EFFECTIVE METHODS OF REGENERATING WHITEBARK PINE (*PINUS ALBICAULIS*) THROUGH DIRECT SEEDING

by

Clay Robert DeMastus

A thesis submitted in partial fulfillment
of the requirements for the degree

of

Master of Science

in

Biological Sciences

MONTANA STATE UNIVERSITY
Bozeman, Montana

April 2013

© COPYRIGHT

by

Clay Robert DeMastus

2013

All Rights Reserved

APPROVAL

of a thesis submitted by

Clay Robert DeMastus

This thesis has been read by each member of the thesis committee and has been found to be satisfactory regarding content, English usage, format, citation, bibliographic style, and consistency, and is ready for submission to The Graduate School.

Dr. David Roberts

Approved for the Department of Ecology

Dr. David Roberts

Approved for The Graduate School

Dr. Ronald W. Larsen

STATEMENT OF PERMISSION TO USE

In presenting this thesis in partial fulfillment of the requirements for a master's degree at Montana State University, I agree that the Library shall make it available to borrowers under rules of the Library.

If I have indicated my intention to copyright this thesis by including a copyright notice page, copying is allowable only for scholarly purposes, consistent with "fair use" as prescribed in the U.S. Copyright Law. Requests for permission for extended quotation from or reproduction of this thesis in whole or in parts may be granted only by the copyright holder.

Clay Robert DeMastus

April 2013

ACKNOWLEDGEMENTS

I would like to thank the Whitebark Pine Restoration Program in cooperation with the United States Forest Service for their financial support of this project. I thank Dr. John Schwandt, Project Advisor and committee member, for his advice, support, and encouragement throughout this process and for his excitement and passion that he displayed and continues to display towards this continuing project. I am thankful for my major professor, Dr. Dave Roberts, for his guidance and support in my time spent at Montana State University as well my final committee member, Dr. Laura Burkle, for her advice and support.

I also thank the many others who played roles in the initial planning stages, site identification, site construction, and data collection. This project was truly a group effort and would not have been possible otherwise.

I thank my grandparents, Leigh and Janice, and James and Barbara, for their support and encouragement.

TABLE OF CONTENTS

1. INTRODUCTION 1

2. METHODS 8

Study Area 8
Study Design 8
Direct Seeding 8
Nursery Seedling and Seed Caches 10
Treatment Descriptions 11
Installation and Measurements 12
Data Analysis 13

3. RESULTS AND DISCUSSION 16

Germination 17
Survival 30
Combined Germination and Survival 34
Caging 38
Caging Effects on Germination 39
Caging Effects on Survival 42
Summary 46
Directly Sown Seed Versus Outplanted Nursery Grown Seedlings 47
Seeds Cached Versus Non-Cached 48
Temperature 50

4. CONCLUSIONS 56

Management Implications 58
Treatment Type 58
Caging 59
Seed Caching 60
Future Research 60

REFERENCES CITED 62

APPENDICES 66

APPENDIX A – Additional Study Map Information 67
APPENDIX B – Germination Figures, Tables, and Calculations 69
APPENDIX C – Survival Tables and Calculations 76

TABLE OF CONTENTS – CONTINUED

APPENDIX D – Combined Germination and Survival Tables and Calculations 84
APPENDIX E – Temperature Final Model Summary and Calculations 92
APPENDIX F – R code 95
APPENDIX G – Original Data 109

LIST OF TABLES

Table Page

1. Installation and data collection date....12
2. Degrees of freedom for the saturated model of germination....17
3. Excerpt of summary of model 1 (germination) showing large standard error of the scarification treatment at block 3 at the Ulm Peak site....20
4. Results of the drop in deviance Chi-squared test of model 4 (germination) compared to model 3 (germination)....23
5. Results of the drop in deviance Chi-squared test of model 5 (germination) compared to model 4 (germination)....24
6. Results of the drop in deviance Chi-squared test of model 6 (germination) compared to model 5 (germination)....25
7. Results of the drop in deviance Chi-squared test of model 7 (germination) compared to model 6 (germination)....25
8. Results of the drop in deviance Chi-squared test of model 8 (germination) compared to model 7 (germination)....26
9. Results of the drop in deviance Chi-squared test of model 9 (germination) compared to model 8 (germination)....26
10. Excerpt of the summary of the final model of germination....27
11. Estimated germination percent and 95% confidence intervals at each site by treatment....29
12. Excerpt of the summary of the final model of survival....32
13. Estimated survival percent and 95% confidence intervals at each site by treatment....33
14. Excerpt of the summary of the final model of germinated and survived....36

LIST OF TABLES - CONTINUED

Table Page

15. Estimated combined germination and survivalpercent and 95% confidence intervals at each site by treatment 37

16. Caged versus non-caged estimated germination rates comparison by treatment and site 42

17. Results of the drop in deviance Chi-squared test of model 4 (survival) compared to model 3 (survival)....43

18. Results of the drop in deviance Chi-squared test of model 5 (survival) compared to model 4 (survival)....44

19. Results of the drop in deviance Chi-squared test of model 6 (survival) compared to model 5 (survival)....44

20. Results of the drop in deviance Chi-squared test of model 7 (survival) compared to model 6 (survival)....45

21. Caged versus non-caged estimated survival rates comparison by treatment and site 45

22. Extreme high and low recorded temperatures at each site....51

23. Excerpt from the summary of model 1 (temperature) 55

A.1. Complete summary of final model of germination....70

A.2. Results of the drop in deviance Chi-squared test of model 4 (survival) compared to model 3 (survival)....77

A.3. Results of the drop in deviance Chi-squared test of model 5 (survival) compared to model 4 (survival)....77

A.4. Results of the drop in deviance Chi-squared test of model 6 (survival) compared to model 5 (survival)....78

A.5. Results of the drop in deviance Chi-squared test of model 7 (survival) compared to model 6 (survival)....78

LIST OF TABLES – CONTINUED

Table Page

A.6. Results of the drop in deviance Chi-squared test of model 8 (survival) compared to model 7 (survival)....78

A.7. Results of the drop in deviance Chi-squared test of model 9 (survival) compared to model 8 (survival)....78

A.8. Complete summary of final model of survival....79

A.9. Results of the drop in deviance Chi-squared test of model 4 (combined germination and survival) compared to model 3 (combined germination and survival)....85

A.10. Results of the drop in deviance Chi-squared test of model 5 (combined germination and survival) compared to model 4 (combined germination and survival)....85

A.11. Results of the drop in deviance Chi-squared test of model 6 (combined germination and survival) compared to model 5 (combined germination and survival)....86

A.12. Results of the drop in deviance Chi-squared test of model 7 (combined germination and survival) compared to model 6 (combined germination and survival)....86

A.13. Results of the drop in deviance Chi-squared test of model 8 (combined germination and survival) compared to model 7 (combined germination and survival)....86

A.14. Results of the drop in deviance Chi-squared test of model 9 (combined germination and survival) compared to model 8 (combined germination and survival)....86

A.15. Complete summary of final model of combined germination and survival....87

A.16. Complete summary of final model of temperature....93

A.17. Original data used in study's analyses....110

LIST OF FIGURES

Figure Page

1. Study area map....9
2. Schematic layout of a site....10
3. Pioneer Mountain caged and non-caged germination counts by treatment and block....18
4. Exploratory plot of model 1 (germination) showing residual versus fitted values....19
5. The means of the scarifcation treatment by block at the Ulm Peak site before and after blocks 1 and 3 were combined....21
6. Plot of residuals versus predicted values of model 2 (germination)....22
7. Germination estimates and 80% confidence intervals....30
8. Survival estimates and 80% confidence intervals....33
9. Combined germination and survival estimates and 80% confidence intervals....38
10. Nursery seedling survival versus cache seeds combined germination and survival....48
11. Cache germination versus non-cache germination....49
12. Cache survival versus non-cache survival....50
13. Extreme maximum and minimum temperatures by site....52
14. Observed difference of surface temperature minus sub-surface temperature at the Pioneer Mountain site....52
15. Plot of Pioneer Mountain surface and sub-surface temperatures....53
16. Charts showing the variations of daily minimum and daily maximum temperatures for each site throughout varying data collection dates....54

LIST OF FIGURES (CONTINUED)

Figure Page

A.1. Germination counts by site, treatment, and block.....70

ABSTRACT

Rapidly diminishing populations of whitebark pine (*Pinus albicaulis*) have sparked efforts to restore this ecologically important species and the communities they support. Current restoration efforts have proven to be costly, time consuming, and labor intensive. Implementation of direct seeding as a restoration method, if found effective, would likely decrease the amount of time, money, and labor expended on these efforts.

This study looks at the effectiveness of direct seeding through a series of tests performed at six sites throughout the northern Rocky Mountains. The tests consist of a complete randomized block design with five blocks of eight treatments at each site. Treatments include seed treatments of warm stratification, scarification, and both warm stratification and scarification combined. Caging treatments are also implemented into each block. Testing the effectiveness of seed caching and long term survival rates of outplanted nursery grown seedling versus directly sown seeds was also carried out by planting caches next to nursery seedlings throughout each site.

A logistic regression analysis consistently estimated seeds undergoing the warm stratification treatment to have the highest combined germination and survivalrates. Caging was found to be effective at increasing germination under certain circumstances as well as increasing survival possibly due to the shading properties the cages provided.

Seed caching did not appear to have an effect on survival of directly sown seeds. Caching also did not appear to have an effect on germination with the exception of one site.

Initial results of long term survival rates of outplanted nursery grown seedlings compared to germination and survival rates of directly sown seeds showed higher rates for the nursery grown seedlings. Additional monitoring will be needed to determine long-term survival differences.

From the results of this study, it is felt that the implementation of direct seeding of warm stratified seed as a restoration method will be successful and cost effective. Caging, although found effective in this study, is felt to posses more disadvantages than advantages. Its advantages in the aspect of survival could be replaced with other microsite planting techniques. Seed caching, at this time, is not recommended as more research is needed.

INTRODUCTION

Whitebark pine (*Pinus albicaulis*) is a keystone species for upper subalpine ecosystems in the northern Rocky Mountains. As a keystone species, its presence determines the ability of a large number of other species to persist within a community (Primack 1998). Unlike many keystone species that only play a single important role, whitebark pine preserves biodiversity in numerous ways (Tomback et al. 1993). The seeds are an important source of food for many species (Hutchins and Lanner 1982) including the grizzly bear (*Ursus arctos horriblis*) (Mattson et al. 1991) which is also considered a keystone species (Helfield and Naiman 2006). Whitebark pine communities are diverse—varying greatly over a large geographic range, including wet and dry meadows, wetlands, and alpine tundra—that host a wide variety of plants, animals, and fungi. Runoff is regulated and soil erosion is reduced by the ability of whitebark pine to grow where other conifers cannot (Tomback et al. 2001). Whitebark pine is often the first species to establish itself after a disturbance in the upper subalpine forest which helps facilitate succession by furthering community development (Tomback et al. 1993).

Unfortunately, populations of this ecologically important species are declining at an alarming rate. Spread of the highly invasive exotic disease of white pine blister rust (*Cronartium ribicola*) has taken its toll on whitebark pine populations. This coupled with recent mountain pine beetle (*Dendroctonus ponderosae)* outbreaks and the successional advances of subalpine fir (*Abies lasiocarpa*) and Englemann spruce (*Picea englemannii*) into habitats historically dominated by whitebark pine have put the future of this keystone species in question.

White pine blister rust was first introduced to North America from shipments of eastern white pine (*Pinus strobus)* from nurseries in Germany and France. Infections in North America were first found in 1906 (Spaulding 1911). The disease has a complicated lifecycle in which there are five kinds of spores on two host species. Two of these spores occur on the white pines and the other three occur on its alternate host, the genus *Ribes* (McDonald and Hoff 2001). Recent studies show that some species of *Pedicularis* and *Castilleja* can serve as alternate hosts but their importance has yet to be determined (McDonald et al. 2006). Infection in pines occurs through the needles and grows into branches, killing cells as it spreads. Cankers form from the accumulation of these dead cells. The disease eventually spreads from the branches, and once infecting the bole, usually causes mortality by girdling the tree. Smaller trees are more susceptible to the disease as infections have shorter distances to travel before reaching the bole.

Unlike white pine blister rust, the mountain pine beetle is native to the environment of the whitebark pine. The beetle plays an important ecological role by attacking mature pine which allows younger, healthier pines to take their place. Historically, pine beetle populations would build in lower elevation lodgepole pine (*Pinus contorta*) forests and move into the higher elevation forests of whitebark pine (Arno and Hoff 1989). The harsh environments were too extreme and the pine beetle populations would die off (Arno and Hoff 1989). However, with rising temperatures, this die-off is no longer as dramatic, if it occurs at all. This change has thrown the system out of balance and has caused tree mortality in these areas to climb to levels never seen before (Kurz et al. 2008).

In many whitebark pine communities, fire plays an important role. Historically these communities burned every 50 to 400 years (Brown 1995). For about the last 80 years, the practice of fire suppression has greatly reduced the frequency of fires in these areas. As a result of this practice, the fire intolerant species subalpine fir and Englemann spruce have started to dominate communities that were once dominated by whitebark pine.

Currently, there are various types of restoration efforts taking place. A level of resistance to white pine blister rusts seems to be present in nearly all whitebark pine populations. Very rarely is 100% mortality seen in a stand of whitebark pine that has been infected with the disease. Collecting cones from trees that phenotypically appear to have a resistance to the disease, establishing their offspring and then exposing them to the rust determines if there is a resistance within a population. Scion collected from mature trees that have been tested and shown to have a resistance to white pine blister rust are grafted to a rootstock and planted in a closely monitored and protected seed orchards constructed in designated whitebark pine habitat (Mahalovich and Dickerson 2004). The mature scion allows the tree the ability to start producing cones within a couple of years after being grafted. The cones can then be harvested and processed for their seed. These seeds are grown up in a nursery and the seedlings planted back out into the forest armored with a resistance to white pine blister rust. The seed orchard allows a large number blister rust resistant trees to be more easily cared for and managed due to being confined within a couple of acres rather than spread over millions of acres of entire forests.

The importance of whitebark pine as a keystone species has become a common topic in the literature over the last 20 years (Ellison et al. 2005; Resler and Tomback 2008; Smith et al. 2008; Soule et al. 2005; Tomback and Achuff 2010; Tomback et al. 2001). Considering the current population declines along with this ecological importance provides convincing justification for intervention through management (Samman et al. 2003; Smith et al. 2008; Tomback and Achuff 2010; Tomback et al. 2001). Whitebark pine restoration efforts that are currently taking place have proven to be expensive, time consuming, and somewhat complex (Burr et al. 2001; Farmer 1997). If proven successful in the field, direct seeding could augment the current efforts by providing a less costly and less labor intensive restoration method.

As previously mentioned, it takes two years to establish whitebark pine seedlings in a nursery setting to the point where they can be pulled from their plugs and taken to the site of restoration. With direct seeding, the seeds are collected, treatments (if any) are applied, and the seeds can be planted back in the field, the following year. Money is saved on greenhouse use, labor and energy used to grow up the seedlings, freight costs to ship them to a site, and personnel hours used carry out the work on the ground. Planting 50,000 seeds in an area is much less labor intensive than planting 50,000 seedlings. This is particularly true if the area of planting is remote, as is typical for whitebark pine habitat. Similar comparisons can be made when dealing with the expensive implementation of seed orchards. Money is needed for finding genetically superior trees, the grafting of scion onto rootstock, surveying and construction of the orchard, and personnel costs of maintaining the orchard.

Despite their economic drawbacks, these restoration efforts do have their place. In fact, seed orchards could likely be a very effective source of seeds for direct seeding in the near future. If direct seeding is effective in the field, the money and time spent on restoration efforts can be greatly reduced. Recent advancements in seed treatments have greatly increased germination in the nursery setting (Burr et al. 2001). However, there is limited information on the success of these same seed treatments under natural field conditions.

Planting under natural settings introduces new factors that could affect the success of sown seeds. Seed predation from rodents, birds, and other animals is one of these factors. Several studies have tested the effects on germination of various methods aimed to prevent seed predation. Smith et al. (2011) found that protection of sown limber pine (*Pinus flexilus*) seeds by caging had little effect on germination. Conversely, McCaughey and Weaver (1990) observed high levels of rodent predation in seeds planted in litter without rodent exclosures. Schwandt et al. (2011) tested the effectiveness of treating seeds with animal deterrents Thiram®, Ropel®, and hot pepper. While these treatments may have been effective in fending off rodents, they showed strong negative effects on seed germination. Cages enclosing the sown seeds showed moderate success in prevention of predation by rodents.

Exposure to uncontrolled environmental factors can also affect the success of sown seeds. Studies have tested methods of minimizing the amount of extreme environmental fluctuations a seed endures by strategic planting. Izlar (2007) found that planting whitebark pine seedlings in microsites, or small areas of the landscape that

experience more favorable environmental conditions due to their location, significantly increased first year survival. McCaughey and Weaver (1990) similarly found that planting in mineral soil and shade cover was shown to significantly increase germination.

Treatments of warm stratification have been shown to be successful in increasing germination while treatments of scarification and warm stratification and scarification combined have shown less success (Schwandt et al. 2011). However, more investigation is necessary to confirm these findings.

This particular study was designed to help make these confirmations and additionally to determine the effectiveness of direct seeding in the field and to develop guidelines for the implementation of restoration practices of whitebark pine throughout its range. The six main objectives are as follows:

1. Investigate what treatments (if any) are most effective at increasing germination of directly sown seeds.
2. Investigate what treatments (if any) are most effective at increasing survival of germinants from directly sown seeds.
3. Investigate if caging affects germination of directly sown seeds and survival of germinants from directly sown seeds.
4. Compare long term survival of directly sown seeds versus long term survival of outplanted nursery grown seedlings.
5. Compare germination and survival rate of directly sown seeds in seed caches versus non-cached or individually directly sown seeds.

6. Investigate what effect (if any) surface and subsurface soil temperatures have on the survival of germinants from directly sown seed.

METHODS

Study Area

Six sites throughout the northern Rocky Mountains in the states of Montana and Idaho were chosen to carry out the field experiments described in this chapter. These sites were: Fairy Lake on the Gallatin National Forest near Bozeman, MT, Pioneer Mountain within The Yellowstone Club Ski Area near Big Sky, MT, Toboggan Ridge on the Clearwater National Forest in Idaho, Thompson Peak on the Lolo National Forest near Plains, MT, Ulm Peak on the Idaho-Montana state line west of Thompson Falls, MT, and Gold Pass on Idaho-Montana state line west of St. Regis, MT (Figure 1). These sites were chosen for their whitebark pine habitat and accessibility for ease in set-up and data collection.

Study Design

Direct Seeding

In this portion of the experiment, 800 seeds collected from local seed sources were used at each site. The seeds were planted in a complete randomized block design with five replicates of eight treatments with 20 seeds per treatment. Each of the 20 seeds in each treatment was planted 3.25″ apart from one another at a depth of 1.5″ in bare mineral soil. The treatments included; 1) warm stratification (strat), 2) scarification (scar), 3) both the stratification and scarification together (scar + strat), and 4) a control.

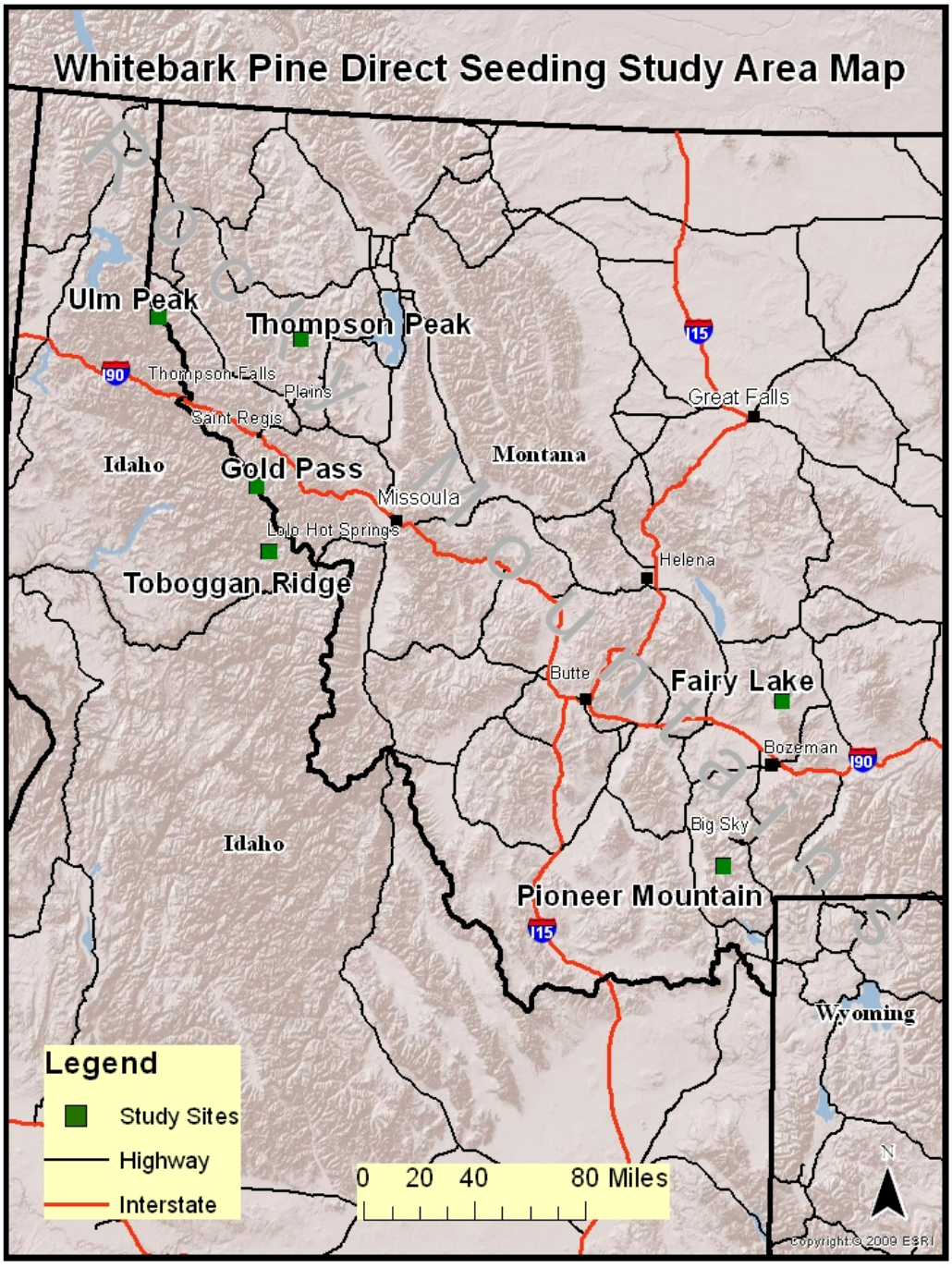


Figure 1: Study area map

These four treatments were installed with and without a 1/2 ″ mesh wire cage in each replicate to make up the eight blocks and treatments. Figure 2 is an example that shows the layout of one site broken down by blocks and treatments. This consisted of eight rows of eight treatments spaced approximately three feet apart for ease in data collection with 20 seeds in each row. Two HOBO® data loggers were also installed at each site to record ground surface temperatures as well as soil temperatures 1.5″ below the surface (depth of sown seed). These were placed in selected caged treatments in various locations throughout the site.

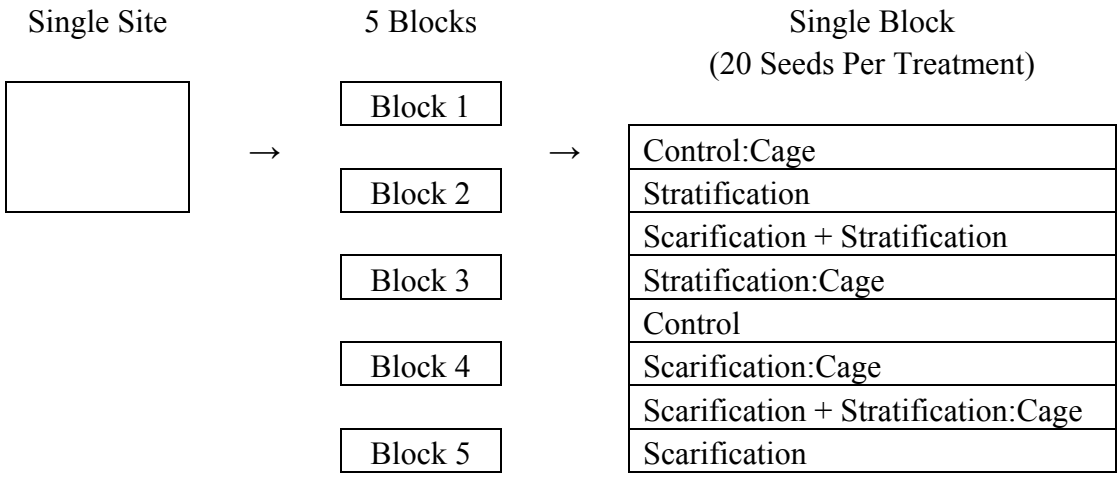


Figure 2: Schematic layout of a site.

