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CLIMATE CHANGE AND FOREST TREES IN THE PACIFIC NORTHWEST: GUIDE TO VULNERABILITY ASSESSMENT METHODOLOGY



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CLIMATE CHANGE AND FOREST TREES IN THE PACIFIC NORTHWEST: GUIDE TO VULNERABILITY ASSESSMENT METHODOLOGY

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CHAPTER 1. INTRODUCTION

This guide provides a step-by-step description of the methodology used to apply the Forest Tree Genetic Risk Assessment System (ForGRAS; Potter and Crane 2010) to the tree species of the Pacific Northwest in a recent climate change vulnerability assessment (Devine et al. 2012). We describe our modified version of the ForGRAS model, and we review the model's basic principles and operation. We also discuss further adjustments to the model that managers may find useful if applying it to other regions or to fit other objectives. Chapter 2 of this guide describes the overall methodology of the vulnerability assessment; chapters 3 through 7 describe each of the five risk factors that we selected for the Pacific Northwest vulnerability assessment. Appendices provide step-by-step procedures used to prepare the model input data.

Background: The Pacific Northwest Forest Tree Vulnerability Assessment

Climate change projections for the Pacific Northwest include year-round warming and potentially increased winter precipitation and decreased summer precipitation (Mote and Salathé 2009). The extent and duration of the regional snowpack is projected to decrease, particularly at lower elevations (Elsner et al. 2010, Mote 2003). In addition to potential direct effects of climate on individual tree vigor and survival, climate-related stress could increase vulnerability of forests to large-scale disturbance

including fire and damage from insects and diseases (Dale et al. 2001). The effects of long-term climate changes on the composition and structure of Pacific Northwest plant communities are difficult to predict. There is limited information on the climatic tolerances of many species and even less information on what complex interactions could result from ecosystem-wide exposure to a changing environment.

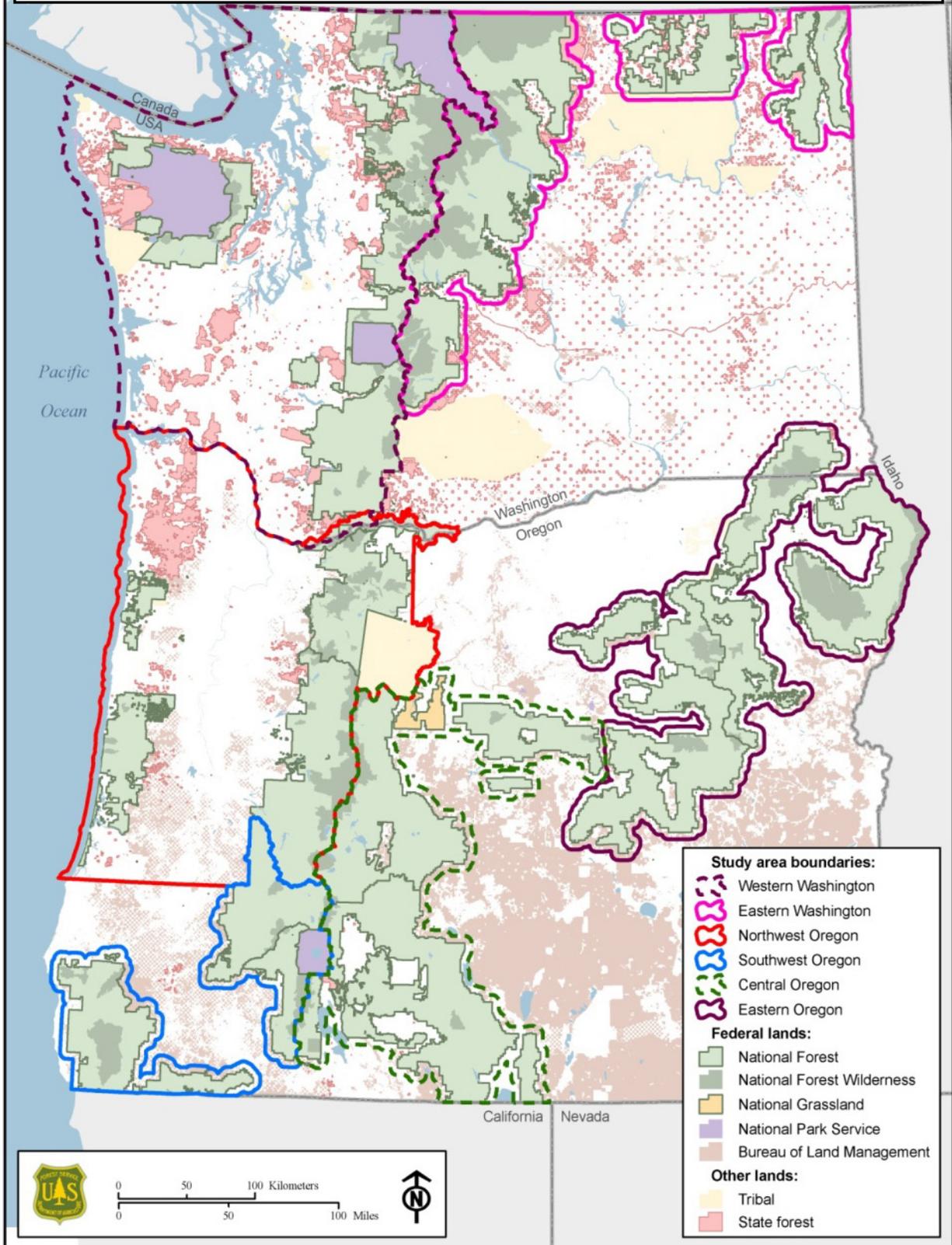
The goal of this guide is to describe the methodology used to apply the Forest Tree Genetic Risk Assessment System (Potter and Crane 2010) to the tree species of the Pacific Northwest.