Nursery Seedlings and Seed Caches

Two year old nursery seedlings grown from local seed sources were planted at each site spread throughout the areas encompassing the five blocks. Thirty-four nursery seedlings were planted at the Gold Pass and Thompson Peak sites while 100 were planted at the remaining sites.

At the Fairy Lake, Thompson Peak, Ulm Peak, and Gold Pass sites, caches of three untreated seeds were planted directly next to 32 of the nursery grown seedlings. An untreated seed cache of four was planted next to one of the nursery grown seedlings for a total of 100 seeds in 33 caches. At the Pioneer Mountain and Toboggan Ridge sites, untreated seed caches of three were planted next to 50 of the nursery grown seedlings and warm stratified seed caches of three were planted next to the remaining 50 nursery grown seedlings for a total of 300 seeds in 100 caches.

Treatment Descriptions

After extraction from cold storage, seeds undergoing the warm stratification treatment were placed under running cold tap water for 48 hours. Following this, the seeds were placed in an incubator at room temperature (20C to 30C) for 30 days. At weekly intervals during this time, the seed were given a one hour cold water rinse to reduce mold.

Seeds undergoing the scarification treatment were placed in a container lined with sandpaper and spun mechanically for three hours.

Seeds undergoing both treatments were first placed under the warm stratification treatment followed by the scarification treatment.

Once treatments concluded, the seeds were separated by treatment and by block and planted at each particular site within 24 hours.

Installation and Measurements

Due to logistical and manpower constraints, not all six sites were installed at the same time. Four of the six sites (Gold Pass, Ulm Peak, Thompson Peak, and Fairy Lake) were installed in the fall of 2009. The remaining two sites (Toboggan Ridge and Pioneer Mountain) were installed in the fall of 2010. After the installation of each site, data collection started the following summer, soon after snow melt. The goal was to collect data at least twice each year for three years; as early as possible in the summer to document early germination and late in the fall to document additional germination and any summer mortality. Toboggan Ridge was the only site where this did not occur; due to road washouts in the spring of 2011, only fall measurements were taken. See Table 1 for more detail on the exact dates of installation and data collection.

Site	Installed	1st Year Measurement(s)	2nd Year Meas.	3rd Year Meas.
Gold Pass	Fall 2009	7/1/10, 7/13/10, 7/26/10, 9/23/10	8/4/11	7/30/12
Thompson Peak	Fall 2009	7/14/10, 10/6/10	8/3/11	8/1/12
Ulm Peak	Fall 2009	7/20/10, 9/23/10	8/22/11	8/2/12
Fairy Lake	Fall 2009	7/27/10, 9/14/10	8/1/11	8/8/12
Toboggan Ridge	Fall 2010	9/20/11	7/31/12, 9/21/12	NA
Pioneer Mountain	Fall 2010	8/2/11, 9/15/11	8/14/12, 9/20/12	NA

Table 1: Installation and data collection dates.

Data Analysis

To investigate what treatments (if any) are most effective at increasing germination of directly sown seeds, a logistic regression model was used. The response variable of individual seed germination is assumed to have a binomial distribution (the seed either germinates or it does not germinate). A saturated model was first created and analyzed with appropriate tests and plots. Due to evidence of extra-binomial variation, the model was fit using quasi-likelihood methods in order to more accurately estimate the standard errors. Starting with the saturated model, a step by step exclusion of terms within this model followed by drop in deviance Chi-squared tests was used to test for evidence against the more reduced model in order to help guide the decision on whether or not to include a particular term in the final model. A final model was then used to interpret the treatment effects using estimated probabilities from the logistic regression.

The second objective of this study was to investigate what treatments (if any) are most effective at increasing survival of germinants from directly sown seeds. This was carried out in the same manner as the first objective. The response variable was now individual seed survival which is also assumed to have a binomial distribution (the germinant either lives or dies). Once again, a step by step exclusion of terms from a saturated model followed by drop in deviance Chi-squared tests was used to guide in the decision for a final model from which estimated probabilities were calculated from the logistic regression. A model was also created to estimate rates of seeds that both combined germination and survival.

The third objective of this study was to investigate if caging affects germination of directly sown seeds and survival of germinants from directly sown seeds. The initial saturated models used in the previous analyses included caging interaction terms. These caging interactions were removed and tested for evidence without them in the model at some point during the step by step exclusion of terms followed by drop in deviance Chi-squared tests. The results of these various tests were used to interpret the effect caging may have had on the germination of the directly sown seed and the effect they may have had on survival of germinants from directly sown seeds.

The fourth objective of the study was to compare long term survival of directly sown seeds versus long term survival of outplanted nursery grown seedlings. This was done by calculating the current survival rates of the outplanted nursery-grown seedlings for each site and the current rates of seeds that combined germination and survivalthat were planted in the seed caches directly next to the nursery grown seedlings at each site and performing a paired t-test to show the mean difference between the two. A bar chart was constructed presenting these rates for each respective site.

The fifth objective of the study was to compare germination and survival data of directly sown seeds in seed caches versus non-cached or individually directly sown seeds. This was carried out by calculating germination and survival rates of seeds in caches as well as germination and survival rates of seeds not in caches with corresponding treatments at the same site. Paired t-tests showing the mean difference between the two groups for both germination and survival were carried out. Bar charts of both germination and survival were created contrasting the results of each group separated by site.

The sixth and final objective of the study was to investigate what effect (if any) surface and subsurface soil temperatures have on the survival of germinants from directly sown seed. This was done by constructing a chart in which sub-surface temperature data were plotted over surface temperature data collected in the same area. Another chart was constructed showing the difference between surface and sub-surface temperature readings taken at the same time every hour and six minutes over the course of two calendar years. Charts tracking the daily maximum and minimum temperatures at each site were also constructed.

Logistic regression was used to investigate if temperature has an effect on survival of directly sown seeds. With the idea that the continuing occurrence of extreme temperatures is likely a possible cause of mortality in newly germinated seedlings, a count of how many times the temperature reached above 32.2 degrees Celsius (90F) and -1.1 degrees C (30F) was tallied for each site. These values were then standardized by the number of measurement days at each site. A logistic regression model was then created using these standardized values and seed treatment type as variable terms and a response variable of number of germinants that survived from directly sown seeds. The coefficient for the temperature term was then used to estimate what effect (if any) temperature had on survival.

RESULTS AND DISCUSSION

This study's initial intent was to analyze the results of direct seeding tests performed in six whitebark pine habitats throughout the northern Rocky Mountains. One of these six sites (Fairy Lake) had very low germination rates and even poorer survival rates. This particular site is unique because it has both limber pine (*Pinus flexilus*) and whitebark pine growing within the same general area. In Montana, this is a rarity as there are only few sites that posses this same characteristic (Pfister et al. 1977). Limber pine is phenotypically similar to whitebark pine. The best visual discerning feature that separates the two species is the difference in their unique cones. Whitebark and limber pine use mast seeding to improve their fitness. Some years there are bountiful amounts of cones and other years it is difficult to find even one cone on a particular tree. The year the Fairy Lake site was installed (2009) was not a mast year. Because of this, the difference between the two species at this site was very difficult to discern. The site was thought to be installed in whitebark pine habitat because there where known whitebark pine plus trees that where used in past cone and scion collections by local Forest Service crews close by and were marked with identification tags. However, throughout the course of the study, it became apparent in mast years (2010 and 2011) that the site had been installed in a zone transitioning from limber habitat to whitebark habitat. It is thought that this along with the fact that it was a dry, rocky and more harsh site could have been the reason such poor germination and survival occurred here. Because of this, the decision was made to not include the data from the Fairy Lake site in the final analysis.

Germination

Table 2 shows the degrees of freedom for the saturated model including all possible terms and interaction terms. Inclusion of all these terms within a model creates a problem as it leaves no degrees of freedom to calculate the residual deviance. In other words, there are not enough independent observations to create enough information to estimate the variability. To gain residual degrees of freedom, some of these terms need to be removed from the model. This is all under the assumption that it is appropriate to consider some of these terms as "background noise".

Source of Variation			df
Site	(5-1)	=	4
Block(Site)	(5-1)(5)	=	20
Seed	(4-1)	=	3
Cage	(2-1)	=	1
Cage*Seed	(1)(3)	=	3
Cage*Site	(1)(4)	=	4
Seed*Site	(3)(4)	=	12
Seed*Block(Site)	(3)(20)	=	60
Cage*Block(Site)	(1)(20)	=	20
Cage*Seed*Site	(1)(3)(4)	=	12
Cage*Seed*Block(Site)	(1)(3)(20)	=	60
Residuals	(199-199)	=	0
Total			199

Table 2: Degrees of freedom for the saturated model of germination

The study was designed without replication within the blocks assuming that the cage*seed*block(site) interaction may be ignored. Figure 3 helps illustrate this assumption.

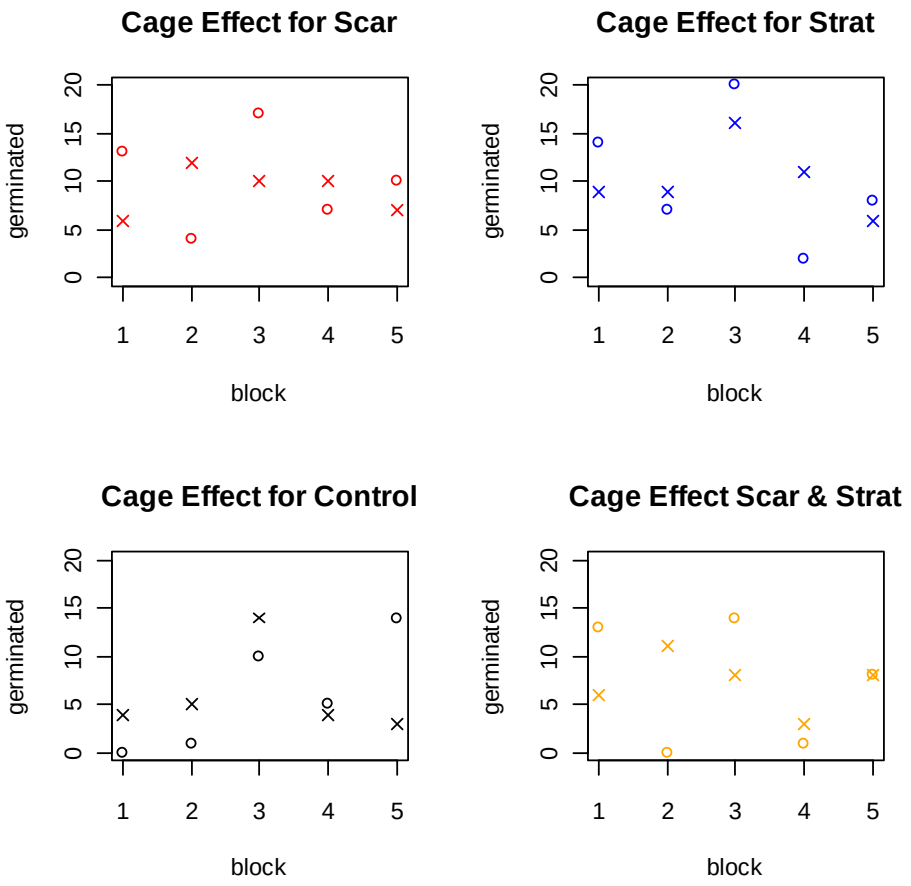


Figure 3: Pioneer Mountain caged and non-caged germination counts by treatment and block

This plot shows the caged and non-caged germination counts for each treatment paired for each block at the Pioneer Mountain site (see Figure A.1 in appendix B showing similar plots for all sites with comparable trends). The difference for the pairs in each block is fairly consistent which helps in the justification of ignoring the cage*seed*block(site) interaction. Although some inconsistency certainly exists and is apparent in these plots, one has to consider the amount of background variability that is going to be naturally inherent in a design such as this. Considering the magnitude of

these inconsistencies with this is mind, it is felt that it is reasonable to assume that these deviations are likely from background noise and not from systematic variation due to an interaction, thus justifying the omission of the cage*seed*block(site) interaction in the model.

Model 1 (Germination): Omiting the cage*seed*block(site) term

model.1 <- glm(cbind(germ, nogerm) ~ site/block + cage * seed + cage * site + seed * site + seed *(site/block) + cage * (site/block) + cage * seed * site, family = binomial, data = dat)

Omission of this term freed up 60 degrees of freedom but after further examining model 1, a problem with the accuracy of the standard errors of the estimates from the model surfaced. An exploratory plot of the residuals versus the fitted values shows two residual values separated by a substantial distance from the bulk of the others (Figure 4). This is the first indication of a potential problem. A summary on model 1 shows the standard error of one of the seed*block(site) terms at the Ulm Peak site to be implausibly large (See Table 3).

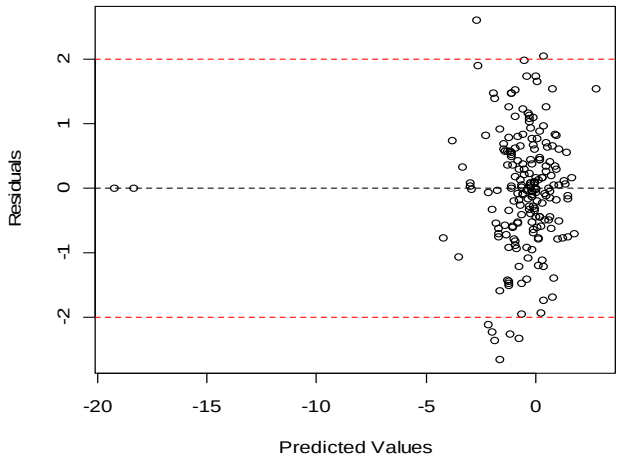


Figure 4: Exploratory plot of model 1 (germination) showing residual versus fitted values.

	Estimate	Std. Error	z value	Pr(>|z|)
(Intercept)	-0.7514	0.4030	-1.864	0.062288
siteulm:block3:seedscar	-17.52	1105	-0.016	0.987347

Table 3: Excerpt of summary of model 1 (germination) showing large standard error of the scarification treatment at block 3 at the Ulm Peak site.

To further investigate this, another plot of the Ulm Peak data was constructed (Figure 5). As one can see from this plot, none of the scarified treated seeds in block 3 germinated, thus producing zeros in the data. The red line signifies the mean of only the scarified treated seeds that germinated in block 3. These zeros in the data are causing the separation of the residual plots in Figure 4 as well as the extremely large standard error of one of the estimates found in the summary of model 1.

Logistic regression estimates probabilities. In the case of this study, the probabilities that a seed germinates, the probability that germinated seed survives, as well as the probability that a seed germinates and survives ($\Pr(Yi = 1|Xi)$) is what is of interest. The link function for logistic regression is $\log(Yi / 1 - Yi)$. Because of this it becomes a problem when taking the log of extremely small Yi's, or in other words, taking the log of zero. The logistic model assumes $0 < Yi < 1$. When data are close to these boundaries, the estimates produced will have large standard errors similar to the one found in Table 3.

To deal with this issue it was decided to combine blocks 1 and 3 at Ulm Peak as if they were one. This decision is justified by the fact that these blocks were under similar environmental conditions. This restructuring was signified by the label block.new(corresponding number) instead of block(corresponding number). The black line in figure 5 shows the mean of the blocks at Ulm Peak before and after 1 and 3 were

combined with each other. This increase in the mean will allow for more meaningful and more accurate estimates in the logistic model.

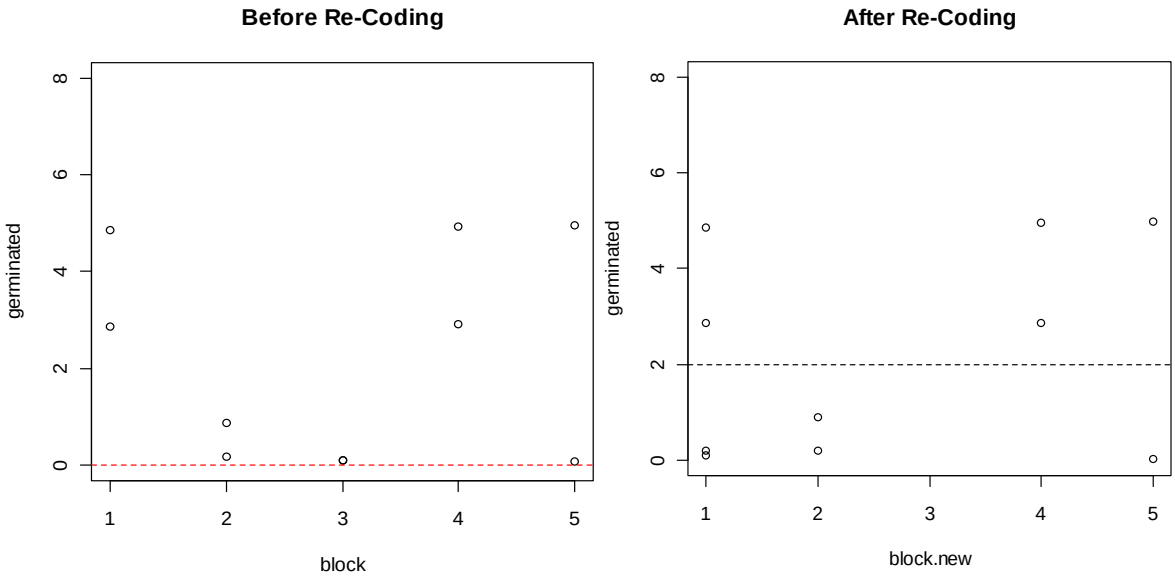


Figure 5: The means of the scarification treatment by block at the Ulm Peak site before and after blocks 1 and 3 were combined.

Model 2 (Germination): Combining blocks 1 and 3 at Ulm Peak

model.2 <- glm(cbind(germ, nogerm) ~ site/block.new + cage * seed + cage * site + seed * site + seed* (site/block.new) + cage * (site/block.new) + cage * seed * site, family = binomial, data = dat)

Combining the blocks at the Ulm Peak site gained 1 more degree of freedom to the model for a total of 61. After running a summary of model 2, it was found to have a residual deviance of 175.70. A goodness-of-fit test using the residual deviance on 61 degrees of freedom yields an extremely small p-value that is essentially zero. This provides strong evidence that the model is inadequate. This inadequacy can be attributed to one or a combination of three things: 1) outliers, 2) extra-binomial variation or 3) the exclusion of relevant explanatory variables. The exclusion of relevant explanatory

variables is not likely because the model contains all the main effects and a large number of interaction terms. In this case, extra-binomial variation is expected. In the binomial model it is assumed that each experimental unit has the same probability and that outcomes are independent. Unrecorded environmental influences can change these probabilities. There is a multitude of these factors that vary from site to site and block to block in this experiment; soil type, soil temperature, weather, habitat type and elevation are just a few speculative examples. Variations such as these are what is likely causing this violation.

Figure 6 shows that there is a large number of residuals outside the expected range (the red lines on the plot). The variance is greater than what would be expected from a binomial distribution, confirming what would be expected from extra-binomial variation. To more accurately estimate the standard errors of the coefficients, the model was refit using quasi-likelihood methods. This corrects the extra-binomial variation by inflating the standard errors.

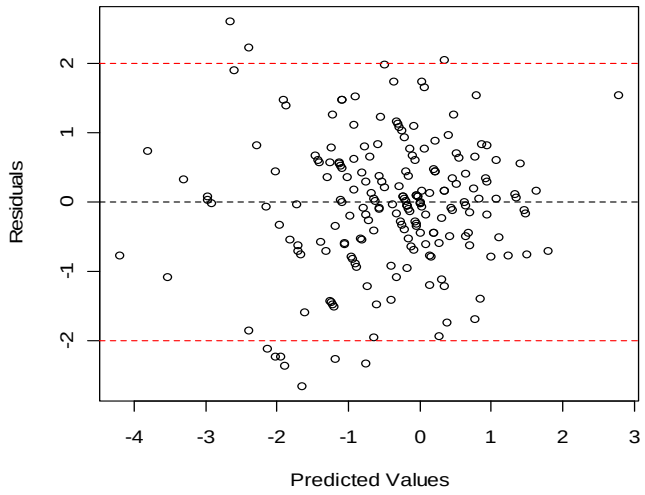


Figure 6: Plot of residuals versus predicted values of model 2 (germination).

Model 3 (Germination): The Quasi-Binomial Model

model.3 <- glm(cbind(germ, nogerm) ~ site/block.new + cage * seed + cage * site + seed * site + seed* (site/block.new) + cage * (site/block.new) + cage * seed * site, family = quasibinomial, data = dat)

A summary of model 3 provides the dispersion parameter of 2.696. The square root of the dispersion parameter (1.642) provides the number by which to multiply the standard errors of the coefficients in the final model of choice.

A step by step omission of terms in the model followed by a drop in deviance Chi-squared test with the previous model still containing the particular term being omitted was carried out to determine if there is any statistical evidence against the reduced model. These tests start with model 4 below in which the cage*seed*site interaction is removed.

Model 4 (Germination): Removing cage*seed*site

model.4 <- glm(cbind(germ, nogerm) ~ site/block.new + cage * seed + cage * site + seed * site + seed* (site/block.new) + cage * (site/block.new), family = quasibinomial, data = dat)

Table 4 shows the results of the drop in deviance Chi-squared test performed using the following R code: anova(model.4, model.3, test= "Chisq"). The p-value from this test (0.8483) provides little evidence against the reduced model without this three way interaction term and therefore, dropping this term appears to be justified statistically.

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	73	194.94			
2	61	175.7	12	19.246	0.8483

Table 4: Results of the drop in deviance Chi-squared test of model 4 (germination) compared to model 3 (germination).

Model 5 (Germination): Removing cage*(site/block.new)

model.5 <- glm(cbind(germ, nogerm) ~ site/block.new + cage * seed + cage * site + seed * site + seed * (site/block.new), family = quasibinomial, data = dat)

Table 5 shows the results of the drop in deviance Chi-squared test performed using the following R code: anova(model.5, model.4, test= "Chisq"). The small p-value (0.000623) from this test provides strong evidence against the reduced model without the interaction term cage*(site/block.new). In other words, the cage*(site/block.new) interaction is likely an important term to keep in the final model. This is suggestive of a cage effect that is dependent upon site as well as block.

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	93	310.35			
2	73	194.94	20	115.41	0.000623

Table 5: Results of the drop in deviance Chi-squared test of model 5 (germination) compared to model 4 (germination).

Model 6 (Germination): Removing cage*site

model.6 <- glm(cbind(germ, nogerm) ~ site/block.new + cage * seed + seed * site + seed*(site/block.new), family = quasibinomial, data = dat)

Table 6 shows the results of the drop in deviance Chi-squared test performed using the following R code: anova(model.6, model.5, test= "Chisq"). The p-value from this test (0.4943) provides little evidence against the reduced model without the cage*site interaction term and therefore, omitting this term from the final model appears to be justified statistically.

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	97	320.69			
2	93	310.35	4	10.339	0.4943

Table 6: Results of the drop in deviance Chi-squared test of model 6 (germination) compared to model 5 (germination).

Model 7 (Germination) : Removing cage*seed

```
model.7 <- glm(cbind(germ, nogerm) ~ site/block.new + seed*site +
seed*(site/block.new), family = quasibinomial, data = dat)
```

Table 7 shows the results of the drop in deviance Chi-squared test performed using the following R code: anova(model.7, model.6, test="Chisq"). The large p-value from this test (0.9008) provides little evidence against the reduced model without the cage*seed interaction and therefore, removing this term appears to be justified statistically.

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	101	323.89			
2	97	320.69	4	3.1951	0.9008

Table 7: Results of the drop in deviance Chi-squared test of model 7 (germination) compared to model 6 (germination).

Model 8 (Germination) - Removing seed*(site/block.new)

```
model.8 <- glm(cbind(germ, nogerm) ~ site/block.new + seed*site,
family = quasibinomial, data = dat)
```

Table 8 shows the results of the drop in deviance Chi-squared test performed using the following R code: anova(model.8, model.7, test="Chisq"). The large p-value from this test (0.8689) provides little evidence against the reduced model without the

seed*(site/block.new) interaction and therefore, removing this term appears to be justified statistically.

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	160	461.72			
2	101	323.89	59	137.83	0.8689

Table 8: Results of the drop in deviance Chi-squared test of model 8 (germination) compared to model 7 (germination).

Model 9 (Germination) : Removing seed*site

```
model.9 <- glm(cbind(germ, nogerm) ~ site/block.new,
family = quasibinomial, data = dat)
```

Table 9 shows the results of the drop in deviance Chi-squared test performed using the following R code: anova(model.9, model.8, test = "Chisq"). The extremely small p-value from this test (1.2110 E-15) provides very strong evidence against the reduced model without the seed*site interaction. It appears that the seed*site interaction should be kept in the final model. This is showing that the treatment effect varies with site.

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	175	746.51			
2	160	461.72	15	284.8	1.2110E-15

Table 9: Results of the drop in deviance Chi-squared test of model 9 (germination) compared to model 8 (germination).

From the results of the tests performed above, the final model chosen to evaluate the germination data is as follows:

Final Model (Germination)

model.final.germ<-glm(cbind(germ,nogerm)~ site/block.new + seed*site + cage*(site/block.new),family=quasibinomial, data = dat)

An excerpt of the summary of the model can be seen in Table 10.

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	-9.592e-01	4.308e-01	-2.226	0.027650
sitepioneer	-4.254e-01	6.200e-01	-0.686	0.493810
sitethompson	3.483e-01	6.050e-01	0.576	0.565746
sitetoboggan	1.311e+00	5.870e-01	2.233	0.027199
siteulm	2.014e-01	6.043e-01	0.333	0.739397
seedscar	-6.190e-01	3.335e-01	-1.856	0.065591
seedscar+strat	4.171e-01	3.203e-01	1.302	0.195087
seedstrat	1.299e+00	3.339e-01	3.891	0.000156
sitepioneer:seedscar	1.526e+00	4.832e-01	3.158	0.001960
sitethompson:seedscar	-2.116e-01	4.922e-01	-0.430	0.667936
sitetoboggan:seedscar	4.911e-01	4.612e-01	1.065	0.288851
siteulm:seedscar	-7.624e-01	5.488e-01	-1.389	0.167047
sitepioneer:seedscar+strat	-1.038e-01	4.768e-01	-0.218	0.827923
sitethompson:seedscar+strat	5.249e-01	4.615e-01	1.137	0.257411
sitetoboggan:seedscar+strat	-7.191e-01	4.534e-01	-1.586	0.115078
siteulm:seedscar+strat	1.809e-01	4.625e-01	0.391	0.696288
sitepioneer:seedstrat	-2.715e-01	4.831e-01	-0.562	0.575062
sitethompson:seedstrat	-5.780e-01	4.700e-01	-1.230	0.220905
sitetoboggan:seedstrat	-1.470e+00	4.618e-01	-3.183	0.001807
siteulm:seedstrat	-3.002e-01	4.724e-01	-0.636	0.526156

Null deviance: 928.68 on 199 degrees of freedom
Residual deviance: 339.13 on 135 degrees of freedom

Table 10: Excerpt of the summary of the final model of germination.

Although the final model is greatly simplified from the saturated model, interpretation is not without complication. The reference level is the estimate of the

control treatment at Gold Pass which is shown as the intercept in the summary. Estimates for other sites and treatments are derived from this reference level. The estimated probability of germination for a particular seed treatment at a particular site can be calculated from the logit link function mentioned earlier (logit = log(Yi / 1 – Yi)). For example, the estimated probability that a control seed germinates at Gold Pass (the reference level) can be calculated from the inverse of the logit link function ($logit^{-1}$ = exp (Yi) / (1 + exp (Yi))) as:

Y1 = Pr(germination) = $logit^{-1}$ (Intercept) = exp (Intercept) / (1 + exp (Intercept))

= exp (-0.9592) / (1 + exp (-0.9592))

= 0.278

The estimated probability that a warm stratified seed germinates at Thompson Peak can be calculated as:

Y2 = Pr(germination) = $logit^{-1}$(Intercept + sitethompson + seedstrat + sitethompson:seedstrat)

= exp (-0.9592 + 0.3483 + 1.299 – 0.5780) / (1 + exp 0.9592 + 0.3483 + 1.299 – 0.5780))

= 0.528

For this particular analysis, treatment is confounded by site. This also makes for some minor inconveniences when trying to make generalized field practice recommendations based on the entirety of the data from this study on which treatment is most effective. Due to this, Table 11 and Figure 7 were constructed with the estimated germination at each site for each treatment along with 80% confidence intervals. This

compilation of estimated percent germination is the most effective way to get an idea which treatment is best suited for increasing germination.

Germination Estimates

Site	Treatment	Estimated Germination (%)	80% CI (%)
Gold Pass	Control	27.8	17.4 to 41.0
Gold Pass	Scar	17.1	10.0 to 27.7
Gold Pass	Scar + Strat	36.8	24.4 to 51.2
Gold Pass	Strat	58.4	43.5 to 71.9
Pioneer Mountain	Control	20.0	11.9 to 31.7
Pioneer Mountain	Scar	38.3	25.5 to 52.9
Pioneer Mountain	Scar + Strat	22.5	13.7 to 34.6
Pioneer Mountain	Strat	41.5	27.9 to 55.9
Thompson Peak	Control	35.2	23.2 to 49.4
Thompson Peak	Scar	19.1	11.3 to 30.6
Thompson Peak	Scar + Strat	58.2	43.8 to 71.4
Thompson Peak	Strat	52.8	38.3 to 66.7
Toboggan Ridge	Control	58.7	45.0 to 71.2
Toboggan Ridge	Scar	55.6	41.9 to 68.5
Toboggan Ridge	Scar + Strat	51.2	37.7 to 64.6
Toboggan Ridge	Strat	54.5	40.9 to 67.5
Ulm Peak	Control	31.9	20.7 to 45.7
Ulm Peak	Scar	10.5	5.8 to 18.5
Ulm Peak	Scar + Strat	46.0	32.4 to 60.2
Ulm Peak	Strat	56.0	41.7 to 69.3

Table 11: Estimated germination percent and 80% confidence intervals at each site by treatment.

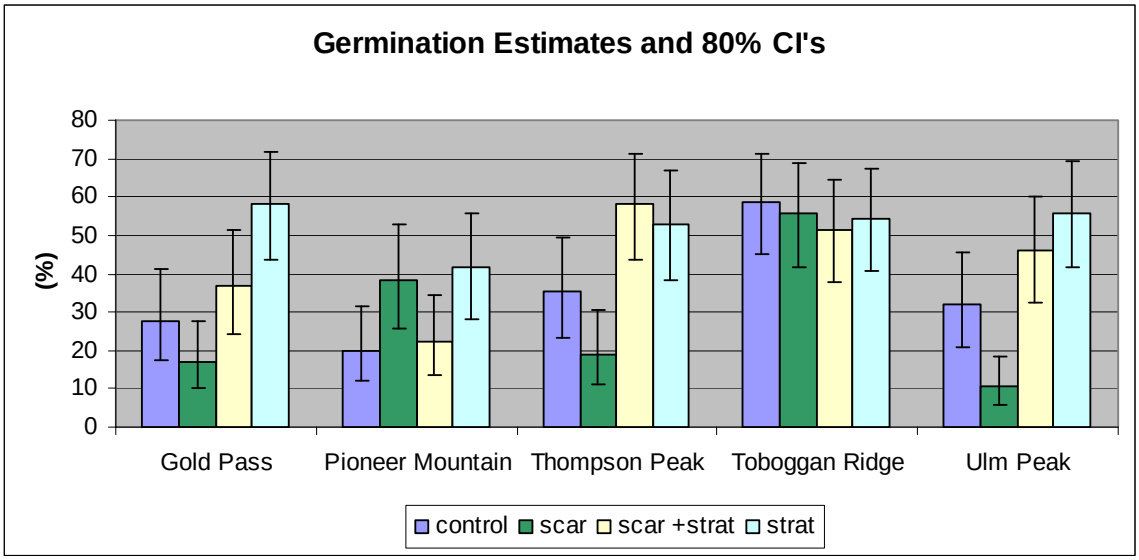


Figure 7: Germination estimates and 80% confidence intervals

Looking at this table and chart, one can see that germination was highest at the Toboggan Ridge site. Germination by treatment at this site was very similar with no significant differences. Warm stratified seed and seed undergoing both warm stratification and scarification were found to have significantly higher germination rates than seed only undergoing the scarification treatment at the Ulm Peak and Thompson Peak sites. Warm stratified seed at the Gold Pass site was found to have significantly higher germination rates than scarified seed. As a whole, warm stratified seed had the highest germination rates as it never dropped lower than 41% at any of the sites. The other three treatments had germination rates below this mark at multiple sites.

Survival

The overall study objective is to determine what seed treatment method is most effective under natural field settings. This knowledge can help guide and shape field

management practices and techniques. Germination is what is initially of interest but the next aspect of interest is survival. From the analysis of the germination data it appears that the warm stratification seed treatment does increase germination in whitebark pine. From here it is necessary to investigate how the ability of these germinants to survive may or may not be affected by the seed treatments.

The saturated model used to do this included all of the same terms and interactions used in the saturated model of the germination analysis. The only difference being the new response variable of individual germinants from the directly sown seeds that survived.

Model 1 (Survival): Saturated Model

```
model.1 <- glm(cbind(survived, totgermsurv) ~ site/block + cage * seed + cage * site +
seed * site + seed *(site/block) + cage * (site/block) + cage * seed * site, family =
binomial, data = dat)
```

As in the germination analysis, data from several blocks had to be combined at some sites in order to eliminate zeros in the data and make more meaningful and accurate estimates. Running a summary of the model with some blocks combined resulted in a residual deviance of 142.0. A goodness-of-fit test using the residual deviance on 82 degrees of freedom yielded a small p-value that is essentially zero, suggesting that the model is inadequate. As seen in the germination analysis, this inadequacy can be attributed to extra-binomial variation. Because of the extra-binomial variation the model was refit using quasi-likelihood methods to allow for the proper inflation of the standard errors.

Once again, terms from the model were removed one at a time and a drop in deviance Chi-squared test with the previous model still containing the particular term being omitted was carried out to determine if there is any statistical evidence against the reduced model. Each model and Chi-squared test can be found in Appendix C in Tables A.2 to A.7.

A final model was determined from these steps. Table 12 is an excerpt of the summary of this final model. Figure 8 and Table 13 show estimated survival of germinants from directly sown seeds by site and treatment as well as 80% confidence intervals for each estimate.

Coefficients:

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	-0.43262	0.57004	-0.759	0.449178
sitepioneer	1.32350	0.82193	1.610	0.109614
sitethompson	1.68553	0.71830	2.347	0.020360
sitetoboggan	2.37399	0.74875	3.171	0.001872
siteulm	-1.48856	0.74456	-1.999	0.047531
seedscar	0.06709	0.45638	0.147	0.883346
seedscar+strat	-0.18488	0.39546	-0.467	0.640879
seedstrat	-0.57778	0.36279	-1.593	0.113519
sitepioneer:seedscar	-0.04934	0.63264	-0.078	0.937942
sitethompson:seedscar	-0.72066	0.69032	-1.044	0.298319
sitetoboggan:seedscar	-0.61050	0.68719	-0.888	0.375858
siteulm:seedscar	-0.30251	0.90995	-0.332	0.740053
sitepioneer:seedscar+strat	-1.02198	0.60630	-1.686	0.094114
sitethompson:seedscar+strat	-0.19623	0.55727	-0.352	0.725271
sitetoboggan:seedscar+strat	0.20137	0.68780	0.293	0.770133
siteulm:seedscar+strat	1.46592	0.61491	2.384	0.018479
sitepioneer:seedstrat	0.07272	0.55811	0.130	0.896522
sitethompson:seedstrat	0.69073	0.54866	1.259	0.210161
sitetoboggan:seedstrat	0.68328	0.67702	1.009	0.314612
siteulm:seedstrat	2.02245	0.58307	3.469	0.000697

Table 12: Excerpt of the summary of the final model of survival.

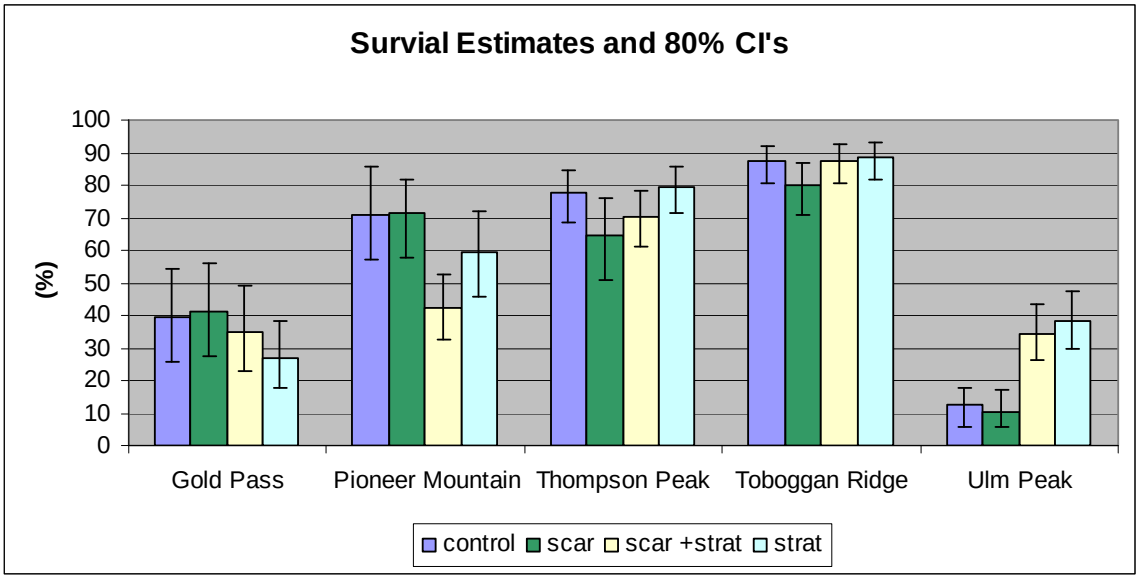


Figure 8: Survival estimates and 80% confidence intervals.

Survival Estimates

Site	Treatment	Survival (%)	80% CI (%)
Gold Pass	Control	39.4	26.0 to 54.5
Gold Pass	Scar	41	27.5 to 56.0
Gold Pass	Scar + Strat	35	23.1 to 49.2
Gold Pass	Strat	26.7	17.5 to 38.5
Pioneer Mountain	Control	70.9	56.4 to 82.1
Pioneer Mountain	Scar	71.3	57.8 to 81.8
Pioneer Mountain	Scar + Strat	42.2	32.5 to 52.5
Pioneer Mountain	Strat	59.5	45.5 to 72.2
Thompson Peak	Control	77.8	68.7 to 84.8
Thompson Peak	Scar	64.6	51.2 to 76.0
Thompson Peak	Scar + Strat	70.5	61.0 to 78.5
Thompson Peak	Strat	79.7	71.5 to 85.9
Toboggan Ridge	Control	87.5	80.6 to 92.1
Toboggan Ridge	Scar	80.2	71.1 to 86.9
Toboggan Ridge	Scar + Strat	87.6	80.3 to 92.5
Toboggan Ridge	Strat	88.6	81.5 to 93.2
Ulm Peak	Control	12.8	8.1 to 19.7
Ulm Peak	Scar	10.4	4.9 to 20.8
Ulm Peak	Scar + Strat	34.5	26.4 to 43.7
Ulm Peak	Strat	38.3	30.0 to 47.4

Table 13: Estimated survival percent and 80% confidence intervals at each site by treatment.

Figure 8 and Table 13 show that estimated survival is highest at the Toboggan Ridge site with no treatment type with lower than 80% survival. The site was followed closely by the Thompson Peak site and the Pioneer Mountain site with estimated survival rates well over 50% for almost all treatment types. The Gold Pass and Ulm Peak sites had considerably lower estimates.

There were no significant differences found in regards to treatment survival with a few exceptions. The control and scarification treatments were found to have significantly higher survival rates than seed undergoing both scarification and warm stratification at the Pioneer Mountain site. Warm stratified seed and seed undergoing both stratification and scarification were found to have significantly higher survival rates than the untreated control and scarified seed at the Ulm Peak site.

Treatments may increase germination but if survival rates of these treatments are poor to the point to where they negate any increased germination advantage that they may have on other methods then this is obviously something that needs to be determined before any field management practice recommendations are made. This is what the third analysis of this study looks at.

Combined Germination and Survival

In review of the first two analyses, seed treatments appear to increase germination in certain cases. Estimated survival rates were similar between seed treatments with a few significant differences. The next step is to look at which treatments have the highest percentage of seeds that have both germinated and survived. It is understood that these

rates can be calculated by simply multiplying germination by survival but because the analysis looks at variation at site, block, and treatment levels it is likely that the dispersion parameter by which the standard errors are inflated will differ. Because of this, performing a direct analysis will provide a complete overview of the results with accurate confidence intervals.

Just as in the other analyses, the saturated model includes the same terms and interactions but has a different response variable. This time the response variable is individual seed germination and survival.

Model 1 (Combined Germination and Survival): Saturated Model

```
model.1 <- glm(cbind(survived, nogermsurv) ~ site/block + cage * seed + cage * site +
seed * site + seed *(site/block) + cage * (site/block) + cage * seed * site, family =
binomial, data = dat)
```

Again, a few of the blocks had to be combined to eliminate zeros. Inadequacies in the model were found due to extra-binomial variation making it necessary to refit it using quasi-likelihood methods. Again, a series of exclusion of terms coupled with drop in deviance Chi-squared tests was carried out to determine the final model used in the analysis. Each model and Chi-squared test can be found in Appendix D in Tables A.9 to A.14.

Table 14 is an excerpt of the summary from the final model. Table 15 and Figure 9 show estimated survival of germinants from directly sown seeds by site and treatment as well as 80% confidence intervals for each estimate.

Coefficients:

	Estimate	Std. Error	t value	Pr(>|t|)	
(Intercept)	-2.14591	0.53677	-3.998	0.000103	
sitepioneer	0.37338	0.71148	0.525	0.600554	
sitethompson	1.43538	0.67178	2.137	0.034351	
sitetoboggan	2.28682	0.64660	3.537	0.000549	
siteulm	-0.96513	0.72999	-1.322	0.188271	
seedscar	-0.50209	0.35262	-1.424	0.156689	
seedscar+strat	0.19741	0.32645	0.605	0.546337	
seedstrat	0.44583	0.31686	1.407	0.161621	
sitepioneer:seedscar	1.25092	0.49292	2.538	0.012243	
sitethompson:seedscar	-0.57429	0.54868	-1.047	0.297048	
sitetoboggan:seedscar	0.20929	0.46074	0.454	0.650344	
siteulm:seedscar	-0.73468	0.88739	-0.828	0.409123	
sitepioneer:seedscar+strat	-0.53308	0.50279	-1.060	0.290853	
sitethompson:seedscar+strat	0.19249	0.46788	0.411	0.681407	
sitetoboggan:seedscar+strat	-0.51369	0.44140	-1.164	0.246482	
siteulm:seedscar+strat	1.09962	0.57993	1.896	0.059991	.
sitepioneer:seedstrat	0.13055	0.46984	0.278	0.781528	
sitethompson:seedstrat	0.07096	0.45988	0.154	0.877592	
sitetoboggan:seedstrat	-0.60093	0.43202	-1.391	0.166428	
siteulm:seedstrat	1.30631	0.56441	2.314	0.022086	

Table 14: Excerpt of the summary of the final model of combined germination and survival.

From Table 15 and Figure 9 one can see that estimated percentage of seeds that both combined germination and survival was highest at the Toboggan Ridge site with ranges from 54% to 46% depending on treatment. The Thompson Peak site also had high percentages with the exception of the scarified seed which performed poorly with a combined germination and survival rate of 14%. Warm stratified seed and seed undergoing both warm stratification and scarification were found to have significantly higher combined germination and survival rates than scarified seed at the Thompson Peak site and significantly higher combined germination and survival rates than untreated control seed and scarified seed at the Ulm Peak site. Warm stratified seed had the highest

estimated combined germination and survival rates at three of the five sites. This same treatment had the second highest estimated combined germination and survival rates at the remaining two sites and only trailed the treatment with the highest estimates rates by three percent at both of these two sites.

Combined Germination and Survival Estimates

Site	Treatment	Estimated Germ. + Surv. (%)	80% CI (%)
Gold Pass	Control	10.5	5.9 to 18.0
Gold Pass	Scar	6.6	3.6 to 11.9
Gold Pass	Scar + Strat	12.5	7.1 to 21.0
Gold Pass	Strat	15.5	9.0 to 25.3
Pioneer Mountain	Control	14.5	8.6 to 23.5
Pioneer Mountain	Scar	26.4	16.9 to 38.8
Pioneer Mountain	Scar + Strat	10.8	6.2 to 18.3
Pioneer Mountain	Strat	23.2	14.6 to 34.9
Thompson Peak	Control	33.0	22.5 to 45.3
Thompson Peak	Scar	14.3	8.5 to 23.2
Thompson Peak	Scar + Strat	42.1	32.8 to 51.9
Thompson Peak	Strat	45.2	32.9 to 58.0
Toboggan Ridge	Control	53.5	41.6 to 65.0
Toboggan Ridge	Scar	46.2	34.7 to 58.1
Toboggan Ridge	Scar + Strat	45.6	34.2 to 57.6
Toboggan Ridge	Strat	49.7	37.9 to 61.4
Ulm Peak	Control	4.3	2.7 to 6.5
Ulm Peak	Scar	1.3	0.5 to 3.2
Ulm Peak	Scar + Strat	14.0	11.0 to 17.8
Ulm Peak	Strat	20.4	13.8 to 29.1

Table 15: Estimated combined germination and survival percent and 80% confidence intervals at each site by treatment

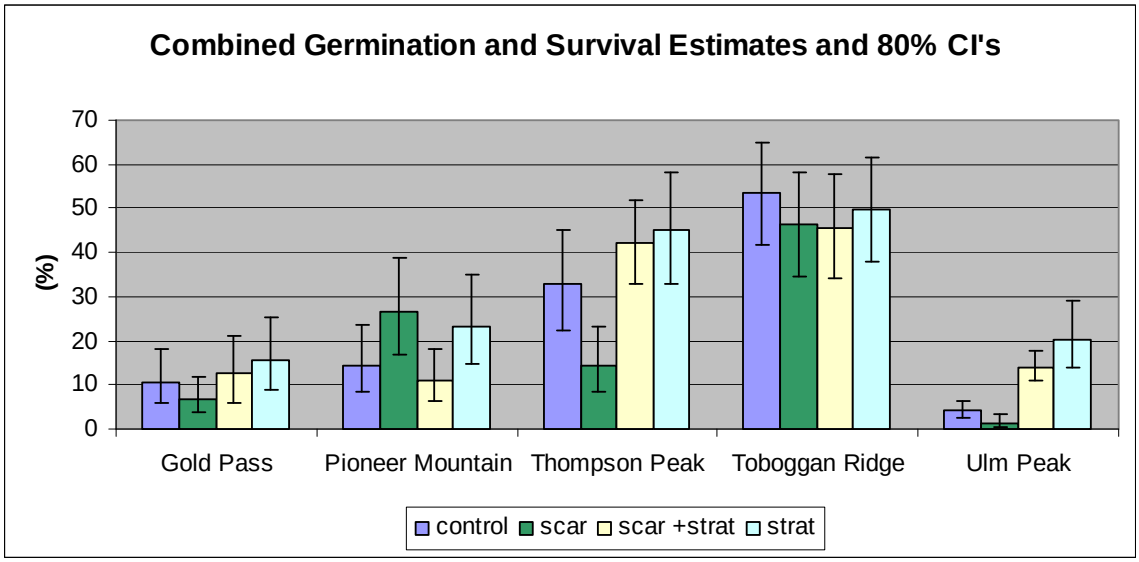


Figure 9: Combined germination and survival estimates and 80% confidence intervals.

Caging

When thinking of the potential problems of using direct seeding as a regeneration tool, seed predation immediately comes to mind. This is especially true for whitebark pine seeds as they contain high levels of fat and protein. When dealing with single seeds or small caches of two to three seeds the biggest threat of predation is from small rodents and, perhaps to a lesser degree, birds. As stated in the methods, half of all of the seeds planted in this study were covered with 1/2″ wire mesh cages to investigate whether or not the cages had an effect on the germination rates and the survival of germinants with the theory that the cages may prevent or deter seed predation.

The caging effect was actually tested while completing portions of the first two analyses. The initial saturated models used in the analyses included caging interaction terms. These caging interaction terms were removed at some point during the step by step exclusion of terms. Following the removal, drop in deviance Chi-squared tests were

used to test for evidence against the more reduced model without these interaction terms. The following subsections take models and Chi-squared tests from the first two analyses to show the effects of caging on germination and survival of whitebark pine seeds and germinants.

Caging Effects on Germination

Model 3 (Germination): The Quasi-Binomial Model

```
model.3 <- glm(cbind(germ, nogerm) ~ site/block.new + cage * seed + cage * site + seed * site + seed* (site/block.new) + cage * (site/block.new) + cage * seed * site, family = quasibinomial, data = dat)
```

Model 3 is the quasi-binomial model from which the removal of terms starts. As one can see, there are four caging interaction terms included in this model. They are as follows: cage*seed, cage*site, cage*(site/block.new), and cage*seed*site. The following steps remove each of these interactions and test for evidence against their absence in the more reduced model.

Model 4 (Germination) : Removing cage*seed*site

```
model.4 <- glm(cbind(germ, nogerm) ~ site/block.new + cage * seed + cage * site + seed * site + seed* (site/block.new) + cage * (site/block.new), family = quasibinomial, data = dat)
```

Table 4 shows the results of the drop in deviance Chi-squared test performed using the following R code: anova(model.4, model.3, test= "Chisq"). The p-value from this test (0.8483) provides little evidence against the reduced model without this three way interaction term and therefore little evidence for a caging effect on germination that is dependent both on site and seed treatment.

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	73	194.94			
2	61	175.7	12	19.246	0.8483

Table 4: Results of the drop in deviance Chi-squared test of model 4 (germination) compared to model 3 (germination).

Model 5 (Germination) : Removing cage*(site/block.new)

model.5 <- glm(cbind(germ, nogerm) ~ site/block.new + cage * seed + cage * site + seed * site + seed * (site/block.new), family = quasibinomial, data = dat)

Table 5 shows the results of the drop in deviance Chi-squared test performed using the following R code: anova(model.5, model.4, test= "Chisq"). The small p-value (0.000623) from this test does provide good evidence against the reduced model without the interaction term cage*(site/block.new). This is suggestive of a cage effect on germination that is dependent upon site as well as block.