In 2010, we launched an effort to address the projected effects of climate change on forest tree species in Washington and Oregon (Forest Service Pacific Northwest Region). We sought to determine the potential implications of climate change on the management, restoration, and conservation of forest tree species of the Pacific

Northwest. The project emphasized National Forest System lands and management issues but considered the full distribution of each tree species, across all land ownerships.

This project led to the publication of a climate change vulnerability assessment focused on the forests of western Washington, with emphasis on the Olympic, Mt. Baker-Snoqualmie, and Gifford-Pinchot National Forests (Aubry et al. 2011). In 2012, we completed a regional report that included six subregional vulnerability assessments that covered all of the national forests of the Pacific Northwest Region (Devine et al. 2012) (fig. 1). Based on the results of these assessments, the reports include recommendations and specific actions for managers to address the projected effects of climate change on forest tree species in Washington and Oregon.

Figure 1. Boundaries of the six study areas of the Pacific Northwest forest tree climate change vulnerability assessment (Devine et al. 2012)



At the heart of the project was a vulnerability assessment—a systematic process of identifying and quantifying areas of vulnerability within a system (Glick et al. 2011). The assessment was undertaken to identify: (1) characteristics of individual forest tree species that could influence their response to long-term changes in climate, and (2) relative levels of vulnerability to climate change among tree species. This vulnerability assessment is a tool for prioritizing tree species to help managers more efficiently allocate limited resources to the most vulnerable tree species.

In contrast to some of the previously published analyses of climate change effects on forests, the Pacific Northwest forest tree vulnerability assessment was *not* designed to create maps of projected future suitable habitat for each species. Instead, we used documented life history traits, current distribution, and pest and pathogen data for individual tree species—combined with consensus regional climate projections—to rate each species' relative vulnerability to a changing climate. We chose this approach because we felt that it would be most useful to managers and would provide a biological basis to assist decision-making in the near future.

After evaluating several different vulnerability assessment models, we chose ForGRAS because it is straightforward to apply, transparent, and can

The Forest Tree Genetic Risk Assessment System

ForGRAS was developed to evaluate the vulnerability of individual tree species within a region of interest, under anticipated long-term climate change. Given projected changes in climate, conservation of species' existing adaptedness (specifically variation in adaptive traits) is key to long-term viability. However, because this detailed level of genetic information does not currently exist for many tree species, ForGRAS uses documented ecological and life-history traits to assess the vulnerability of individual tree species to climate change and related threats (Myking 2002, Potter and Crane 2010).