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	93	310.35			
2	73	194.94	20	115.41	0.000623

Table 5: Results of the drop in deviance Chi-squared test of model 5 (germination) compared to model 4 (germination).

Model 6 (Germination): Removing cage*site

model.6 <- glm(cbind(germ, nogerm) ~ site/block.new + cage * seed + seed * site + seed*(site/block.new), family = quasibinomial, data = dat)

Table 6 shows the results of the drop in deviance Chi-squared test performed using the following R code: anova(model.6, model.5, test= "Chisq"). The p-value from this test (0.4943) provides little evidence against the reduced model without the cage*site

interaction term and therefore little evidence of a caging effect on germination that is dependent on site.

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	97	320.69			
2	93	310.35	4	10.339	0.4943

Table 6: Results of the drop in deviance Chi-squared test of model 6 (germination) compared to model 5 (germination).

Model 7 (Germination) : Removing cage*seed

```
model.7 <- glm(cbind(germ, nogerm) ~ site/block.new + seed*site +
seed*(site/block.new), family = quasibinomial, data = dat)
```

Table 7 shows the results of the drop in deviance Chi-squared test performed using the following R code: anova(model.7, model.6, test="Chisq"). The large p-value from this test (0.9008) provides little evidence against the reduced model without the cage*seed interaction and therefore very little evidence of a caging effect on germination that is dependent on the seed treatment.

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	101	323.89			
2	97	320.69	4	3.1951	0.9008

Table 7: Results of the drop in deviance Chi-squared test of model 6 (germination) compared to model 7 (germination).

Caged and Non-Caged Germination Estimates

Site	Treatment	Non-Caged Germ. (%)	Caged Germ. (%)
Gold Pass	Control	27.8	29.6
Gold Pass	Scar	17.1	18.4
Gold Pass	Scar + Strat	36.8	38.9
Gold Pass	Strat	58.4	60.6
Pioneer Mountain	Control	20.0	36.3
Pioneer Mountain	Scar	38.3	58.5
Pioneer Mountain	Scar + Strat	22.5	39.7
Pioneer Mountain	Strat	41.2	61.4
Thompson Peak	Control	35.2	20.6
Thompson Peak	Scar	19.1	10.2
Thompson Peak	Scar + Strat	58.2	40.0
Thompson Peak	Strat	52.8	65.2
Toboggan Ridge	Control	58.7	50.0
Toboggan Ridge	Scar	55.6	46.8
Toboggan Ridge	Scar + Strat	51.2	42.5
Toboggan Ridge	Strat	54.5	45.7
Ulm Peak	Control	31.9	35.6
Ulm Peak	Scar	10.5	12.2
Ulm Peak	Scar + Strat	46.0	50.1
Ulm Peak	Strat	56.0	60.0

Table 16: Caged versus non-caged estimated germination rates comparison by treatment and site.

Caging Effects on Survival

Model 3 (Survival) – The Quasi-Binomial Model

model.3 <- glm(cbind(survived, totgermsurv) ~ site/block.new + cage * seed + cage * site + seed * site + seed* (site/block.new) + cage * (site/block.new) + cage * seed * site, family = quasibinomial, data = dat)

As with testing for caging effects on germination, model 3 is the quasi-binomial from which the removal of terms starts. Once again, there are the same four caging interaction terms included in this model. The following steps remove each of these interactions and test for evidence against their absence in the more reduced model.

Model 4 (Survival) - Removing cage*seed*site

model.4 <- glm(cbind(survived, totgermsurv) ~ site/block.new + cage * seed + cage * site + seed * site + seed* (site/block.new) + cage * (site/block.new), family = quasibinomial, data = dat)

Table 17 shows the results of the drop in deviance Chi-squared test performed using the following R code: anova(model.4, model.3, test= "Chisq"). The p-value from this test (0.6343) provides little evidence against the reduced model without this three way interaction term and therefore little evidence for a caging effect on survival that is dependent both on site and seed treatment.

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	94	157.88			
2	82	142	12	15.883	0.6343

Table 17: Results of the drop in deviance Chi-squared test of model 4 (survival) compared to model 3 (survival).

Model 5 (Survival) - Removing cage*(site/block.new)

model.5 <- glm(cbind(survived, totgermsurv) ~ site/block.new + cage * seed + cage * site + seed * site + seed* (site/block.new), family = quasibinomial, data = dat)

Table 18 shows the results of the drop in deviance Chi-squared test performed using the following R code: anova(model.5, model.4, test= "Chisq"). The small p-value (0.0365) from this test does provide good evidence against the reduced model without the interaction term cage*(site/block.new). This is suggestive of a cage effect on survival that is dependent upon site as well as block.

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	108	195.73			
2	94	157.88	14	37.845	0.0365

Table 18: Results of the drop in deviance Chi-squared test of model 5 (survival) compared to model 4 (survival).

Model 6 (Survival) - Removing cage*site

model.6 <- glm(cbind(survived, totgermsurv) ~ site/block.new + cage * seed + seed * site + seed*(site/block.new), family = quasibinomial, data = dat)

Table 19 shows the results of the drop in deviance Chi-squared test performed using the following R code: anova(model.6, model.5, test= "Chisq"). The p-value from this test (0.1736) provides little evidence against the reduced model without the cage*site interaction term and therefore little evidence of a caging effect on survival that is dependent on site.

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	112	206.38			
2	108	195.73	4	10.655	0.1736

Table 19: Results of the drop in deviance Chi-squared test of model 6 (survival) compared to model 5 (survival).

Model 7 (Survival) - Removing cage*seed

model.7 <- glm(cbind(survived, totgermsurv) ~ site/block.new + seed*site + seed*(site/block.new), family = quasibinomial, data = dat)

Table 20 shows the results of the drop in deviance Chi-squared test performed using the following R code: anova(model.7, model.6, test= "Chisq"). The very small p-value from this test (7.742 E-07) provides strong evidence against the reduced model

without the cage*site interaction term. This is suggestive of a caging effect on survival that is dependent on seed treatment.

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	116	263.19			
2	112	206.38	4	56.802	7.7420E-07

Table 20: Results of the drop in deviance Chi-squared test of model 7 (survival) compared to model 6 (survival).

Cage and Non-Caged Survival Estimates

Site	Treatment	Non-Caged Surv. (%)	Caged Surv.(%)
Gold Pass	Control	39.4	61.2
Gold Pass	Scar	41.0	63.5
Gold Pass	Scar + Strat	35.0	57.5
Gold Pass	Strat	26.7	47.7
Pioneer Mountain	Control	70.9	84.8
Pioneer Mountain	Scar	71.3	85.1
Pioneer Mountain	Scar + Strat	42.2	62.6
Pioneer Mountain	Strat	59.5	77.2
Thompson Peak	Control	77.8	74.9
Thompson Peak	Scar	64.6	60.9
Thompson Peak	Scar + Strat	70.5	67.1
Thompson Peak	Strat	79.7	77.0
Toboggan Ridge	Control	87.5	94.8
Toboggan Ridge	Scar	80.2	91.4
Toboggan Ridge	Scar + Strat	87.6	94.9
Toboggan Ridge	Strat	88.6	95.3
Ulm Peak	Control	12.8	25.6
Ulm Peak	Scar	10.4	21.4
Ulm Peak	Scar + Strat	34.5	55.4
Ulm Peak	Strat	38.3	59.4

Table 21: Caged versus non-caged estimated survival rates comparison by treatment and site.

Summary

When looking at all of the germination data from the entire study, overall, there appears to be very little difference between sown seeds covered with a cage and sown seeds not covered with a cage. This is why it is interesting that when the data are analyzed with a little more scrutiny there actually is a cage effect on germination.

Thinking about some of the caging interaction terms that were tested for in this analysis, such as cage*seed and cage*seed*site, it does not make intuitive sense that these interactions are actually explaining a biological process that is occurring. One would not expect a cage effect on germination that is dependent on the treatment type. That is not to say that it could not happen, it is just not expected. The drop in deviance Chi-squared tests confirm this line of thinking with very high p-values of 0.9008 and 0.8483 for the cage*seed and cage*seed*site interactions respectively.

When dealing with other interactions such as the cage*site and cage*(site/block.new) terms, one might expect these interactions to explain a biological process that is occurring. For example, rodent activity may be high at one site but not at another. If this was the case, it would be expected that a large amount of the deviance could be explained by the cage*site term. A p-value of 0.4943 in the Chi-squared test shows that this is not case in this study. However, a small p-value of 0.0006 for the cage*(site/block.new) term suggest that there is a cage effect on germination that is dependent on both site and block. This could be because there was a large amount of rodent activity at certain blocks at a site but not necessarily throughout an entire site.

It seems that one might expect similar Chi-squared test results for survival data. For the most part, this is the case. P-values of 0.6343 for the cage*seed*site interaction and 0.1736 for the cage*site interaction suggests there is not a cage effect for survival that is dependent on both seed treatment and site or a cage effect for survival that is dependent on site alone. A somewhat small p-value of 0.0365 for the cage*(site/block.new) interaction term is suggestive of a cage effect for survival that is dependent on both site and block just as it was for germination. The big difference between the germination data and the survival data is the rather surprising small p-value of 7.74 E-07 for the cage*seed interaction term suggesting a cage effect for survival that is dependent on seed treatment. One speculative idea of why this is occurring is because the cages in certain cases are actually creating a cooler more habitable environment for the germinants to survive by providing more shade than that of a row of germinants without a cage.

Directly Sown Seed versus Outplanted Nursery Grown Seedlings

Figure 10 shows that outplanted nursery seedling survival is considerably higher than cached seeds that combined germination and survivalat each site. This is no surprise, especially this early on considering the nursery seedlings start with the advantage of already being established two-year old seedlings. The results of a paired t-test show the mean of the difference of the survival rate of outplanted nursery seedlings and combined germination and survivalrate of directly sown seed is 53.6% with a 95% confidence interval of 36.6% to 70.6% (p-value = 0.0009). These observed results are

very similar to the results of Smith et al. (2011) where limber pine, a whitebark pine relative, was used instead. It is important to keep in mind that these rates are after only two years of data for the Pioneer Mountain and Toboggan Ridge sites and three years of data for the others. Ideally, data will continue to be collected yearly for this aspect of the study, as long term survival is what is of interest.

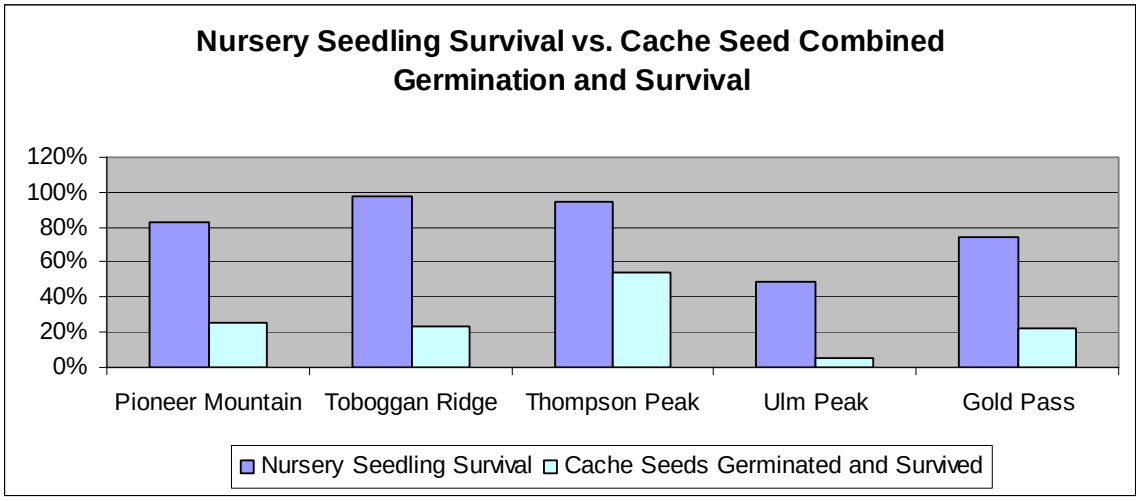


Figure 10: Nursery seedling survival versus cache seed combined germination and survival

Cached Seed versus Non-Cached Seed

Figure 11 shows that seeds in caches had a significantly lower germination rate than seeds not in caches at every site with one exception. Cached seeds at the Thompson Peak site had a germination rate of 68% while non-cached seeds had a germination rate of 38%. The results at the Thompson Peak site are more similar to what was observed in the Smith et al. (2011) study using limber pine in which seed germination and germinant survival both increased when planted in caches of three and five.

Across sites, there is very little difference between cached and non-cached seeds. A paired t-test show the mean of the difference between cached seed germination and non-cached seed germination show the mean to be -1.8% with a 95% confidence interval of -2.5% to 2.1% (p-value = 0.8394). However, the difference between the two groups observed at the Thompson Peak site is fairly sizeable which could lead one to believe that cached seeds have an advantage under certain circumstances. Perhaps nutrient availability is more abundant at the Thompson Peak site and therefore multiple seeds planted together carry an advantage over seeds planted by themselves. Perhaps soil moisture is higher at this site or a combination of soil moisture and nutrients or other unknown factors.

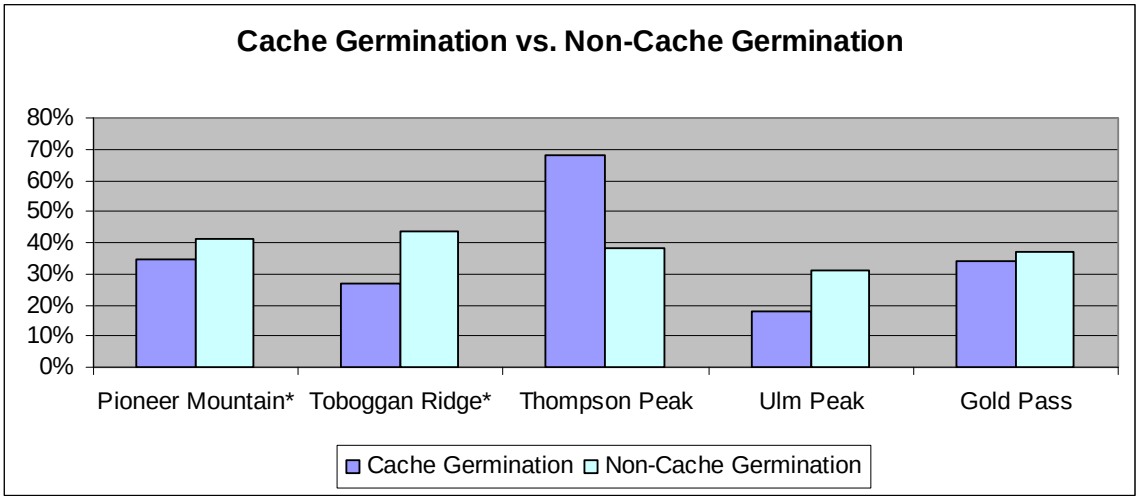


Figure 11: Cache germination vs. non-cache germination
*Caches included both control and warm stratified seeds.

Two sites (Toboggan Ridge and Gold Pass) had slightly higher cached seeds survival rates compared to non-cached seeds. Non-cached seed survival was slightly higher at the remaining three sites (See Figure 12). Considering the amount of natural

variation that is inherent in a study such as this, the observed differences from site to site are not convincing that one method has an advantage over the other. This is also confirmed with a paired t-test that found the mean of the difference between cached seed survival and non-cached seed survival to be 4.2% with a 95% confidence interval of -6.5% to 14.9% (p-value = 0.3383). However, it should be noted that the results were collected over a small time frame (2-3 years).

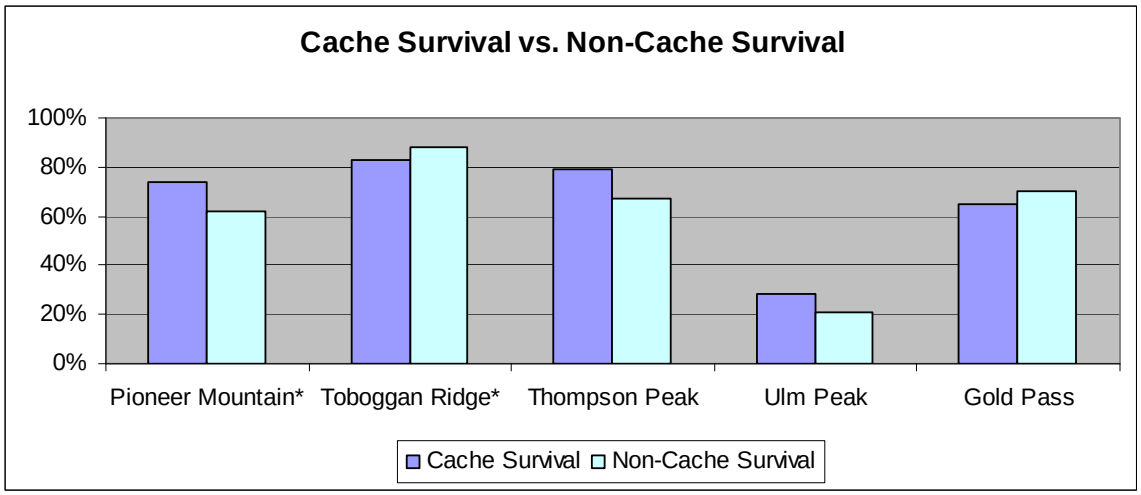


Figure 12: Cache survival versus non-cache survival
*Caches included both control and warm stratified seeds.

Temperature

Plotting sub-surface temperatures on top of surface temperatures as in Figure 15 makes it difficult to distinguish between the two. The red (surface temperature) does appear at the extremes showing the temperature is more variable on the surface than the sub-surface which is to be expected. Perhaps a more effective way to look at the differences between the two is by plotting the temperature difference of the surface readings and the sub-surface readings taken at the same time (Figure 14). This plot

shows temperature readings taken every hour and six minutes from both the surface and sub-surface at the same location and same time. It is very effective at showing the growing seasons and even some summer weather patterns. When the majority of the points are negative that is indicative of hot days and cool nights. When there is a shift to more positive points, it is indicative of hot days and warm nights. It also shows that the winter of 2010-2011 had a much better snow pack then the winter of 2011-2012. Both Figure 14 and Figure 15 are effective at showing how constant the temperature is during the winter months under this snow cover.

Table 22 and Figure 13 show the extreme high and low temperatures that occurred at each site while temperature data was being recorded. The lowest temperatures for all the sites occurred in the fall before there was any snow cover.

Site	Max Temp (F/C)	Min Temp (F/C)
Pioneer Mountain	120.9 / 49.4	23.1 / -4.9
Gold Pass	146.2 / 63.4	26.5 / -3.1
Thompson Peak	140.9 / 60.5	21.9 / -5.6
Ulm Peak	113.1 / 45.1	23.6 / -4.7
Toboggan Ridge	132.2 / 55.6	25.8 / -3.4

Table 22: Extreme high and low recorded temperatures at each site.

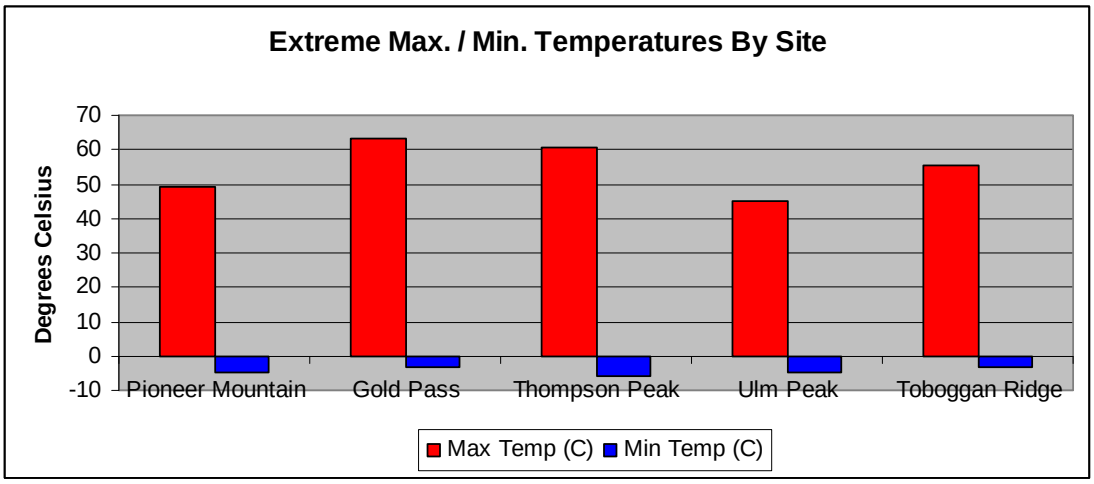


Figure 13: Extreme maximum and minimum temperatures by site.

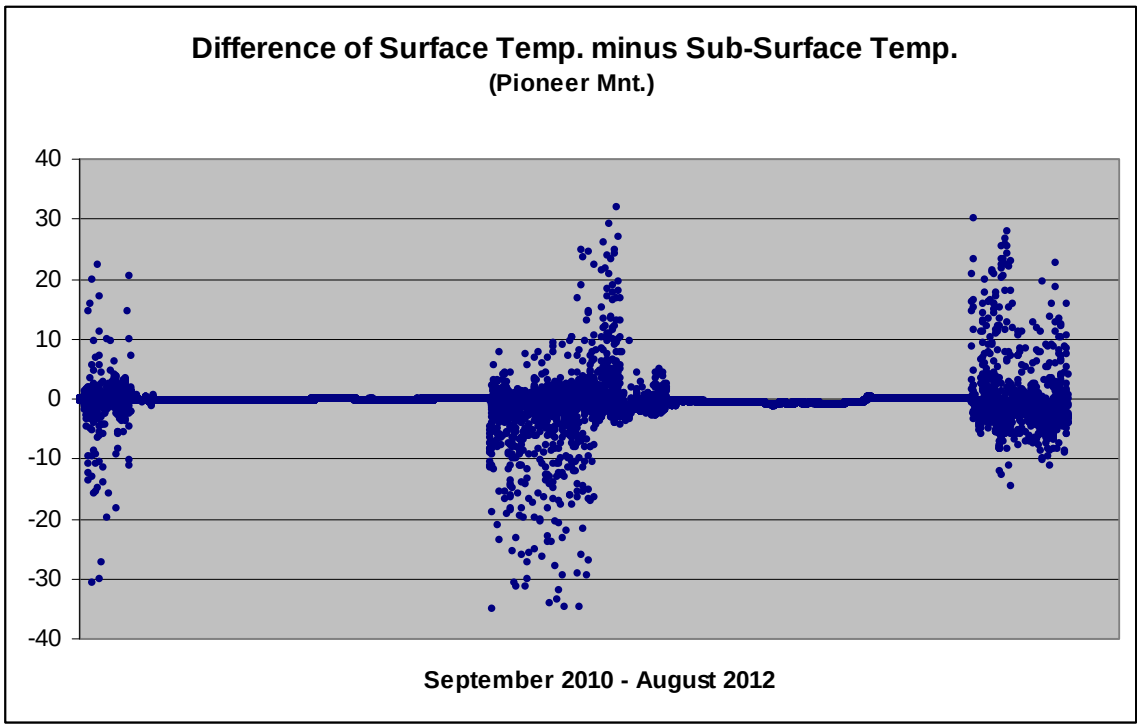


Figure 14: Difference of surface temperature minus sub-surface temperature at Pioneer Mountain site.

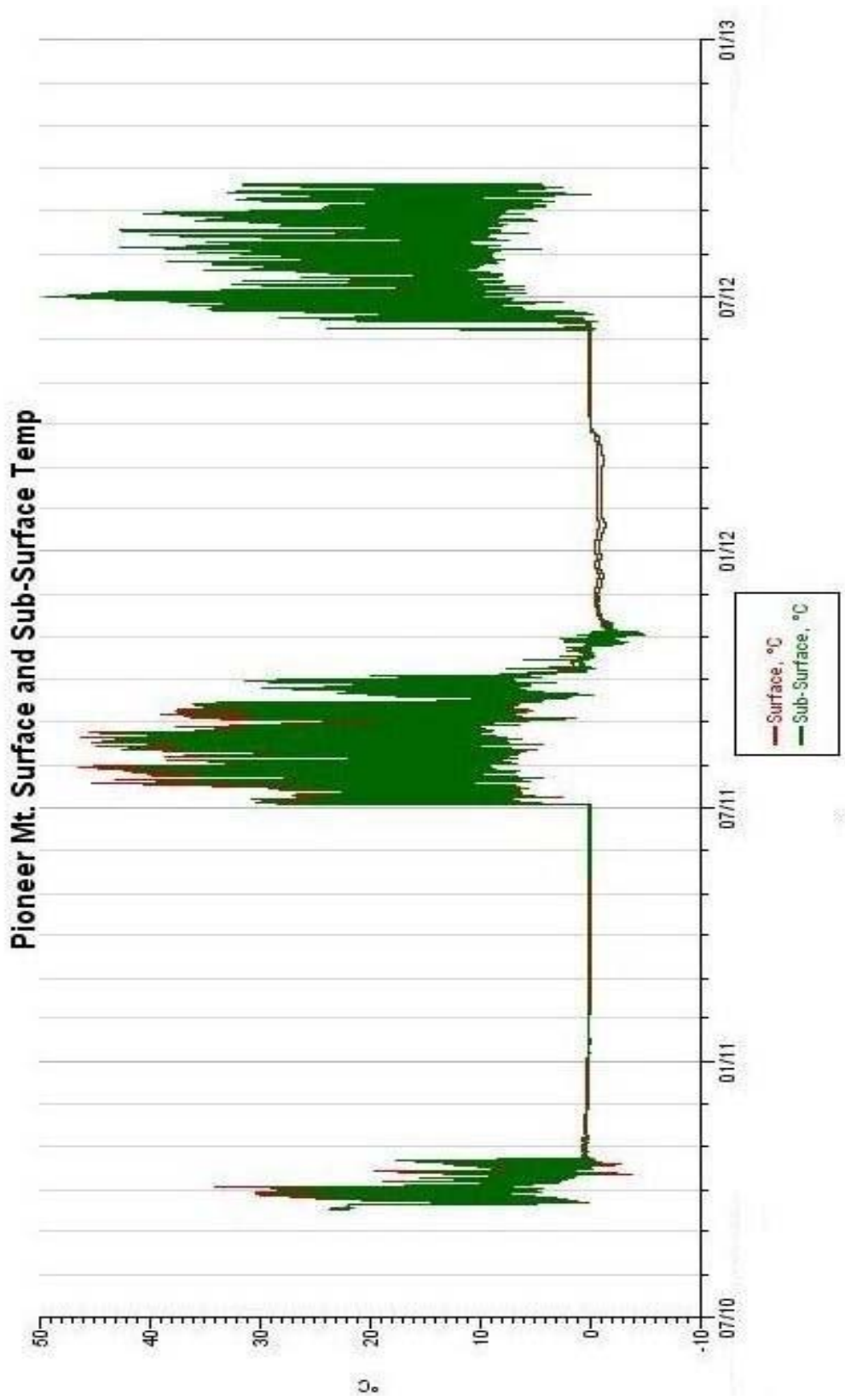


Figure 15: Plot of Pioneer Mountain surface and sub-surface temperatures

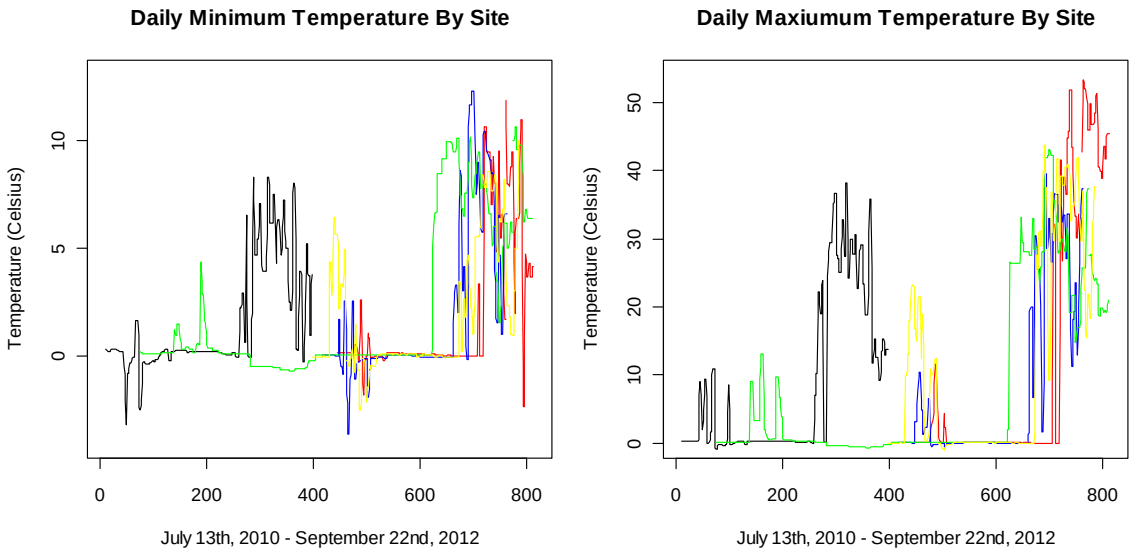


Figure 16: Charts showing the variations of daily minimum and maximum temperatures for each site throughout varying data collection dates. Key: Black = Thompson Peak; Green = Pioneer Mountain; Yellow = Gold Pass; Blue = Ulm Peak; Red = Toboggan Ridge

Model 1 (Temperature): Temperature Effect

model.1 <- glm(cbind(survived, totgermsurv) ~ treatment + temp, family=binomial, data = dat)

Table 23 is an excerpt of the summary of model 1 (temperature). The temperature term is from the scaled value of number of extreme temperature events at each site as explained in the methods. The estimate for this term is 0.008784 with a p-value of 0.07. The positive estimate is suggestive that an increasing amount of extreme temperatures have a positive effect on the survival of whitebark pine germinants. This is probably not the case and it is likely that one or many other important variables that explain survival have not been taken into account. Some examples of this may be soil moisture, soil nutrients, humidity, etc. (de Chantal et al. 2003).

Coefficients:

	Estimate	Std. Error	z value	Pr(>|z|)
(Intercept)	-0.093940	0.351435	-0.267	0.7892
treatmentsc	0.039685	0.160561	0.247	0.8048
treatmentscst	-0.281237	0.143328	-1.962	0.0497
treatmentst	-0.130792	0.138742	-0.943	0.3458
temp	0.008784	0.004893	1.795	0.0726

Table 23: Excerpt from the summary of model 1 (temperature).

CONCLUSIONS

Whitebark pine seed treatments of warm stratification and warm stratification and scarification together were found to have significantly increased germination under natural field settings compared to the scarification treatment at two sites. Warm stratified seed was found to have significantly higher germination rates than scarified seed and untreated control seed at one of the other three sites. As a whole, warm stratified seed had the highest germination rates as estimates did not drop lower than 41% at any of the sites. The other three treatments had germination rates below this mark at multiple sites.

Survival rates of whitebark pine germinants from directly sown seed were similar between treatments with a few exceptions. The control and scarification treatments were found to have significantly higher survival rates than seed undergoing both scarification and warm stratification at one of the five sites. Warm stratified seed and seed undergoing both stratification and scarification were found to have significantly higher survival rates than the untreated control and scarified seed at one of the remaining four sites.

Warm stratified seed and seed undergoing both warm stratification and scarification were found to have significantly higher combined germination and survival rates than scarified seed at one of the five sites and significantly higher combined germination and survival rates than untreated control seed and scarified seed at the one of the remaining four sites. Warm stratified seed had the highest estimated combined germination and survival rates at three of the five sites. This same treatment had the second highest estimated combined germination and survival rates at the remaining two

sites and was surpassed by the treatment with the highest estimated rates by only three percent at both of these two sites.

Caging directly sown seed was shown to have a positive effect on germination and survival that is dependent on both site and block. Caging was also shown to have a positive effect on survival that is dependent on seed treatment. It is thought that this caging effect on survival could be due to an unexpected cooling effect brought about by the shade provided by the cage. The shade provided by the cage is minimal but possibly significant enough to decrease temperatures, which results in a decrease in evapotranspiration, ultimately resulting in an increase in survival.

Outplanted nursery grown seedlings had significantly higher survival rates than the combined germination and survivalrates of seeds sown in caches after two and three years of observation. Ideally the data concerning this aspect of the experiment will continue to be recorded on a yearly basis in the future to monitor long term survival.

Cache seed germination rates were lower than seeds planted alone (non-cached) at all sites except one, Thompson Peak. Cache seed survival rates and non-cache seed survival rates were very similar at all five sites as no significant difference was found.

Soil surface temperatures had higher volatility than subsurface temperatures and winter temperatures stayed very close to freezing once there was snow cover. The number of extreme temperature events at a site is estimated to increase survival of germinants from directly sown seeds. However, this is probably not the cause of increased survival and results such as this are likely an indicator that one or many other important variables affecting survival are not accounted for in this study.

Management Implications

As a keystone species, whitebark pine not only plays important roles in the upper subalpine ecosystems in which it resides but also the surrounding ecosystems that feel the indirect effects of the existence of this tree. The rapid population decline of this ecologically important tree over the years has made apparent the need for restoration. Current methods of restoring whitebark pine populations have proven to be costly and time consuming. Considering the pressing nature of the situation, the less expensive and quick- to- implement methods of direct seeding could greatly benefit restoration efforts if found effective in the field.

The question now becomes: What percent level of germination and survival is deemed as successful? The question may be answered by a cost/benefit analysis comparing the cost of how much it takes to get a nursery grown seedling in the ground compared to the cost of getting a treated seed directly sown in the ground and then looking at their respective survival rates. These rates would vary depending on site location and accessibility but educated guesses of combined germination and survival rates of directly sown seed as low as 10% could be deemed as a success (Schwandt; Roberts personal communication 2012).

Treatment Type

The statistical analyses of this study have estimated combined germination and survival rates of warm stratified seed and both warm stratified and scarified seed at all sites to be above 10%. The lower reaches of the 80% confidence intervals of warm

stratified seed only dips below 10% on one occasion (9% at Gold Pass site). Overall, warm stratified seeds have the highest estimated proportion of seed that had germinated and were still living throughout the course of the study making this treatment the most logical choice for implementation into field management practices.

Caging

A caging effect that is dependent on both site and block is suggestive that there is an advantage to caging directly sown seeds under certain circumstances. This is likely when there is high rodent activity in a certain area. This is not always the case as rodent activity was found inside the cage on more than one occasion but the cage itself does appear to act as a deterrent. Caging also appears to increase survival. However, this increase in survival is thought to come about from an increase in shade and cooler more hospitable environments. These results bring to light the importance of selecting good microsites.

From a restoration management practices standpoint, the real question is: Should caging be used as restoration practice in the field? Caging is a very labor intensive process when looked at in the scope of how many seeds it is actually protecting. The advantages it brings to the establishment and survival of germinants do not outweigh its disadvantages. Whitebark pine habitat is often in remote areas in which the benefits of direct seeding are magnified from a logistics standpoint. Caging in these situations would probably negate any advantage gained from direct seeding as the cages are heavy and cumbersome to transport. Cages also possess the disadvantage that they have to be removed several years after installation to prevent them from impeding future seedling

growth. For these reasons caging is not recommended from a restoration management standpoint.

Seed Caching

Overall, seed caching did not appear to have much effect on seed germination and germinant survival unlike the results from Smith et al (2011) using limber pine seeds. On an individual site level, cached seeds at the Thompson Peak site did appear to increase germination suggesting that site specific unaccounted for variables may be responsible for the difference. More research is necessary to confirm this and to make any management recommendations.

Future Research

Continuing direct seeding trials under the same format as was carried out at the six sites in this study will improve information on its effectiveness and likely narrow the confidence intervals that this study produced with its data. Two sites doing just this were installed in the fall of 2012 to provide additional data: one site was at the Jackson Hole Ski Resort in Wyoming and the other near Island Park, Idaho. Continued monitoring of temperature data and inclusion of monitoring of other climatic and site variables could lead to some interesting findings on what factors affect survival. Precipitation, humidity, soil moisture, and soil nutrient availability are a few examples of variables that could be useful.

For this study, sowing depth was kept at a constant 1.5 inches and sowing time was always in the fall season. Other direct seeding proposals may be established to look

at how changing sowing depth and sowing timing may effect germination and survival (Schwandt, personal communication 2013).

REFERENCES CITED

REFERENCES CITED

Arno, S. F., & Hoff, R. J. (1989). *Silvics of whitebark pine (Pinus albicaulis)*. US Department of Agriculture, Forest Service, Intermountain Research Station. General Technical Report INT-253.

Brown, J. K. (1995). Fire regimes and their relevance to ecosystem management. *Proceedings of Society of American Foresters Convention*. p. 171 -178.

Burr, K. E., Eramian, A., & Eggleston, K. (2001). Growing whitebark pine seedlings for restoration. *Whitebark pine communities: Ecology and restoration*, p. 325-345.

Ellison, A. M., Bank, M. S., Clinton, B. D., Colburn, E. A., Elliott, K., Ford, C. R., Foster, D.R., Kloeppel, B.D., Knoepp, J.D., Lovett, G.M., Mohan, J., Orwig, D.A., Rodenhouse, N.L., Sobczak, W.V., Stinson, K.A., Stone, J.K., Swan, C.M., Thompson, J., Von Holle, B., Webster, J.R. & Webster, J. R. (2005). Loss of foundation species: consequences for the structure and dynamics of forested ecosystems. *Frontiers in Ecology and the Environment*, *3*(9), p. 479-486.

de Chantal, M., Leinonen, K., Ilvesniemi, H., & Westman, C. J. (2003). Combined effects of site preparation, soil properties, and sowing date on the establishment of Pinus sylvestris and Picea abies from seeds. *Canadian Journal of Forest Research,* 33(5), p. 931-945.

Farmer, R. E. (1997). Germination and establishment: temperature, water and light. *Seed ecophysiology of temperate and boreal zone forest trees. St. Lucie Press, Delray Beach, Fl*, p. 155-198.

Helfield, J. M., & Naiman, R. J. (2006). Keystone interactions: salmon and bear in riparian forests of Alaska. *Ecosystems*, *9*(2), p. 167-180.

Hutchins, H. E., & Lanner, R. M. (1982). The central role of Clark's nutcracker in the dispersal and establishment of whitebark pine. *Oecologia*, *55*(2), p. 192-201.

Izlar, D. K. (2007). *Assessment of whitebark pine seedling survival for Rocky Mountain plantings* (Doctoral dissertation, Université Laval).

Kurz, W. A., Dymond, C. C., Stinson, G., Rampley, G. J., Neilson, E. T., Carroll, A. L., Ebata, L., & Safranyik, L. (2008). Mountain pine beetle and forest carbon feedback to climate change. *Nature*, *452*(7190), p. 987-990.

Mahalovich, M. F., & Dickerson, G. A. (2004). Whitebark pine genetic restoration program for the Intermountain West (United States). *Breeding and genetic resources of five-needle pines: Growth, adaptability and pest resistance, IUFRO Working Party*, *2*(15), p. 23-27.

Mattson, D. J., Blanchard, B. M., & Knight, R. R. (1991). Food habits of Yellowstone grizzly bears, 1977-1987. *Canadian Journal of Zoology*, *69*(6), p. 1619-1629.

McCaughey, W. W., & Weaver, T. (1990). Biotic and microsite factors affecting whitebark pine establishment. US Department of Agriculture, Forest Service, Intermountain Research Station, General Technical Report INT-270, p. 140-150.

McDonald, G. I., & Hoff, R. J. (2001). Blister rust: an introduced plague. *Whitebark pine communities: ecology and restoration. Edited by DF Tomback, SF Arno, and RE Keane. Island Press, Washington, DC*, p. 193-220.

McDonald, G. I., Richardson, B. A., Zambino, P. J., Klopfenstein, N. B., & Kim, M. S. (2006). Pedicularis and Castilleja are natural hosts of Cronartium ribicola in North America: a first report. *Forest Pathology*, *36*(2), p. 73-82.

Pfister, R. D., Kovalchik, B. L., Arno, S. F., & Presby, R. C. (1977). *Forest habitat types of Montana*. Intermountain Forest and Range Experiment Station, Forest Service, US Department of Agriculture. General Technical Report INT-GTR-34.

Primack, R.B. (1998). Essentials of Conservation Biology. Sinauer Associates, Inc.

Resler, L. M., & Tomback, D. F. (2008). Blister rust prevalence in krummholz whitebark pine: implications for treeline dynamics, northern Rocky Mountains, Montana, USA. *Arctic, Antarctic, and Alpine Research*, *40*(1), p. 161-170.

Samman, S., Schwandt, J. W., & Wilson, J. L. (2003). Managing for healthy white pine ecosystems in the United States to reduce the impacts of white pine blister rust. USDA Forest Service, Missoula, MT. Report. R1-03-118.

Schwandt, J., Chadwick, K., Kearns, H., & Jensen, C. (2011). Whitebark pine direct seeding trials in the Pacific Northwest. USDA Forest Service. Proceedings RMRS-P-63.

Smith, C. M., Poll, G., Miranda, E., & Hill, J. (2011). Limber pine seed and seedling planting experiment in Waterton Lakes National Park, Canada. USDA Forest Service. Proceedings RMRS-P-63.

Smith, C. M., Wilson, B., Rasheed, S., Walker, R.C., Carolin, T., & Shepherd, B. (2008). Whitebark pine and white pine blister rust in the Rocky Mountains of Canada and northern Montana. *Canadian Journal of Forest Research*, *38*(5), p. 982-995.

Soulé, M. E., Estes, J. A., Miller, B., & Honnold, D. L. (2005). Strongly interacting species: conservation policy, management, and ethics. *BioScience*, *55*(2), p. 168-176.

Spaulding, P. (1911). The blister rust of white pine*. US Department of Agriculture Bureau of Plant Industry Bui, 206*(88), p. 61-78.

Tomback, D. F., & Achuff, P. (2010). Blister rust and western forest biodiversity: ecology, values and outlook for white pines. *Forest Pathology*, *40*(3−4), p. 186-225.

Tomback, D. F., Arno, S. F., & Keane, R. E. (2001). The compelling case for management intervention. *Whitebark pine communities: ecology and restoration. Island Press, Washington, DC*, p. 3-25.

Tomback, D. F., Sund, S. K., & Hoffmann, L. A. (1993). Post-fire regeneration of Pinus albicaulis: height-age relationships, age structure, and microsite characteristics. *Canadian Journal of Forest Research*, *23*(2), p. 113-119.

APPENDICES

APPENDIX A

ADDITIONAL STUDY MAP INFORMATION

Appendix A - Additional Study Map Information

Created By: Clay DeMastus
Date Created: 10/02/2012
Sources used: nris.mt.gov/gis/
http://inside.uidaho.edu/
http://www.uwyo.edu/wygisc/

Projection Info:
NAD 1983 State Plane Montana FIPS 2500 meters
Lambert Conformal Conic Projection

APPENDIX B

GERMINATION FIGURES, TABLES, AND CALCULATIONS

Appendix B – Germination Figures, Tables, and Calculations

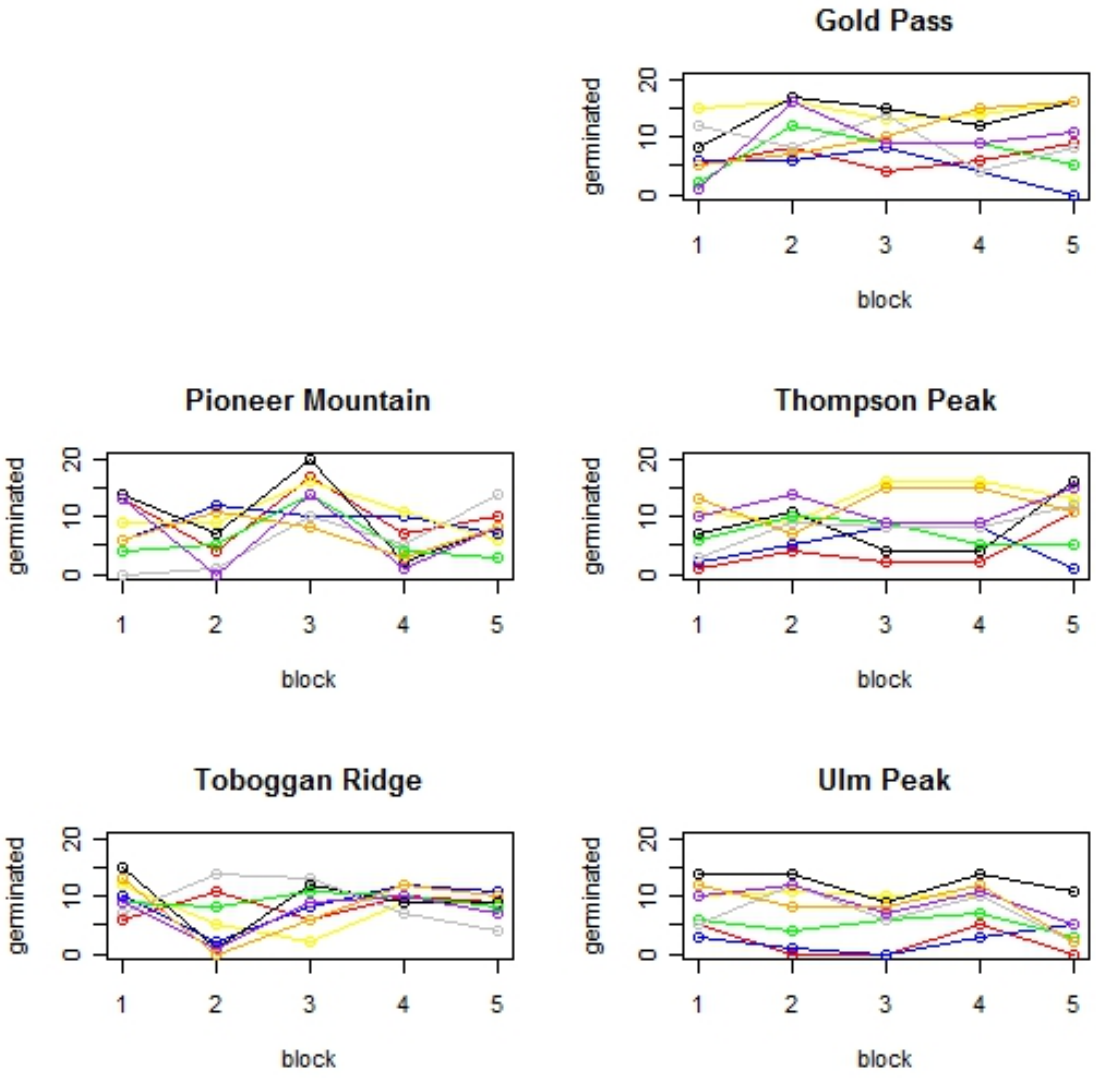


Figure A.1: Germination counts by site, treatment, and block. (Key: red = scar and cage; blue = scar; yellow = strat; black = strat and cage; green = control; grey = control and cage; purple = scar and strat and cage; orange = scar and strat).