For a defined study area, ForGRAS produces an overall vulnerability score for each tree species; this score is then used to rank the species according to their climate change vulnerability. A species' overall vulnerability score is calculated by averaging the scores of multiple risk factors (e.g., distribution, reproductive capacity), each of which range from 0 to 100. Each risk factor contains a set of variables that are used to quantify a species' climate change vulnerability according to intrinsic attributes or external threats.

be easily modified to fit specific objectives and assumptions. Originally developed for the Southern Appalachian region, the ForGRAS model quantifies each tree species' climate change vulnerability, as well as the specific factors that contribute to that vulnerability (Potter and Crane 2010). The primary goal of this guide is to provide a detailed description of the methodology that we recently used (Devine et al. 2012) to apply the ForGRAS model to the tree species of the Pacific Northwest.

CHAPTER 2. APPLICATION OF THE FORGRAS VULNERABILITY ASSESSMENT

In this section, we describe the four steps used to perform the Pacific Northwest vulnerability assessment using the ForGRAS model: (1) determine the area and species of interest, (2) select risk factors, (3) collect data and calculate risk factor values, and (4) calculate overall scores and rank species (Potter and Crane 2010). We

also describe, in detail, the procedures used to acquire and prepare data for the model.

This section describes the process of applying the ForGRAS model to an individual study area, as we did in each of the six subregional analyses (Devine et al. 2012) (fig. 1). In the regional report, we also calculated region-level scores by averaging each tree species' vulnerability score across the six study areas (Devine et al. 2012).

Step 1: Determine Area and Species of Interest

Area of Interest

ForGRAS can be applied at a range of different geographic scales. We delineated six study areas within the Pacific Northwest Region so that we could focus on the species and management issues unique to each area. Although we assessed all of the national forests of the region, we chose not to conduct analyses at the individual-forest level because it would have been more difficult to identify broad trends. For example, if the analysis included only the Olympic National Forest, it would not account for the fact that populations of high-elevation tree species in the Olympic Range are geographically separated from Cascade Range populations. Conversely, if a study area were too large and ecologically diverse, it could be more difficult to identify trends. In the case of Washington, combining eastern and western portions of the state in a single analysis would involve simultaneously evaluating the

Minimum Technical Skills Needed to Run the ForGRAS Model

The original ForGRAS spreadsheet model (Potter and Crane 2010), and the version of ForGRAS modified for the Pacific Northwest assessment, is designed to be run by users possessing only a basic knowledge of Microsoft Excel. However, some of the data preparation that is necessary to calculate the model input data requires additional software skills. Detailed procedures for calculating the model input data appear in appendices 1 through 3. The software and skills needed to perform these procedures are:

Microsoft Excel: Basic knowledge only; detailed steps are provided in the appendix procedures.

Microsoft Access: No prior experience needed for analyzing the FIA annual inventory tree data; detailed steps are provided. *Optional* analyses of other types of map data may, in some cases, require additional skills, such as managing variable relationships and creating queries.

ESRI ArcGIS: An intermediate skill level is necessary, including ability to create and edit shapefiles and to run tabular statistical analysis, including use of tools such as the Frequency Tool.

Procedures described in this publication are based on the 2010 versions of Microsoft Excel and Access and on ArcGIC 10.

influences of substantially different disturbance regimes and climates.

The study area can be based on ownership boundaries, ecological considerations, or a combination of both. In the study areas in eastern Washington and Oregon, where study area boundaries were based on the extent of the national forests, we added a 5-km-wide buffer so that the study area would fully encompass populations of tree species occurring at the edge of the national forest that would have otherwise been partially excluded from the analysis. Thus, these study areas were determined by a combination of ownership and ecological factors.

Species List

After defining the study area, the next task is to assemble a complete list of forest tree species within that area. In the Pacific Northwest assessment, we defined a tree as a woody perennial capable of producing a single stem with apical dominance and reaching at least 20 ft (6 m) in height.