Coefficients:

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	-9.592e-01	4.308e-01	-2.226	0.027650
sitepioneer	-4.254e-01	6.200e-01	-0.686	0.493810
sitethompson	3.483e-01	6.050e-01	0.576	0.565746
sitetoboggan	1.311e+00	5.870e-01	2.233	0.027199

siteulm	2.014e-01	6.043e-01	0.333	0.739397
seedscar	-6.190e-01	3.335e-01	-1.856	0.065591 .
seedscar+strat	4.171e-01	3.203e-01	1.302	0.195087
seedstrat	1.299e+00	3.339e-01	3.891	0.000156
cage	9.085e-02	5.563e-01	0.163	0.870510
sitegold:block.new2	7.476e-01	5.282e-01	1.415	0.159275
sitepioneer:block.new2	6.645e-01	5.182e-01	1.282	0.201909
sitethompson:block.new2	-1.184e-01	5.273e-01	-0.224	0.822722
sitetoboggan:block.new2	-1.671e+00	5.621e-01	-2.973	0.003489
siteulm:block.new2	-3.138e-01	5.409e-01	-0.580	0.562838
sitegold:block.new3	6.918e-01	5.281e-01	1.310	0.192492
sitepioneer:block.new3	1.245e+00	5.230e-01	2.380	0.018688
sitethompson:block.new3	8.452e-01	5.287e-01	1.599	0.112255
sitetoboggan:block.new3	-8.776e-01	5.037e-01	-1.742	0.083723 .
siteulm:block.new3	-1.981e-01	5.570e-01	-0.356	0.722677
sitegold:block.new4	8.036e-01	5.285e-01	1.520	0.130732
sitepioneer:block.new4	1.759e-01	5.284e-01	0.333	0.739736
sitethompson:block.new4	6.155e-01	5.243e-01	1.174	0.242452
sitetoboggan:block.new4	-5.053e-02	4.902e-01	-0.103	0.918047
siteulm:block.new4	2.269e-01	5.271e-01	0.430	0.667570
sitegold:block.new5	5.519e-01	5.303e-01	1.041	0.299881
sitepioneer:block.new5	-6.099e-02	5.386e-01	-0.113	0.910005
sitethompson:block.new5	-1.392e-01	5.313e-01	-0.262	0.793652
sitetoboggan:block.new5	-3.016e-01	4.898e-01	-0.616	0.539078
siteulm:block.new5	-1.280e+00	6.190e-01	-2.068	0.040566
sitepioneer:seedscar	1.526e+00	4.832e-01	3.158	0.001960
sitethompson:seedscar	-2.116e-01	4.922e-01	-0.430	0.667936
sitetoboggan:seedscar	4.911e-01	4.612e-01	1.065	0.288851
siteulm:seedscar	-7.624e-01	5.488e-01	-1.389	0.167047
sitepioneer:seedscar+strat	-1.038e-01	4.768e-01	-0.218	0.827923
sitethompson:seedscar+strat	5.249e-01	4.615e-01	1.137	0.257411
sitetoboggan:seedscar+strat	-7.191e-01	4.534e-01	-1.586	0.115078
siteulm:seedscar+strat	1.809e-01	4.625e-01	0.391	0.696288
sitepioneer:seedstrat	-2.715e-01	4.831e-01	-0.562	0.575062
sitethompson:seedstrat	-5.780e-01	4.700e-01	-1.230	0.220905
sitetoboggan:seedstrat	-1.470e+00	4.618e-01	-3.183	0.001807
siteulm:seedstrat	-3.002e-01	4.724e-01	-0.636	0.526156
sitepioneer:cage	7.307e-01	7.599e-01	0.961	0.338027
sitethompson:cage	-8.292e-01	7.847e-01	-1.057	0.292483
sitetoboggan:cage	-4.428e-01	7.415e-01	-0.597	0.551355
siteulm:cage	7.266e-02	7.543e-01	0.096	0.923402
sitegold:block.new2:cage	3.630e-01	7.622e-01	0.476	0.634702
sitepioneer:block.new2:cage	-2.381e+00	7.970e-01	-2.987	0.003349
sitethompson:block.new2:cage	1.136e+00	7.605e-01	1.493	0.137688

sitetoboggan:block.new2:cage	1.146e+00	7.543e-01	1.519	0.131176
siteulm:block.new2:cage	6.977e-01	7.481e-01	0.933	0.352690
sitegold:block.new3:cage	6.386e-02	7.596e-01	0.084	0.933120
sitepioneer:block.new3:cage	-3.101e-02	7.526e-01	-0.041	0.967198
sitethompson:block.new3:cage	-7.168e-01	7.759e-01	-0.924	0.357222
sitetoboggan:block.new3:cage	1.028e+00	7.020e-01	1.465	0.145294
siteulm:block.new3:cage	-3.101e-01	7.799e-01	-0.398	0.691576
sitegold:block.new4:cage	-7.147e-01	7.635e-01	-0.936	0.350945
sitepioneer:block.new4:cage	-1.696e+00	7.776e-01	-2.182	0.030868
sitethompson:block.new4:cage	-4.872e-01	7.730e-01	-0.630	0.529588
sitetoboggan:block.new4:cage	5.600e-08	6.933e-01	0.000	1.000000
siteulm:block.new4:cage	2.757e-01	7.388e-01	0.373	0.709578
sitegold:block.new5:cage	2.730e-01	7.608e-01	0.359	0.720284
sitepioneer:block.new5:cage	6.099e-02	7.338e-01	0.083	0.933883
sitethompson:block.new5:cage	2.087e+00	7.779e-01	2.683	0.008219
sitetoboggan:block.new5:cage	-1.138e-01	6.991e-01	-0.163	0.870955
siteulm:block.new5:cage	3.761e-01	8.325e-01	0.452	0.652204

(Dispersion parameter for quasibinomial family taken to be 2.3774)

Null deviance: 928.68 on 199 degrees of freedom
Residual deviance: 339.13 on 135 degrees of freedom

Table A.1: Complete summary of final model of germination

Calculations:

Calculation for Standard Error Multiplier to Correct for Extra-Binomial Variation:

Sqrt(dispersion parameter from saturated model)
Sqrt(2.6957)
= 1.641858616

Calculation of Inflated Standard Errors

sqrt(sum of variance and co-variance terms used) * (dispersion parameter) = inflated SE

Gold Pass

Control	0.4308 * 1.641858616 = 0.70731
Scar	sqrt(0.19962) * 1.641858616 = 0.73356
Scar + Strat	sqrt(0.18228) * 1.641858616 = 0.70097
Strat	sqrt(0.18828) * 1.641858616 = 0.7124

Pioneer Mountain

Control	sqrt(0.19873) * 1.641858616 = 0.73193
Scar	sqrt(0.18351) * 1.641858616 = 0.70334
Scar + Strat	sqrt(0.190722) * 1.641858616 = 0.71703
Strat	sqrt(0.18511) * 1.641858616 = 0.69728

Thompson Peak

Control	sqrt(0.18036) * 1.641858616 = 0.69728
Scar	sqrt(0.202178) * 1.641858616 = 0.73825
Scar + Strat	sqrt(0.177662) * 1.641858616 = 0.69185
Strat	sqrt(0.179492) * 1.641858616 = 0.6956

Toboggan Ridge

Control	sqrt(0.15892) * 1.641858616 = 0.6545
Scar	sqrt(0.15874) * 1.641858616 = 0.6542
Scar + Strat	sqrt(0.15917) * 1.641858616 = 0.65504
Strat	sqrt(0.15878) * 1.641858616 = 0.65423

Ulm Peak

Control	sqrt(0.17957) * 1.641858616 = 0.69575
Scar	sqrt(0.22597) * 1.641858616 = 0.78048
Scar + Strat	sqrt(0.18561) * 1.641858616 = 0.68132
Strat	sqrt(0.17289) * 1.641858616 = 0.68269

80% Confidence Interval Calculations

Germination probabilities of estimates and confidence intervals are in parentheses. These were calculated from logit link function: (logit = log(Yi / 1 – Yi).
Y1 = Pr(germination) = $logit^{-1}$(estimate)
$logit^{-1}$ can be calculated in R via the 'arm' package using the following code: invlogit(estimate).

Gold Pass

Control	-0.9592 or (27.8%) + and – 0.842(0.70731) = (-1.5547, -0.3636) or (17.4%, 41.0%)
Scar	-1.5782 or (17.1%) + and – 0.842(0.73356) = (-2.1959, -0.9605) or (10.0%, 27.7%)

Scar + Strat -0.5421 or (36.8%) + and – 0.842(0.70097) = (-1.1323, 0.04812) or (24.4%, 51.2%)
Strat 0.3398 or (58.4%) + and – 0.842(0.7124) = (-0.2600, 0.9396) or (43.5%, 71.9%)

Pioneer Mountain

Control -1.3846 or (20.0%) + and – 0.842(0.73193) = (-2.0009, -0.7683) or (11.9%, 31.7%)
Scar -0.4776 or (38.3%) + and – 0.842(0.70334) = (-1.0698, 0.1146) or (25.5%, 52.9%)
Scar + Strat -1.239 or (22.5%) + and – 0.842(0.71703) = (-1.8427, -0.6353) or (13.7%, 34.6%)
Strat -0.3571 or (41.2%) + and – 0.842(0.69728) = (-1.198, -0.02379) or (23.2%, 49.4%)

Thompson Peak

Control -0.6109 or (35.2%) + and – 0,842(0.69728) = (-1.198, -0.02379) or (23.2%, 49.4%)
Scar -1.4415 or (19.1%) + and – 0.842(0.73825) = (-2.0631, -0.8199) or (11.3%, 30.6%)
Scar + Strat 0.3311 or (58.2%) + and – 0.842(0.69185) = (-0.2514, 0.91364) or (42.8%, 71.4%)
Strat 0.1101 or (52.8%) + and – 0.842(0.6956) = (-0.4756, 0.6958) or (38.3%, 66.7%)

Toboggan Ridge

Control 0.3518 or (58.7%) + and – 0.842(0.6545) = (-0.1993, 0.90289) or (45.0%, 71.2%)
Scar 0.2239 or (55.6%) + and – 0.842(0.6542) = (-0.32694, 0.77474) or (41.9%, 68.5%)
Scar + Strat 0.0498 or (51.2%) + and – 0.842(0.65504) = (-0.50174, 0.6013) or (37.7%, 64.6%)
Strat 0.1808 or (54.5%) + and – 0.842(0.65423) = (-0.3701, 0.73167) or (40.9%, 67.5%)

Ulm Peak

Control -0.7578 or (31.9%) + and – 0.842(0.69575) = (-1.3436, -0.172) or (20.7%, 45.7%)
Scar -2.1392 or (10.5%) + and – 0.842(0.78048) = (-2.7964, -1.482) or (5.8%, 18.5%)

Scar + Strat -0.1598 or (46.0%) + and – 0.842(0.68132) = (-0.7335, 0.41387) or (32.4%, 60.2%)
Strat 0.241 or (56.0%) + and – 0.842(0.68269) = (-0.3338, 0.81583) or (41.7%, 69.3%)

APPENDIX C

SURVIVAL TABLES AND CALCULATIONS

Appendix C – Survival Tables and Calculations

Model 2 (Survival) – Model after combining blocks
model.2 <- glm(cbind(survived, totgermsurv) ~ site/block.new + cage * seed + cage * site + seed * site + seed* (site/block.new) + cage * (site/block.new) + cage * seed * site, family = binomial, data = dat)

Model 3 (Survival) – Quasibinomial Model
model.3 <- glm(cbind(survived, totgermsurv) ~ site/block.new + cage * seed + cage * site + seed * site + seed
* (site/block.new) + cage * (site/block.new) + cage * seed * site, family = quasibinomial, data = dat)

Model 4 (Survival) - Removing cage*seed*site
model.4 <- glm(cbind(survived, totgermsurv) ~ site/block.new + cage * seed + cage * site + seed * site + seed
* (site/block.new) + cage * (site/block.new), family = quasibinomial, data = dat)

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	94	157.88			
2	82	142	12	15.883	0.6343

Table A.2: Results of the drop in deviance Chi-squared test of model 4 (survival) compared to model 3 (survival).

Model 5 (Survival) - Removing cage*(site/block.new)
model.5 <- glm(cbind(survived, totgermsurv) ~ site/block.new + cage * seed + cage * site + seed * site + seed* (site/block.new), family = quasibinomial, data = dat)

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	108	195.73			
2	94	157.88	14	37.845	0.0365

Table A.3: Results of the drop in deviance Chi-squared test of model 5 (survival) compared to model 4 (survival).

Model 6 (Survival) - Removing cage*site
model.6 <- glm(cbind(survived, totgermsurv) ~ site/block.new + cage * seed + seed * site + seed*(site/block.new), family = quasibinomial, data = dat)

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	112	206.38			
2	108	195.73	4	10.655	0.1736

Table A.4: Results of the drop in deviance Chi-squared test of model 6 (survival) compared to model 5 (survival).

Model 7 (Survival) - Removing cage*seed

model.7 <- glm(cbind(survived, totgermsurv) ~ site/block.new + seed*site + seed*(site/block.new), family = quasibinomial, data = dat)

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	116	263.19			
2	112	206.38	4	56.802	7.7420E-07

Table A.5: Results of the drop in deviance Chi-squared test of model 7 (survival) compared to model 6 (survival).

Model 8 (Survival) - Removing seed*(site/block.new)

model.8 <- glm(cbind(survived, totgermsurv) ~ site/block.new + seed*site, family = quasibinomial, data = dat)

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	158	307.22			
2	116	263.19	42	44.03	0.9965

Table A.6: Results of the drop in deviance Chi-squared test of model 8 (survival) compared to model 7 (survival).

Model 9 (Survival) - Removing seed*site

model.9 <- glm(cbind(survived, totgermsurv) ~ site/block.new, family = quasibinomial, data = dat)

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	173	357.11			
2	158	307.22	15	49.893	0.0223

Table A.7: Results of the drop in deviance Chi-squared test of model 9 (survival) compared to model 8 (survival).

	Estimate	Std. Error	t value	Pr(>|t|)
(Intercept)	-0.43262	0.57004	-0.759	0.449178
sitepioneer	1.32350	0.82193	1.610	0.109614
sitethompson	1.68553	0.71830	2.347	0.020360
sitetoboggan	2.37399	0.74875	3.171	0.001872
siteulm	-1.48856	0.74456	-1.999	0.047531
seedscar	0.06709	0.45638	0.147	0.883346
seedscar+strat	-0.18488	0.39546	-0.467	0.640879
seedstrat	-0.57778	0.36279	-1.593	0.113519
cage	0.91934	0.68620	1.340	0.182514
sitegold:block.new2	0.22487	0.61924	0.363	0.717051
sitepioneer:block.new2	-0.51996	0.58062	-0.896	0.372058
sitethompson:block.new2	NA	NA	NA	NA
sitetoboggan:block.new2	NA	NA	NA	NA
siteulm:block.new2	NA	NA	NA	NA
sitegold:block.new3	0.44845	0.61556	0.729	0.467521
sitepioneer:block.new3	-0.08776	0.61218	-0.143	0.886222
sitethompson:block.new3	-2.29846	0.53495	-4.297	3.24e-05
sitetoboggan:block.new3	NA	NA	NA	NA
siteulm:block.new3	NA	NA	NA	NA
sitegold:block.new4	-0.01860	0.62558	-0.030	0.976324
sitepioneer:block.new4	NA	NA	NA	NA
sitethompson:block.new4	-2.04632	0.53227	-3.845	0.000183
sitetoboggan:block.new4	-0.15508	0.61491	-0.252	0.801263
siteulm:block.new4	-1.08258	0.70546	-1.535	0.127162
sitegold:block.new5	0.92694	0.63023	1.471	0.143606
sitepioneer:block.new5	-0.73016	0.70764	-1.032	0.303946
sitethompson:block.new5	-1.41317	0.56086	-2.520	0.012878
sitetoboggan:block.new5	-0.30248	0.62068	-0.487	0.626794
siteulm:block.new5	0.79938	0.86066	0.929	0.354604
sitepioneer:seedscar	-0.04934	0.63264	-0.078	0.937942
sitethompson:seedscar	-0.72066	0.69032	-1.044	0.298319
sitetoboggan:seedscar	-0.61050	0.68719	-0.888	0.375858
siteulm:seedscar	-0.30251	0.90995	-0.332	0.740053
sitepioneer:seedscar+strat	-1.02198	0.60630	-1.686	0.094114
sitethompson:seedscar+strat	-0.19623	0.55727	-0.352	0.725271
sitetoboggan:seedscar+strat	0.20137	0.68780	0.293	0.770133
siteulm:seedscar+strat	1.46592	0.61491	2.384	0.018479
sitepioneer:seedstrat	0.07272	0.55811	0.130	0.896522
sitethompson:seedstrat	0.69073	0.54866	1.259	0.210161
sitetoboggan:seedstrat	0.68328	0.67702	1.009	0.314612
siteulm:seedstrat	2.02245	0.58307	3.469	0.000697
sitepioneer:cage	-0.08794	0.95675	-0.092	0.926899
sitethompson:cage	-1.07758	0.84073	-1.282	0.202076

sitetoboggan:cage	0.04994	0.92448	0.054	0.956999
siteulm:cage	-0.06304	0.79128	-0.080	0.936621
sitegold:block.new2:cage	-0.42060	0.86480	-0.486	0.627482
sitepioneer:block.new2:cage	-1.22777	0.87187	-1.408	0.161303
sitethompson:block.new2:cage	NA	NA	NA	NA
sitetoboggan:block.new2:cage	NA	NA	NA	NA
siteulm:block.new2:cage	NA	NA	NA	NA
sitegold:block.new3:cage	0.62352	0.90103	0.692	0.490082
sitepioneer:block.new3:cage	-0.19869	0.82828	-0.240	0.810775
sitethompson:block.new3:cage	1.30137	0.80902	1.609	0.109976
sitetoboggan:block.new3:cage	NA	NA	NA	NA
siteulm:block.new3:cage	NA	NA	NA	NA
sitegold:block.new4:cage	1.04755	0.94576	1.108	0.269934
sitepioneer:block.new4:cage	NA	NA	NA	NA
sitethompson:block.new4:cage	1.04923	0.80931	1.296	0.196965
sitetoboggan:block.new4:cage	-2.17702	0.88905	-2.449	0.015582
siteulm:block.new4:cage	1.41641	0.85074	1.665	0.098181 .
sitegold:block.new5:cage	0.35595	0.91754	0.388	0.698660
sitepioneer:block.new5:cage	0.11007	0.93739	0.117	0.906692
sitethompson:block.new5:cage	1.91362	0.77747	2.461	0.015066
sitetoboggan:block.new5:cage	-0.61488	1.01933	-0.603	0.547346
siteulm:block.new5:cage	-0.26229	1.09396	-0.240	0.810868

(Dispersion parameter for quasibinomial family taken to be 1.392353)

Null deviance: 599.20 on 191 degrees of freedom
Residual deviance: 211.81 on 139 degrees of freedom

Table A.8: Complete summary of final model of survival (NA's are a result of combining blocks).

Calculations:

Calculation for Standard Error Multiplier to Correct for Extra-Binomial Variation:

Sqrt(dispersion parameter from saturated model)
Sqrt(1.6222)
= 1.273678138

Calculation of Inflated Standard Errors

sqrt(sum of variance and co-variance terms used) * (dispersion parameter) = inflated SE

Gold Pass

Control	0.57004 * 1.273678138 = 0.72605
Scar	sqrt(0.31866) * 1.273678138 = 0.71899
Scar + Strat	sqrt(0.296556) * 1.273678138 = 0.69361
Strat	sqrt(0.254237) * 1.273678138 = 0.64221

Pioneer Mountain

Control	sqrt(0.35062) * 1.273678138 = 0.7542
Scar	sqrt(0.30783) * 1.273678138 = 0.7067
Scar + Strat	sqrt(0.14961) * 1.273678138 = 0.4927
Strat	sqrt(0.27981) * 1.273678138 = 0.6737

Thompson Peak

Control	sqrt(0.19191) * 1.273678138 = 0.55666
Scar	sqrt(0.26409) * 1.273678138 = 0.65454
Scar + Strat	sqrt(0.156358) * 1.273678138 = 0.50364
Strat	sqrt(0.17156) * 1.273678138 = 0.52755

Toboggan Ridge

Control	sqrt(0.23568) * 1.273678138 = 0.6183
Scar	sqrt(0.21358) * 1.273678138 = 0.5886
Scar + Strat	sqrt(0.26833) * 1.273678138 = 0.6598
Strat	sqrt(0.27895) * 1.273678138 = 0.6727

Ulm Peak

Control	sqrt(0.229428) * 1.273678138 = 0.6101
Scar	sqrt(0.583768) * 1.273678138 = 0.9732
Scar + Strat	sqrt(0.129298) * 1.273678138 = 0.4580
Strat	sqrt(0.119178) * 1.273678138 = 0.4397

80% Confidence Interval Calculations

Survival probabilities of estimates and confidence intervals are in parentheses. These were calculated from logit link function: (logit = log(Yi / 1 – Yi).
Y1 = Pr(survival) = logit^{-1}(estimate)
logit^{-1} can be calculated in R via the 'arm' package using the following code: invlogit(estimate).

Gold Pass

Control -0.43262 or (39.4%) + and – 0.842(0.72605) = (-1.044, 0.1787) or (26.0%, 54.5%)
Scar -0.36553 or (41.0%) + and – 0.842(0.71899) = (-0.9709, 0.2399) or (27.5%, 56.0%)
Scar + Strat -0.61750 or (35.0%) + and – 0.842(0.4927) = (-1.2015, -0.0335) or (23.1%, 49.2%)
Strat -1.01040 or (26.7%) + and – 0.842(0.64221) = (-1.5511, -0.4697) or (17.5%, 38.5%)

Pioneer Mountain

Control 0.89088 or (70.9%) + and – 0.842(0.7542) = (0.2558, 1.5259) or (56.4%, 82.1%)
Scar 0.90863 or (71.3%) + and – 0.842(0.7067) = (0.3136, 1.5037) or (57.8%, 81.8%)
Scar + Strat -0.3160 or (42.2%) + and – 0.842(0.4927) = (-0.7309, 0.0989) or (32.5%, 52.5%)
Strat 0.38582 or (59.5%) + and – 0.842(0.6737) = (-0.1814, 0.9531) or (45.5%, 72.2%)

Thompson Peak

Control 1.25291 or (77.8%) + and – 0.842(0.55666) = (0.7842, 1.7216) or (68.7%, 84.8%)
Scar 0.59934 or (64.6%) + and – 0.842(0.65454) = (0.0482, 1.1505) or (51.2%, 76.0%)
Scar + Strat 0.8718 or (70.5%) + and – 0.842(0.50364) = (0.4477, 1.2959) or (61.0%, 78.5%)
Strat 1.36589 or (79.7%) + and – 0.842(0.52755) = (0.9217, 1.8101) or (71.5%, 85.9%)

Toboggan Ridge

Control 1.94137 or (87.5%) + and – 0.842(0.6183) = (1.4208, 2.4620) or (80.6%, 92.1%)
Scar 1.3980 or (80.2%) + and – 0.842(0.5886) = (0.9024, 1.8936) or (71.1%, 86.9%)
Scar + Strat 1.9579 or (87.6%) + and – 0.842(0.6598) = (1.4023, 2.5135) or (80.3%, 92.5%)
Strat 2.0469 or (88.6%) + and – 0.842(0.6727) = (1.4805, 2.6133) or (81.5%, 93.2%)

Ulm Peak

Control -1.92118 or (12.8%) + and – 0.842(0.6101) = (-2.4349, -1.4075) or (8.1%, 19.7%)
Scar -2.1566 or (10.4%) + and – 0.842(0.9732) = (-2.976, -1.3372) or (4.9%, 20.8%)
Scar + Strat -0.6401 or (34.5%) + and – 0.842(0.4580) = (-1.0257, -0.2545) or (26.4%, 43.7%)
Strat -0.4765 or (38.3%) + and – 0.842(0.4397) = (-0.8467, -0.1063) or (30.0%, 47.4%)

APPENDIX D

COMBINED GERMINATION AND SURVIVAL TABLES AND CALCULATIONS

Appendix D – Combined Germination and Survival Tables and Calculations

Model 2 (Combined Germination and Survival) – Model After Combining Blocks
model.2 <- glm(cbind(survived, nogermsurv) ~ site/block.new + cage * seed + cage * site + seed * site + seed* (site/block.new) + cage * (site/block.new) + cage * seed * site, family = binomial, data = dat)

Model 3 (Combined Germination and Survival) – Quasibinomial Model
model.3 <- glm(cbind(survived, nogermsurv) ~ site/block.new + cage * seed + cage * site + seed * site + seed* (site/block.new) + cage * (site/block.new) + cage * seed * site, family = quasibinomial, data = dat)

Model 4 (Combined Germination and Survival) – Removing cage*seed*site
model.4 <- glm(cbind(survived, nogermsurv) ~ site/block.new + cage * seed + cage * site + seed * site + seed* (site/block.new) + cage * (site/block.new), family = quasibinomial, data = dat)

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	87	176.46			
2	75	154.66	12	21.795	0.5067

Table A.9: Results of the drop in deviance Chi-squared test of model 4 (combined germination and survival) compared to model 3 (combined germination and survival).

Model 5 (Combined Germination and Survival) – Removing cage * (site/block.new)
model.5 <- glm(cbind(survived, nogermsurv) ~ site/block.new + cage * seed + cage * site + seed * site + seed* (site/block.new), family = quasibinomial, data = dat)

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	104	261.85			
2	87	176.46	17	85.387	3.9860E-04

Table A.10: Results of the drop in deviance Chi-squared test of model 5 (combined germination and survival) compared to model 4 (combined germination and survival).

Model 6 (Combined Germination and Survival) - Removing cage*site
model.6 <- glm(cbind(survived, nogermsurv) ~ site/block.new + cage * seed + seed * site + seed*(site/block.new), family = quasibinomial, data = dat)

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	108	279.8			
2	104	261.85	4	17.959	0.1199

Table A.11: Results of the drop in deviance Chi-squared test of model 6 (combined germination and survival) compared to model 5 (combined germination and survival).

Model 7 (Combined Germination and Survival) - Removing cage*seed
model.7 <- glm(cbind(survived, nogermsurv) ~ site/block.new + seed*site + seed*(site/block.new), family = quasibinomial, data = dat)

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	112	322.56			
2	108	279.8	4	42.753	0.0016

Table A.12: Results of the drop in deviance Chi-squared test of model 7 (combined germination and survival) compared to model 6 (combined germination and survival).

Model 8 (Combined Germination and Survival) - Removing seed*(site/block.new)
model.8 <- glm(cbind(survived, nogermsurv) ~ site/block.new + seed*site, family = quasibinomial, data = dat)

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	163	434.03			
2	112	322.56	51	111.48	0.8114

Table A.13: Results of the drop in deviance Chi-squared test of model 8 (combined germination and survival) compared to model 7 (combined germination and survival).

Model 9 (Combined Germination and Survival) - Removing seed*site
model.9 <- glm(cbind(survived, nogermsurv) ~ site/block.new, family = quasibinomial, data = dat)

Analysis of Deviance Table

	Resid. Df	Resid. Dev	Df	Deviance	P(>|Chi|)
1	178	588.42			
2	163	434.03	15	154.38	7.8060E-08

Table A.14: Results of the drop in deviance Chi-squared test of model 9 (combined germination and survival) compared to model 8 (combined germination and survival).

Coefficients:

	Estimate	Std. Error	t value	Pr(>|t|)	
(Intercept)	-2.14591	0.53677	-3.998	0.000103	
sitepioneer	0.37338	0.71148	0.525	0.600554	
sitethompson	1.43538	0.67178	2.137	0.034351	
sitetoboggan	2.28682	0.64660	3.537	0.000549	
siteulm	-0.96513	0.72999	-1.322	0.188271	
seedscar	-0.50209	0.35262	-1.424	0.156689	
seedscar+strat	0.19741	0.32645	0.605	0.546337	
seedstrat	0.44583	0.31686	1.407	0.161621	
cage	0.77583	0.64374	1.205	0.230143	
sitegold:block.new2	0.68845	0.63281	1.088	0.278485	
sitepioneer:block.new2	0.08225	0.49182	0.167	0.867418	
sitethompson:block.new2	-0.37499	0.50250	-0.746	0.456759	
sitetoboggan:block.new2	-1.50567	0.51617	-2.917	0.004114	
siteulm:block.new2	NA	NA	NA	NA	
sitegold:block.new3	0.84069	0.62288	1.350	0.179281	
sitepioneer:block.new3	0.93358	0.52326	1.784	0.076545	.
sitethompson:block.new3	-1.21107	0.57569	-2.104	0.037183	
sitetoboggan:block.new3	-0.98665	0.47287	-2.087	0.038732	
siteulm:block.new3	NA	NA	NA	NA	
sitegold:block.new4	0.52146	0.64563	0.808	0.420638	
sitepioneer:block.new4	NA	NA	NA	NA	
sitethompson:block.new4	-1.10638	0.56315	-1.965	0.051423	.
sitetoboggan:block.new4	-0.15126	0.44297	-0.341	0.733257	
siteulm:block.new4	-0.75544	0.79127	-0.955	0.341353	
sitegold:block.new5	1.00049	0.61556	1.625	0.106326	
sitepioneer:block.new5	-0.49047	0.62465	-0.785	0.433655	
sitethompson:block.new5	-0.97907	0.55360	-1.769	0.079131	.
sitetoboggan:block.new5	-0.40943	0.44769	-0.915	0.361999	
siteulm:block.new5	-0.78440	0.79077	-0.992	0.322924	
sitepioneer:seedscar	1.25092	0.49292	2.538	0.012243	
sitethompson:seedscar	-0.57429	0.54868	-1.047	0.297048	
sitetoboggan:seedscar	0.20929	0.46074	0.454	0.650344	
siteulm:seedscar	-0.73468	0.88739	-0.828	0.409123	
sitepioneer:seedscar+strat	-0.53308	0.50279	-1.060	0.290853	
sitethompson:seedscar+strat	0.19249	0.46788	0.411	0.681407	
sitetoboggan:seedscar+strat	-0.51369	0.44140	-1.164	0.246482	
siteulm:seedscar+strat	1.09962	0.57993	1.896	0.059991	.
sitepioneer:seedstrat	0.13055	0.46984	0.278	0.781528	
sitethompson:seedstrat	0.07096	0.45988	0.154	0.877592	
sitetoboggan:seedstrat	-0.60093	0.43202	-1.391	0.166428	
siteulm:seedstrat	1.30631	0.56441	2.314	0.022086	
sitepioneer:cage	0.21379	0.82872	0.258	0.796807	

sitethompson:cage	-1.51513	0.83270	-1.820	0.070951 .
sitetoboggan:cage	-1.02911	0.78222	-1.316	0.190438
siteulm:cage	0.02753	0.75591	0.036	0.971002
sitegold:block.new2:cage	-0.16561	0.82742	-0.200	0.841650
sitepioneer:block.new2:cage	-2.09632	0.72696	-2.884	0.004547
sitethompson:block.new2:cage	1.05979	0.72796	1.456	0.147662
sitetoboggan:block.new2:cage	1.07545	0.69093	1.557	0.121826
siteulm:block.new2:cage	NA	NA	NA	NA
sitegold:block.new3:cage	0.15583	0.81264	0.192	0.848209
sitepioneer:block.new3:cage	-0.18886	0.69609	-0.271	0.786545
sitethompson:block.new3:cage	0.73930	0.83706	0.883	0.378629
sitetoboggan:block.new3:cage	1.18965	0.64906	1.833	0.068930 .
siteulm:block.new3:cage	NA	NA	NA	NA
sitegold:block.new4:cage	-0.05886	0.83882	-0.070	0.944154
sitepioneer:block.new4:cage	NA	NA	NA	NA
sitethompson:block.new4:cage	0.63461	0.82849	0.766	0.444967
sitetoboggan:block.new4:cage	-0.51830	0.64679	-0.801	0.424284
siteulm:block.new4:cage	1.25923	0.91480	1.377	0.170846
sitegold:block.new5:cage	0.12598	0.80520	0.156	0.875895
sitepioneer:block.new5:cage	0.31987	0.78201	0.409	0.683131
sitethompson:block.new5:cage	2.61895	0.75954	3.448	0.000745
sitetoboggan:block.new5:cage	-0.07857	0.64324	-0.122	0.902956
siteulm:block.new5:cage	0.48613	0.94692	0.513	0.608491

(Dispersion parameter for quasibinomial family taken to be 1.94398)

Null deviance: 822.26 on 199 degrees of freedom
Residual deviance: 296.57 on 141 degrees of freedom

Table A.15: Complete summary of final model of combined germination and survival(NA's are a result of combining blocks).

Calculations:

Calculation for Standard Error Multiplier to Correct for Extra-Binomial Variation:

Sqrt(dispersion parameter from saturated model)
Sqrt(1.9353)
= 1.391166058

Calculation of Inflated Standard Errors

sqrt(sum of variance and co-variance terms used) * (dispersion parameter) = inflated SE

Gold Pass

Control	0.53677 * 1.391166058 = 0.74674
Scar	sqrt(0.30818) * 1.391166058 = 0.77229
Scar + Strat	sqrt(0.28325) * 1.391166058 = 0.74040
Strat	sqrt(0.27550)* 1.391166058 = 0.73020

Pioneer Mountain

Control	sqrt(0.2549) * 1.391166058 = 0.70237
Scar	sqrt(0.23377) * 1.391166058 = 0.67263
Scar + Strat	sqrt(0.27007) * 1.391166058 = 0.72296
Strat	sqrt(0.23727) * 1.391166058 = 0.67764

Thompson Peak

Control	sqrt(0.19999) * 1.391166058 = 0.62213
Scar	sqrt(0.25382) * 1.391166058 = 0.70088
Scar + Strat	sqrt(0.11518) * 1.391166058 = 0.47214
Strat	sqrt(0.19504) * 1.391166058 = 0.61439

Toboggan Ridge

Control	sqrt(0.16679) * 1.391166058 = 0.56815
Scar	sqrt(0.16833) * 1.391166058 = 0.57077
Scar + Strat	sqrt(0.16856) * 1.391166058 = 0.57116
Strat	sqrt(0.16737) * 1.391166058 = 0.56914

Ulm Peak

Control	sqrt(0.28158) * 1.391166058 = 0.53064
Scar	sqrt(0.620406) * 1.391166058 = 1.09576
Scar + Strat	sqrt(0.05780) * 1.391166058 = 0.33446
Strat	sqrt(0.15896) * 1.391166058 = 0.55466

80% Confidence Interval Calculations

Combined germination and survival probabilities of estimates and confidence intervals are in parentheses. These were calculated from logit link function: (logit = log(Yi / 1 – Yi).
Y1 = Pr(germination and survival) = logit^{-1}(estimate)
logit^{-1} can be calculated in R via the ‘arm’ package using the following code: invlogit(estimate).

Gold Pass

Control -2.14591 or (10.5%) + and – 0.842(0.74674) = (-2.7747, -1.51715) or (5.9%, 18.0%)
Scar -2.64800 or (6.6%) + and – 0.842(0.77229) = (-3.2983, -1.99773) or (3.6%, 11.9%)
Scar + Strat -1.94850 or (12.5%) + and – 0.842(0.74040) = (-2.5719, -1.32508) or (7.1%, 21.0%)
Strat -1.70008 or (15.5%) + and – 0.842(0.73020) = (-2.3149, -1.08525) or (9.0%, 25.3%)

Pioneer Mountain

Control -1.77253 or (14.5%) + and – 0.842(0.70237) = (-2.3639, -1.1811) or (8.6%, 23.5%)
Scar -1.02370 or (26.4%) + and – 0.842(0.67263) = (-1.5901, -0.4573) or (16.9%, 38.8%)
Scar + Strat -2.10820 or (10.8%) + and – 0.842(0.72300) = (-2.7170, -1.4994) or (6.2%, 18.3%)
Strat -1.19615 or (23.2%) + and – 0.842(0.67764) = (-1.7667, -0.6256) or (14.6%, 34.9%)

Thompson Peak

Control -0.71053 or (33.0%) + and – 0.842(0.62213) = (-1.2344, -0.1867) or (22.5%, 45.3%)
Scar -1.78691 or (14.3%) + and – 0.842(0.70088) = (-2.3771, -1.1968) or (8.5%, 23.2%)
Scar + Strat -0.32063 or (42.1%) + and – 0.842(0.47214) = (-0.7182, 0.0769) or (32.8%, 51.9%)
Strat -0.19374 or (45.2%) + and – 0.842(0.61439) = (-0.7111, 0.3236) or (32.9%, 58.0%)

Toboggan Ridge

Control 0.14091 or (53.5%) + and – 0.842(0.56815) = (-0.33747, 0.61929) or (41.6%, 65.0%)
Scar -0.15189 or (46.2%) + and – 0.842(0.57077) = (-0.63248, 0.32870) or (34.7%, 58.1%)
Scar + Strat -0.17537 or (45.6%) + and – 0.842(0.57116) = (-0.65629, 0.30555) or (34.2%, 57.6%)
Strat -0.01419 or (49.7%) + and – 0.842(0.56914) = (-0.49341, 0.46503) or (37.9%, 61.4%)

Ulm Peak

Control -3.11104 or (4.3%) + and – 0.842(0.53064) = (-3.55784, -2.66424) or (2.7%, 6.5%)
Scar -4.34781 or (1.3%) + and – 0.842(1.09576) = (-5.27044, -3.42518) or (0.5%, 3.2%)
Scar + Strat -1.81401 or (14.0%) + and – 0.842(0.33446) = (-2.0956, -1.53240) or (11.0%, 17.8%)
Strat -1.35890 or (20.4%) + and – 0.842(0.55466) = (-1.82592, -0.89188) or (13.8%, 29.1%)

APPENDIX E

TEMPERATURE FINAL MODEL SUMMARY AND CALCULATIONS

Appendix E – Temperature Summary of Final Model

Coefficients:

	Estimate	Std. Error	z value	Pr(>|z|)
(Intercept)	-0.093940	0.351435	-0.267	0.7892
treatmentsc	0.039685	0.160561	0.247	0.8048
treatmentscst	-0.281237	0.143328	-1.962	0.0497
treatmentst	-0.130792	0.138742	-0.943	0.3458
temp	0.008784	0.004893	1.795	0.0726

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 599.20 on 191 degrees of freedom
Residual deviance: 590.26 on 187 degrees of freedom

Table A.16: Complete summary of final model of temperature.

Calculations

Scaled total number of days under 30 degrees Fahrenheit and over 90 degrees Fahrenheit

Scaled Total = (Actual Total) * (400 / # of days of data)

Gold Pass

Scaled Total = (107) * (400 / 701)
Scaled Total = 61.1

Thompson Peak

Scaled Total = (85) * (400 / 386)
Scaled Total = 88.1

Pioneer Mountain

Scaled Total = (178) * (400 / 1055)
Scaled Total = 67.5

Toboggan Ridge

Scaled Total = (125) * (400 / 736)
Scaled Total = 67.9

Ulm Peak

Scaled Total = (50) * (400 / 346)
Scaled Total = 57.8

APPENDIX F

R CODE

Appendix F – R code

Germination

```
# INITIAL ENTRY OF THE DATA
Dat  <- read.csv("ClayData4.csv", header = T)
dat$seed <- dat$treatment
dat$planted <- dat$germ + dat$nogerm
dat$died <- with(dat, planted - survived)
dat$Cage <- ifelse(dat$cage == 1, "cage", "nocage")
dat$block <- ifelse(dat$block == "one", "1", ifelse(dat$block == "two", "2",
ifelse(dat$block =="three", "3", ifelse(dat$block == "four", "4", "5"))))
dat$site <- ifelse(dat$site == "goldpass", "gold", ifelse(dat$site == "fairylake", "fairy",
ifelse(dat$site =="tobogganridge", "toboggan", ifelse(dat$site == "thompsonpeak",
"thompson", ifelse(dat$site =="pioneermountain", "pioneer", "ulm")))))
dat$seed <- ifelse(dat$seed == "st", "strat", ifelse(dat$seed == "sc", "scar",
ifelse(dat$seed =="scst", "scar+strat", "control")))

#Model 1
model.1 <- glm(cbind(germ, nogerm) ~ site/block + cage * seed + cage * site + seed *
site + seed *(site/block) + cage * (site/block) + cage * seed * site, family = binomial, data
= dat)

# Before re-coding I saved the data as dat.prelim only to use in the preliminary plots in
the
dat.prelim <- dat

#Recoding Ulm Peak
dat$block.new <- dat$block
dat$block.new[dat$site == "ulm" & dat$block == 3 & dat$seed == "scar"] <- 1

#Model 2
model.2 <- glm(cbind(germ, nogerm) ~ site/block.new + cage * seed + cage * site + seed
* site + seed* (site/block.new) + cage * (site/block.new) + cage * seed * site, family =
binomial, data = dat)

#Model 3
model.3 <- glm(cbind(germ, nogerm) ~ site/block.new + cage * seed + cage * site + seed
* site + seed* (site/block.new) + cage * (site/block.new) + cage * seed * site, family =
quasibinomial, data = dat)
```

```
#Model 4
model.4 <- glm(cbind(germ, nogerm) ~ site/block.new + cage * seed + cage * site + seed
* site + seed* (site/block.new) + cage * (site/block.new), family = quasibinomial, data =
dat)

anova(model.4, model.3, test= "Chisq")

#Model 5
model.5 <- glm(cbind(germ, nogerm) ~ site/block.new + cage * seed + cage * site + seed
* site + seed* (site/block.new), family = quasibinomial, data = dat)

anova(model.5, model.4, test= "Chisq")

#Model 6
model.6 <- glm(cbind(germ, nogerm) ~ site/block.new + cage * seed + cage * site + seed
* site, family = quasibinomial, data = dat)

anova(model.6, model.5, test= "Chisq")

#Model 7
model.7 <- glm(cbind(germ, nogerm) ~ site/block.new + cage * seed + cage * site,
family = quasibinomial, data = dat)

anova(model.7, model.6, test="Chisq")

#Model 8
model.8 <- glm(cbind(germ, nogerm) ~ site/block.new + cage*seed + seed*site,
family = quasibinomial, data = dat)

anova(model.8, model.6, test="Chisq")

#Model 9
model.9 <- glm(cbind(germ, nogerm) ~ site/block.new, family = quasibinomial, data =
dat)

anova(model.9, model.8, test="Chisq")

#Final Model Germ
model.final.germ<-glm(cbind(germ,nogerm)~ site/block.new + seed*site +
cage*(site/block.new),
family=quasibinomial, data = dat)
```

```
#Figure 3
par(mfrow = c(2, 2))
scarC <- subset(dat, cage == 1 & site == "pioneer" & seed == "scar")
scar <- subset(dat, cage == 0 & site == "pioneer" & seed == "scar")
stratC <- subset(dat, cage == 1 & site == "pioneer" & seed == "strat")
strat <- subset(dat, cage == 0 & site == "pioneer" & seed == "strat")
controlC <- subset(dat, cage == 1 & site == "pioneer" & seed == "control")
control <- subset(dat, cage == 0 & site == "pioneer" & seed == "control")
scarStratC <- subset(dat, cage == 1 & site == "pioneer" & seed == "scar+strat")
scarStrat <- subset(dat, cage == 0 & site == "pioneer" & seed == "scar+strat")
plot(germ ~ block, ylim = c(0, 20), data = scarC, main = "Cage Effect for Scar", ylab =
"germinated",col = "red")with(scar, points(block, germ, col = "red", pch = 4))
plot(germ ~ block, ylim = c(0, 20), data = stratC, main = "Cage Effect for Strat", ylab =
"germinated",col = "blue")with(strat, points(block, germ, col = "blue", pch =
4))plot(germ ~ block, ylim = c(0, 20), data = controlC, main = "Cage Effect for Control",
ylab = "germinated",col = "black")with(control, points(block, germ, col = "black", pch =
4))plot(germ ~ block, ylim = c(0, 20), data = scarStratC, main = "Cage Effect Scar &
Strat", ylab = "germinated",col = "orange")with(scarStrat, points(block, germ, col =
"orange", pch = 4))

#Figure 4
resid1 <- resid(model.1)
predict1 <- predict(model.1)
plot(resid1 ~ predict1, main = "", xlab = "Predicted Values", ylab = "Residuals")
abline(a = 0, 0, col = "black", lty = 8)
abline(a = 2, b = 0, col = "red", lty = 2)
abline(a = -2, b = 0, col = "red", lty = 2)

#Figure 6
resid2 <- resid(model.2)
predict2 <- predict(model.2)
plot(resid2 ~ predict2, main = "", xlab = "Predicted Values", ylab = "Residuals")
abline(a = 0, 0, col = "black", lty = 8)
abline(a = 2, b = 0, col = "red", lty = 2)
abline(a = -2, b = 0, col = "red", lty = 2)

#Figure A.1
par(mfrow = c(4, 2))
scarC <- subset(dat.prelim, cage == 1 & site == "fairy" & seed == "scar")
scar <- subset(dat.prelim, cage == 0 & site == "fairy" & seed == "scar")
stratC <- subset(dat.prelim, cage == 1 & site == "fairy" & seed == "strat")
strat <- subset(dat.prelim, cage == 0 & site == "fairy" & seed == "strat")
controlC <- subset(dat.prelim, cage == 1 & site == "fairy" & seed == "control")
control <- subset(dat.prelim, cage == 0 & site == "fairy" & seed == "control")
```

```
scarStratC <- subset(dat.prelim, cage == 1 & site == "fairy" & seed == "scar+strat")
scarStrat <- subset(dat.prelim, cage == 0 & site == "fairy" & seed == "scar+strat")
plot(germ ~ block, ylim = c(0, 20), data = scarC, main = "Fairy Lake", ylab =
"germinated", col = "red")
with(scarC, lines(stats::lowess(germ), col = "red"))
with(scar, lines(stats::lowess(germ), col = "blue"))
with(scar, points(block, germ, col = "blue"))
with(strat, lines(stats::lowess(germ), col = "yellow"))
with(strat, points(block, germ, col = "yellow"))
with(stratC, lines(stats::lowess(germ), col = "black"))
with(stratC, points(block, germ, col = "black"))
with(control, lines(stats::lowess(germ), col = "green"))
with(control, points(block, germ, col = "green"))
with(controlC, lines(stats::lowess(germ), col = "grey"))
with(controlC, points(block, germ, col = "grey"))
with(scarStratC, lines(stats::lowess(germ), points = germ, col = "purple"))
with(scarStratC, points(block, germ, col = "purple"))
with(scarStrat, lines(stats::lowess(germ), points = germ, col = "orange"))
with(scarStrat, points(block, germ, col = "orange"))
scarC <- subset(dat.prelim, cage == 1 & site == "gold" & seed == "scar")
scar <- subset(dat.prelim, cage == 0 & site == "gold" & seed == "scar")
stratC <- subset(dat.prelim, cage == 1 & site == "gold" & seed == "strat")
strat <- subset(dat.prelim, cage == 0 & site == "gold" & seed == "strat")
controlC <- subset(dat.prelim, cage == 1 & site == "gold" & seed == "control")
control <- subset(dat.prelim, cage == 0 & site == "gold" & seed == "control")
scarStratC <- subset(dat.prelim, cage == 1 & site == "gold" & seed == "scar+strat")
scarStrat <- subset(dat.prelim, cage == 0 & site == "gold" & seed == "scar+strat")
plot(germ ~ block, ylim = c(0, 20), data = scarC, main = "Gold Pass", ylab =
"germinated", col = "red")
with(scarC, lines(stats::lowess(germ), col = "red"))
with(scar, lines(stats::lowess(germ), col = "blue"))
with(scar, points(block, germ, col = "blue"))
with(strat, lines(stats::lowess(germ), col = "yellow"))
with(strat, points(block, germ, col = "yellow"))
with(stratC, lines(stats::lowess(germ), col = "black"))
with(stratC, points(block, germ, col = "black"))
with(control, lines(stats::lowess(germ), col = "green"))
with(control, points(block, germ, col = "green"))
with(controlC, lines(stats::lowess(germ), col = "grey"))
with(controlC, points(block, germ, col = "grey"))
with(scarStratC, lines(stats::lowess(germ), points = germ, col = "purple"))
with(scarStratC, points(block, germ, col = "purple"))
with(scarStrat, lines(stats::lowess(germ), points = germ, col = "orange"))
with(scarStrat, points(block, germ, col = "orange"))
```

```
scarC <- subset(dat.prelim, cage == 1 & site == "pioneer" & seed == "scar")
scar <- subset(dat.prelim, cage == 0 & site == "pioneer" & seed == "scar")
stratC <- subset(dat.prelim, cage == 1 & site == "pioneer" & seed == "strat")
strat <- subset(dat.prelim, cage == 0 & site == "pioneer" & seed == "strat")
controlC <- subset(dat.prelim, cage == 1 & site == "pioneer" & seed == "control")
control <- subset(dat.prelim, cage == 0 & site == "pioneer" & seed == "control")
scarStratC <- subset(dat.prelim, cage == 1 & site == "pioneer" & seed == "scar+strat")
scarStrat <- subset(dat.prelim, cage == 0 & site == "pioneer" & seed == "scar+strat")
plot(germ ~ block, ylim = c(0, 20), data = scarC, main = "Pioneer Mountain", ylab =
"germinated",
col = "red")
with(scarC, lines(stats::lowess(germ), col = "red"))
with(scar, lines(stats::lowess(germ), col = "blue"))
with(scar, points(block, germ, col = "blue"))
with(strat, lines(stats::lowess(germ), col = "yellow"))
with(strat, points(block, germ, col = "yellow"))
with(stratC, lines(stats::lowess(germ), col = "black"))
with(stratC, points(block, germ, col = "black"))
with(control, lines(stats::lowess(germ), col = "green"))
with(control, points(block, germ, col = "green"))
with(controlC, lines(stats::lowess(germ), col = "grey"))
with(controlC, points(block, germ, col = "grey"))
with(scarStratC, lines(stats::lowess(germ), points = germ, col = "purple"))
with(scarStratC, points(block, germ, col = "purple"))
with(scarStrat, lines(stats::lowess(germ), points = germ, col = "orange"))
with(scarStrat, points(block, germ, col = "orange"))
scarC <- subset(dat.prelim, cage == 1 & site == "thompson" & seed == "scar")
scar <- subset(dat.prelim, cage == 0 & site == "thompson" & seed == "scar")
stratC <- subset(dat.prelim, cage == 1 & site == "thompson" & seed == "strat")
strat <- subset(dat.prelim, cage == 0 & site == "thompson" & seed == "strat")
controlC <- subset(dat.prelim, cage == 1 & site == "thompson" & seed == "control")
control <- subset(dat.prelim, cage == 0 & site == "thompson" & seed == "control")
scarStratC <- subset(dat.prelim, cage == 1 & site == "thompson" & seed == "scar+strat")
scarStrat <- subset(dat.prelim, cage == 0 & site == "thompson" & seed == "scar+strat")
plot(germ ~ block, ylim = c(0, 20), data = scarC, main = "Thompson Peak", ylab =
"germinated", col = "red")
with(scarC, lines(stats::lowess(germ), col = "red"))
with(scar, lines(stats::lowess(germ), col = "blue"))
with(scar, points(block, germ, col = "blue"))
with(strat, lines(stats::lowess(germ), col = "yellow"))
with(strat, points(block, germ, col = "yellow"))
with(stratC, lines(stats::lowess(germ), col = "black"))
with(stratC, points(block, germ, col = "black"))
with(control, lines(stats::lowess(germ), col = "green"))
```

```
with(control, points(block, germ, col = "green"))
with(controlC, lines(stats::lowess(germ), col = "grey"))
with(controlC, points(block, germ, col = "grey"))
with(scarStratC, lines(stats::lowess(germ), points = germ, col = "purple"))
with(scarStratC, points(block, germ, col = "purple"))
with(scarStrat, lines(stats::lowess(germ), points = germ, col = "orange"))
with(scarStrat, points(block, germ, col = "orange"))
scarC <- subset(dat.prelim, cage == 1 & site == "toboggan" & seed == "scar")
scar <- subset(dat.prelim, cage == 0 & site == "toboggan" & seed == "scar")
stratC <- subset(dat.prelim, cage == 1 & site == "toboggan" & seed == "strat")
strat <- subset(dat.prelim, cage == 0 & site == "toboggan" & seed == "strat")
controlC <- subset(dat.prelim, cage == 1 & site == "toboggan" & seed == "control")
control <- subset(dat.prelim, cage == 0 & site == "toboggan" & seed == "control")
scarStratC <- subset(dat.prelim, cage == 1 & site == "toboggan" & seed == "scar+strat")
scarStrat <- subset(dat.prelim, cage == 0 & site == "toboggan" & seed == "scar+strat")
plot(germ ~ block, ylim = c(0, 20), data = scarC, main = "Toboggan Ridge", ylab =
"germinated",
col = "red")
with(scarC, lines(stats::lowess(germ), col = "red"))
with(scar, lines(stats::lowess(germ), col = "blue"))
with(scar, points(block, germ, col = "blue"))
with(strat, lines(stats::lowess(germ), col = "yellow"))
with(strat, points(block, germ, col = "yellow"))
with(stratC, lines(stats::lowess(germ), col = "black"))
with(stratC, points(block, germ, col = "black"))
with(control, lines(stats::lowess(germ), col = "green"))
with(control, points(block, germ, col = "green"))
with(controlC, lines(stats::lowess(germ), col = "grey"))
with(controlC, points(block, germ, col = "grey"))
with(scarStratC, lines(stats::lowess(germ), points = germ, col = "purple"))
with(scarStratC, points(block, germ, col = "purple"))
with(scarStrat, lines(stats::lowess(germ), points = germ, col = "orange"))
with(scarStrat, points(block, germ, col = "orange"))
scarC <- subset(dat.prelim, cage == 1 & site == "ulm" & seed == "scar")
scar <- subset(dat.prelim, cage == 0 & site == "ulm" & seed == "scar")
stratC <- subset(dat.prelim, cage == 1 & site == "ulm" & seed == "strat")
strat <- subset(dat.prelim, cage == 0 & site == "ulm" & seed == "strat")
controlC <- subset(dat.prelim, cage == 1 & site == "ulm" & seed == "control")
control <- subset(dat.prelim, cage == 0 & site == "ulm" & seed == "control")
scarStratC <- subset(dat.prelim, cage == 1 & site == "ulm" & seed == "scar+strat")
scarStrat <- subset(dat.prelim, cage == 0 & site == "ulm" & seed == "scar+strat")
plot(germ ~ block, ylim = c(0, 20), data = scarC, main = "Ulm Peak", ylab =
"germinated", col = "red")
with(scarC, lines(stats::lowess(germ), col = "red"))
```

```
with(scar, lines(stats::lowess(germ), col = "blue"))
with(scar, points(block, germ, col = "blue"))
with(strat, lines(stats::lowess(germ), col = "yellow"))
with(strat, points(block, germ, col = "yellow"))
with(stratC, lines(stats::lowess(germ), col = "black"))
with(stratC, points(block, germ, col = "black"))
with(control, lines(stats::lowess(germ), col = "green"))
with(control, points(block, germ, col = "green"))
with(controlC, lines(stats::lowess(germ), col = "grey"))
with(controlC, points(block, germ, col = "grey"))
with(scarStratC, lines(stats::lowess(germ), points = germ, col = "purple"))
with(scarStratC, points(block, germ, col = "purple"))
with(scarStrat, lines(stats::lowess(germ), points = germ, col = "orange"))
with(scarStrat, points(block, germ, col = "orange"))
plot_colors <- c("red", "blue", "yellow", "black", "green", "grey", "purple", "orange")
text <- c("scar:cage", "scar", "strat", "strat:cage", "control", "control:cage",
"scar+strat:cage",
"scar+strat")
plot.new()
par(xpd = TRUE)
legend("top", legend = text, text.width = max(sapply(text, strwidth)), col = plot_colors,
lwd = 1,
cex = 0.6)
par(xpd = FALSE)
```

Survival

```
#Model 1
model.1 <- glm(cbind(survived, totgermsurv) ~ site/block + cage * seed + cage * site +
seed * site + seed *(site/block) + cage * (site/block) + cage * seed * site, family =
binomial, data = dat)
dat.prelim <- dat

# Re-Coding the data

#Recoding Ulm Peak
dat$block.new <- dat$block
dat$block.new[dat$site == "ulm" & dat$block == 2] <- 1
dat$block.new[dat$site == "ulm" & dat$block == 3] <- 1

#Recoding Toboggan Ridge
dat$block.new[dat$site == "toboggan" & dat$block == 2] <- 1
dat$block.new[dat$site == "toboggan" & dat$block == 3] <- 1
```

```
#Recoding Thompson Peak
dat$block.new[dat$site == "thompson" & dat$block == 2] <- 1

#Recoding Pioneer Mountain
dat$block.new[dat$site == "pioneer" & dat$block == 4] <- 2

#Model 2
model.2 <- glm(cbind(survived, totgermsurv) ~ site/block.new + cage * seed + cage *
site + seed * site + seed* (site/block.new) + cage * (site/block.new) + cage * seed * site,
family = binomial, data = dat)

#Model 3
model.3 <- glm(cbind(survived, totgermsurv) ~ site/block.new + cage * seed + cage *
site + seed * site + seed* (site/block.new) + cage * (site/block.new) + cage * seed * site,
family = quasibinomial, data = dat)

#Model 4 - Removing cage*seed*site
model.4 <- glm(cbind(survived, totgermsurv) ~ site/block.new + cage * seed + cage *
site + seed * site + seed* (site/block.new) + cage * (site/block.new), family =
quasibinomial, data = dat)

anova(model.4, model.3, test= "Chisq")

#Model 5 - Removing cage*(site/block.new)
model.5 <- glm(cbind(survived, totgermsurv) ~ site/block.new + cage * seed + cage *
site + seed * site + seed* (site/block.new), family = quasibinomial, data = dat)

anova(model.5, model.4, test= "Chisq")

#Model 6 - Removing cage*site
model.6 <- glm(cbind(survived, totgermsurv) ~ site/block.new + cage * seed + seed * site
+ seed*(site/block.new),  family = quasibinomial, data = dat)

anova(model.6, model.5, test= "Chisq")

#Model 7 - Removing cage*seed
model.7 <- glm(cbind(survived, totgermsurv) ~ site/block.new + seed*site +
seed*(site/block.new), family = quasibinomial, data = dat)

anova(model.7, model.6, test="Chisq")

#Model 8 - Removing seed*(site/block.new)
model.8 <- glm(cbind(survived, totgermsurv) ~ site/block.new + seed*site, family =
quasibinomial, data = dat)
```

```
anova(model.8, model.7, test="Chisq")

#Model 9 - Removing seed*site
model.9 <- glm(cbind(survived, totgermsurv) ~ site/block.new, family = quasibinomial,
data = dat)

anova(model.9, model.8, test="Chisq")

#Final Model Survival
model.final.survival<-(glm(cbind(survived, totgermsurv)~ site/block.new + seed*site +
cage*(site/block.new), family=quasibinomial, data = dat))
```

Survived and Germinated

```
#Model 1
model.1 <- glm(cbind(survived, nogermsurv) ~ site/block + cage * seed + cage * site +
seed * site + seed *(site/block) + cage * (site/block) + cage * seed * site, family =
binomial, data = dat)
dat.prelim <- dat
# Re-Coding the data

#Recoding Ulm Peak
dat$block.new <- dat$block
dat$block.new[dat$site == "ulm" & dat$block == 2] <- 1
dat$block.new[dat$site == "ulm" & dat$block == 3] <- 1

#Recoding Pioneer Mountain
dat$block.new[dat$site == "pioneer" & dat$block == 4] <- 2

#Model 2
model.2 <- glm(cbind(survived, nogermsurv) ~ site/block.new + cage * seed + cage * site
+ seed * site + seed* (site/block.new) + cage * (site/block.new) + cage * seed * site,
family = binomial, data = dat)

#Model 3
model.3 <- glm(cbind(survived, nogermsurv) ~ site/block.new + cage * seed + cage * site
+ seed * site + seed* (site/block.new) + cage * (site/block.new) + cage * seed * site,
family = quasibinomial, data = dat)

#Model 4 - Removing cage*seed*site
model.4 <- glm(cbind(survived, nogermsurv) ~ site/block.new + cage * seed + cage * site
+ seed * site + seed* (site/block.new) + cage * (site/block.new), family = quasibinomial,
data = dat)
```

```
anova(model.4, model.3, test= "Chisq")

#Model 5 - Removing cage*(site/block.new)
model.5 <- glm(cbind(survived, nogermsurv) ~ site/block.new + cage * seed + cage * site
+ seed * site + seed* (site/block.new), family = quasibinomial, data = dat)

anova(model.5, model.4, test= "Chisq")

#Model 6 - Removing cage*site
model.6 <- glm(cbind(survived, nogermsurv) ~ site/block.new + cage * seed + seed * site
+ seed*(site/block.new), family = quasibinomial, data = dat)

anova(model.6, model.5, test= "Chisq")

#Model 7 - Removing cage*seed
model.7 <- glm(cbind(survived, nogermsurv) ~ site/block.new + seed*site +
seed*(site/block.new), family = quasibinomial, data = dat)

anova(model.7, model.6, test="Chisq")

#Model 8 - Removing seed*(site/block.new)
model.8 <- glm(cbind(survived, nogermsurv) ~ site/block.new + seed*site, family =
quasibinomial, data = dat)

anova(model.8, model.7, test="Chisq")

#Model 9 - Removing seed*site
model.9 <- glm(cbind(survived, nogermsurv) ~ site/block.new, family = quasibinomial,
data = dat)

anova(model.9, model.8, test="Chisq")

#Final Model Combined germination and survival
model.final.germandsurv<-(glm(cbind(survived,nogermsurv)~ site/block.new + seed*site
+ cage*(site/block.new),family=quasibinomial, data = dat))
```

Temperature

```
#Entering Data

goldpass.1 <- read.csv("gptemp.csv", header = T,row.names=1)

goldpass.2 <- read.csv("gp_r2_r7_2242762_Page1.csv", header = T,row.names=1)
```

```
thompsonpeak.1 <- read.csv("tp_r1_r8_chan1s_2242754.csv", header = T,row.names=1)

thompsonpeak.2 <- read.csv("tp_r5_r3_s_2242755.csv", header = T,row.names=1)

tobbaganridge.1 <- read.csv("tr_r2_r4_b_2378734_1_Page1.csv", header =
T,row.names=1)

tobbaganridge.2 <- read.csv("tr_r2_r4_b_2378734_Page1.csv", header = T,row.names=1)

tobbaganridge.3 <- read.csv("tr_r4_r4_b_2378738_0_Page1.csv", header =
T,row.names=1)

tobbaganridge.4 <- read.csv("tr_r4_r4_b_2378738_Page1.csv", header = T,row.names=1)

pioneermountain.1 <- read.csv("pm_r4_r5_lb_2378727_0_Page1.csv", header =
T,row.names=1)

pioneermountain.2 <- read.csv("pm_r4_r5_lb_2378727_Page1.csv", header =
T,row.names=1)

pioneermountain.3 <- read.csv("pm_r5_r5_b_2378731.csv", header = T,row.names=1)

ulmpeak.1 <- read.csv("up_r5_r1_s_2242765_Page1.csv", header = T, row.names=1)

#Function for parsing out daily high and low temps from data files
process <- function(df)
{
   min1 <- tapply(df$Temp_1,df$Date,min)
   min2 <- tapply(df$Temp_2,df$Date,min)
   max1 <- tapply(df$Temp_1,df$Date,max)
   max2 <- tapply(df$Temp_2,df$Date,max)

   min1.na <- seq(1,nrow(min1))[is.na(min1)==TRUE]
   min2.na <- seq(1,nrow(min2))[is.na(min2)==TRUE]
   max1.na <- seq(1,nrow(max1))[is.na(max1)==TRUE]
   max2.na <- seq(1,nrow(max2))[is.na(max2)==TRUE]

   out <- list(min1=min1,min2=min2,max1=max1,max2=max2,
  min1.na=min1.na,min2.na=min2.na,max1.na=max1.na,max2.na=max2.na)out
}
```

```
#Min Figure 12
plot(12:398,smooth(0.5555555*(thompsonpeak.1.temp$min1-
32)),xlim=c(10,816),ylim=c(-4,13),xlab="July 13th, 2010 - September 22nd, 2012",
ylab="Temperature (Celsius)", main = "Daily Minimum Temperature By Site",type='l')
lines(761:814,smooth(0.5555555*(tobbaganridge.1.temp$min1-32)),col="red")
lines(446:761,smooth(0.5555555*(tobbaganridge.2.temp$min1-32)),col="red")
lines(417:763,smooth(0.5555555*(ulmpeak.1.temp$min1-32)),col="blue")
lines(775:812,smooth(0.5555555*(pioneermountain.1.temp$min1-32)),col="green")
lines(77:775,smooth(0.5555555*(pioneermountain.2.temp$min1-32)),col="green")
lines(399:786,smooth(0.5555555*(goldpass.2.temp$min1-32)),col="yellow")

#Max Figure 12
plot(12:398,smooth(0.5555555*(thompsonpeak.1.temp$max1-
32)),xlim=c(10,816),ylim=c(0,54),xlab="July 13th, 2010 - September 22nd, 2012",
ylab="Temperature (Celsius)", main = "Daily Maxiumum Temperature By Site", type='l')
lines(761:814,smooth(0.5555555*(tobbaganridge.1.temp$max1-32)),col="red")
lines(446:761,smooth(0.5555555*(tobbaganridge.2.temp$max1-32)),col="red")
lines(417:763,smooth(0.5555555*(ulmpeak.1.temp$max1-32)),col="blue")
lines(775:812,smooth(0.5555555*(pioneermountain.1.temp$max1-32)),col="green")
lines(77:775,smooth(0.5555555*(pioneermountain.2.temp$max1-32)),col="green")
lines(399:786,smooth(0.5555555*(goldpass.2.temp$max1-32)),col="yellow")

#Days over and under total code
sum(thompsonpeak.1.temp$max1>90)
sum(thompsonpeak.1.temp$max2>90)
sum(thompsonpeak.1.temp$min2<30)
sum(thompsonpeak.1.temp$min1<30)
sum(thompsonpeak.2.temp$max1>90)
sum(thompsonpeak.2.temp$max2>90)
sum(thompsonpeak.2.temp$min2<30)
sum(thompsonpeak.2.temp$min1<30)

sum(tobbaganridge.1.temp$max1>90)
sum(tobbaganridge.1.temp$max2>90)
sum(tobbaganridge.1.temp$min2<30)
sum(tobbaganridge.1.temp$min1<30)
sum(tobbaganridge.2.temp$max1>90)
sum(tobbaganridge.2.temp$max2>90)
sum(tobbaganridge.2.temp$min2<30)
sum(tobbaganridge.2.temp$min1<30)
sum(tobbaganridge.3.temp$max1>90)
sum(tobbaganridge.3.temp$max2>90)
sum(tobbaganridge.3.temp$min2<30)
sum(tobbaganridge.3.temp$min1<30)
```

```
sum(tobbaganridge.4.temp$max1>90)
sum(tobbaganridge.4.temp$max2>90)
sum(tobbaganridge.4.temp$min2<30)
sum(tobbaganridge.4.temp$min1<30)

sum(ulmpeak.1.temp$max1>110)
sum(ulmpeak.1.temp$min1<30)

sum(pioneermountain.1.temp$max1>90)
sum(pioneermountain.1.temp$max2>90)
sum(pioneermountain.1.temp$min2<30)
sum(pioneermountain.1.temp$min1<30)
sum(pioneermountain.2.temp$max1>90)
sum(pioneermountain.2.temp$max2>90)
sum(pioneermountain.2.temp$min2<30)
sum(pioneermountain.2.temp$min1<30)
sum(pioneermountain.3.temp$max1>90)
sum(pioneermountain.3.temp$max2>90)
sum(pioneermountain.3.temp$min2<30)
sum(pioneermountain.3.temp$min1<30)

sum(goldpass.1.temp$max2>90)
sum(goldpass.1.temp$min2<30)
sum(goldpass.2.temp$max2>90)
sum(goldpass.2.temp$min2<30)
sum(goldpass.2.temp$max1>90)
sum(goldpass.2.temp$min1<30)


#Model 1
model.1 <- glm(cbind(survived, totgermsurv) ~ treatment + temp, family=binomial, data
= dat)

#Model 2
model.2 <- glm(cbind(survived, totgermsurv) ~ treatment, family=binomial, data = dat)

anova(model.2, model.1, test="Chisq")
```

APPENDIX G

ORIGINAL DATA

Appendix G - Original Data

germ	nogerm	survived	nogermsurv	totgermsurv	treatment	site	block	cage
2	18	0	20	2	c	gp	one	0
12	8	8	12	4	c	gp	one	1
6	14	1	19	5	sc	gp	one	0
5	15	3	17	2	sc	gp	one	1
15	5	5	15	10	st	gp	one	0
8	12	4	16	4	st	gp	one	1
5	15	3	17	2	scst	gp	one	0
1	10	0	11	1	scst	gp	one	1
12	8	5	15	7	c	gp	two	0
8	12	2	18	6	c	gp	two	1
6	14	2	18	4	sc	gp	two	0
8	12	5	15	3	sc	gp	two	1
16	4	8	12	8	st	gp	two	0
17	3	7	13	10	st	gp	two	1
7	13	1	19	6	scst	gp	two	0
16	4	11	9	5	scst	gp	two	1
9	11	6	14	3	c	gp	three	0
14	6	11	9	3	c	gp	three	1
8	12	6	14	2	sc	gp	three	0
4	16	4	16	0	sc	gp	three	1
13	7	4	16	9	st	gp	three	0
15	4	11	8	4	st	gp	three	1
10	10	2	18	8	scst	gp	three	0
9	11	7	13	2	scst	gp	three	1
9	11	5	15	4	c	gp	four	0
4	16	4	16	0	c	gp	four	1
4	16	2	18	2	sc	gp	four	0
6	14	4	16	2	sc	gp	four	1
14	6	2	18	12	st	gp	four	0
12	8	8	12	4	st	gp	four	1
15	5	5	15	10	scst	gp	four	0
9	11	8	12	1	scst	gp	four	1
5	15	3	17	2	c	gp	five	0
8	12	7	13	1	c	gp	five	1
0	20	0	20	0	sc	gp	five	0
9	11	8	12	1	sc	gp	five	1
16	4	5	15	11	st	gp	five	0
16	4	14	6	2	st	gp	five	1
16	3	12	7	4	scst	gp	five	0
11	9	7	13	4	scst	gp	five	1
9	11	8	12	1	c	tr	one	0
7	13	6	14	1	c	tr	one	1
10	10	10	10	0	sc	tr	one	0
6	14	6	14	0	sc	tr	one	1

12	8	8	12	4	st	tr	one	0
15	5	15	5	0	st	tr	one	1
13	7	13	7	0	scst	tr	one	0
9	11	7	13	2	scst	tr	one	1
8	12	8	12	0	c	tr	two	0
14	6	13	7	1	c	tr	two	1
2	18	2	18	0	sc	tr	two	0
11	9	11	9	0	sc	tr	two	1
5	15	4	16	1	st	tr	two	0
1	19	1	19	0	st	tr	two	1
0	20	0	20	0	scst	tr	two	0
1	19	1	19	0	scst	tr	two	1
11	9	10	10	1	c	tr	three	0
13	7	11	9	2	c	tr	three	1
8	12	4	16	4	sc	tr	three	0
6	14	6	14	0	sc	tr	three	1
2	18	2	18	0	st	tr	three	0
12	8	12	8	0	st	tr	three	1
6	14	5	15	1	scst	tr	three	0
9	11	9	11	0	scst	tr	three	1
10	10	8	12	2	c	tr	four	0
7	13	5	15	2	c	tr	four	1
12	8	11	9	1	sc	tr	four	0
10	10	1	19	9	sc	tr	four	1
9	11	8	12	1	st	tr	four	0
9	11	7	13	2	st	tr	four	1
12	8	9	11	3	scst	tr	four	0
10	10	9	11	1	scst	tr	four	1
8	12	7	13	1	c	tr	five	0
4	16	4	16	0	c	tr	five	1
11	9	9	11	2	sc	tr	five	0
9	11	7	13	2	sc	tr	five	1
9	11	8	12	1	st	tr	five	0
9	11	8	12	1	st	tr	five	1
10	10	7	13	3	scst	tr	five	0
7	13	6	14	1	scst	tr	five	1
6	14	4	16	2	c	tp	one	0
3	17	0	20	3	c	tp	one	1
2	18	2	18	0	sc	tp	one	0
1	18	1	18	0	sc	tp	one	1
11	7	10	8	1	st	tp	one	0
7	13	5	15	2	st	tp	one	1
13	7	10	10	3	scst	tp	one	0
10	10	10	10	0	scst	tp	one	1
10	10	8	12	2	c	tp	two	0
9	11	6	14	3	c	tp	two	1
5	15	3	17	2	sc	tp	two	0
4	16	2	18	2	sc	tp	two	1

9	11	4	16	5	st	tp	two	0
11	9	8	12	3	st	tp	two	1
7	13	6	14	1	scst	tp	two	0
14	6	10	10	4	scst	tp	two	1
9	11	3	17	6	c	tp	three	0
8	12	3	17	5	c	tp	three	1
8	12	1	19	7	sc	tp	three	0
2	18	1	19	1	sc	tp	three	1
16	4	4	16	12	st	tp	three	0
4	16	4	16	0	st	tp	three	1
15	5	3	17	12	scst	tp	three	0
9	11	3	17	6	scst	tp	three	1
5	15	4	16	1	c	tp	four	0
8	12	3	17	5	c	tp	four	1
8	12	1	19	7	sc	tp	four	0
2	18	1	19	1	sc	tp	four	1
16	4	4	16	12	st	tp	four	0
4	16	4	16	0	st	tp	four	1
15	5	3	17	12	scst	tp	four	0
9	11	3	17	6	scst	tp	four	1
5	13	4	14	1	c	tp	five	0
12	8	11	9	1	c	tp	five	1
1	19	0	20	1	sc	tp	five	0
11	9	8	12	3	sc	tp	five	1
13	7	9	11	4	st	tp	five	0
16	4	12	8	4	st	tp	five	1
11	9	0	20	11	scst	tp	five	0
15	5	12	8	3	scst	tp	five	1
4	16	3	17	1	c	pm	one	0
0	20	0	20	0	c	pm	one	1
6	14	4	16	2	sc	pm	one	0
13	7	11	9	2	sc	pm	one	1
9	11	4	16	5	st	pm	one	0
14	6	11	9	3	st	pm	one	1
6	14	4	16	2	scst	pm	one	0
13	7	8	12	5	scst	pm	one	1
5	15	3	17	2	c	pm	two	0
1	19	1	19	0	c	pm	two	1
12	8	4	16	8	sc	pm	two	0
4	12	2	14	2	sc	pm	two	1
9	11	4	16	5	st	pm	two	0
7	13	2	18	5	st	pm	two	1
11	9	5	15	6	scst	pm	two	0
0	20	0	20	0	scst	pm	two	1
14	6	9	11	5	c	pm	three	0
10	10	7	13	3	c	pm	three	1
10	10	5	15	5	sc	pm	three	0
17	3	14	6	3	sc	pm	three	1

16	4	12	8	4	st	pm	three	0
20	0	14	6	6	st	pm	three	1
8	12	3	17	5	scst	pm	three	0
14	6	9	11	5	scst	pm	three	1
4	16	3	17	1	c	pm	four	0
5	15	2	18	3	c	pm	four	1
10	10	9	11	1	sc	pm	four	0
7	13	4	16	3	sc	pm	four	1
11	9	4	16	7	st	pm	four	0
2	18	1	19	1	st	pm	four	1
3	17	0	20	3	scst	pm	four	0
1	19	0	20	1	scst	pm	four	1
3	17	2	18	1	c	pm	five	0
14	6	11	9	3	c	pm	five	1
7	13	4	16	3	sc	pm	five	0
10	10	9	11	1	sc	pm	five	1
6	14	3	17	3	st	pm	five	0
8	12	5	15	3	st	pm	five	1
8	12	1	19	7	scst	pm	five	0
8	12	2	18	6	scst	pm	five	1
6	14	1	19	5	c	up	one	0
5	15	1	19	4	c	up	one	1
3	17	2	18	1	sc	up	one	0
5	15	0	20	5	sc	up	one	1
10	10	1	19	9	st	up	one	0
14	6	10	10	4	st	up	one	1
12	8	5	15	7	scst	up	one	0
10	10	3	17	7	scst	up	one	1
4	16	1	19	3	c	up	two	0
12	8	5	15	7	c	up	two	1
1	19	0	20	1	sc	up	two	0
0	20	0	20	0	sc	up	two	1
11	9	2	18	9	st	up	two	0
14	6	8	12	6	st	up	two	1
8	12	4	16	4	scst	up	two	0
12	8	6	14	6	scst	up	two	1
6	14	1	19	5	c	up	three	0
6	14	2	18	4	c	up	three	1
0	20	0	20	0	sc	up	three	0
0	20	0	20	0	sc	up	three	1
10	10	5	15	5	st	up	three	0
9	11	6	14	3	st	up	three	1
8	12	2	18	6	scst	up	three	0
7	13	4	16	3	scst	up	three	1
7	13	0	20	7	c	up	four	0
10	10	1	19	9	c	up	four	1
3	17	0	20	3	sc	up	four	0
5	15	1	19	4	sc	up	four	1

10	9	2	17	8	st	up	four	0
14	6	11	9	3	st	up	four	1
12	8	2	18	10	scst	up	four	0
11	9	8	12	3	scst	up	four	1
3	17	0	20	3	c	up	five	0
2	18	1	19	1	c	up	five	1
5	15	1	19	4	sc	up	five	0
0	19	0	19	0	sc	up	five	1
2	18	2	18	0	st	up	five	0
11	9	7	13	4	st	up	five	1
2	18	1	19	1	scst	up	five	0
5	15	4	16	1	scst	up	five	1

Table A.17: Original data used in study's analyses. Key: germ = # germinated, no germ = # that did not germinate, survived = # of germinants that survived, nogermsurv = total seeds in row minus # of germinants that survived, totgermsurv = # of seeds that germinated minus # of germinants that survived, treatment: c = control, sc = scarified, scst = scarified and stratified, st = stratified, cage: 1 = cage, 0 = no cage