There are at least four potential approaches for compiling a list of all tree species within a study area (all of these were used in the Pacific Northwest assessment):

1. Use tree species distribution datasets to create a species list; examples of such datasets appear in table 1. Procedures for

Table 1. Primary sources of tree species distribution data used in a climate change vulnerability assessment of the Pacific Northwest Region

Dataset	Source	Coverage	Inventory design
Forest Inventory and Analysis (FIA)	U.S. Forest Service, Pacific Northwest Region	All public and private lands ¹	Regularly spaced plots
Current Vegetation Survey (CVS)	U.S. Forest Service, Pacific Northwest Region	National forests ¹	Regularly spaced plots
USFS Region 6 Ecology Program	U.S. Forest Service, Pacific Northwest Region	National forests	Plots located according to plant community type
Oregon Flora Project	Department of Botany and Plant Pathology, Oregon State University	Public and private land in Oregon	Specimen collections and recorded observations by many individuals with various objectives
University of Washington Herbarium	Burke Museum, University of Washington	Public and private lands in Washington and elsewhere in the Pacific Northwest	Specimen collections and recorded observations by many individuals with various objectives
National parks	National Park Service	Lands managed by the National Park Service	Irregularly spaced plots; data availability varies by park and inventory objectives
Other national forest surveys	USDA Forest Service, Region 6	National forests	Inventory based on individual species of interest
Other	Washington Department of Natural Resources; USDA Forest Service Pacific Northwest Research Station; Department of Defense	Various	Inventory based on individual species of interest

¹ A small amount of random error was intentionally added to the plot locations to protect the identity of landowners.

acquiring and processing data appear in appendix 1. The only tree distribution data source that is mandatory for running this version of the ForGRAS model is the Forest Inventory and Analysis (FIA) annual inventory dataset; however, because FIA sampling is at a low intensity (one plot per 6,000 ac), acquiring data from additional sources may significantly improve understanding of a species' distribution, particularly when working at fine scale or in a relatively small study area. Availability of data varies widely by land ownership ("coverage" column in table 1). Outside of Washington and Oregon, many of these data sources will not apply; however, they should provide a starting point for locating similar data sources available in other regions.

2. Consult local publications and field guides. These are likely to include rare, non-commercial, and small tree species that occasionally are excluded from, or missed by, timber-based forest inventories. In the Pacific Northwest study area, *Northwest Trees* (Arno and Hammerly 2007) was a valuable resource for identifying such tree species. We also consulted local plant association guides that were published by the Forest Service (e.g., Henderson et al. 1989, 1992).
3. Consult local experts, such as botanists or ecologists.
4. Examine national tree species distribution maps (e.g., Little 1971, 1976).

Selecting Species for Analysis

After creating a comprehensive species list for the study area, the next step is to determine how these species will be analyzed in the vulnerability assessment. Four potential approaches include:

1. Analyze all tree species in a single group. It is important to remember that the ForGRAS assessment is only as good as the data on which it is based. Thus, if tree species are included for which data are scarce or unavailable, the analysis will be weakened. For example, if tree distribution is included as a risk factor (chapter 3), comparable distribution data are required for all tree species in order to rate the variables in that risk factor. The primary dataset used for these ratings (in the original ForGRAS model and in the Pacific Northwest assessment) is the national FIA annual inventory dataset. However, in this inventory, some smaller tree species (e.g., willows (*Salix*)) were recorded by genus rather than at the species level. Thus, data availability and selection of variables may influence the tree species list.
2. Select a subset of species that fit the objectives of the study; analyze only these species. It may not be necessary or relevant to include every single tree species in the analysis.
3. Group the tree species, and analyze the groups separately. For example, it may be desirable to separately analyze the vulnerability of overstory trees and understory trees, or to separately analyze riparian species.
4. Group the tree species, but do not analyze all groups. This is the approach that we took in the Pacific Northwest vulnerability assessment (Devine et al. 2012), based on the objective of assessing the major overstory tree species in the study area (group 1) to prioritize these species for conservation and monitoring. We defined other species groups for less-common and non-canopy species (group 2) and for rare species (group 3). We did not apply ForGRAS to

groups 2 or 3 because the full range of data required to rate the risk factor variables was not available (e.g., genetic or distribution data were often lacking).

Instead, we took an alternative approach for group 2 and 3 species (Aubry et al. 2011, Devine et al. 2012).

Step 2: Select Risk Factors and Variables

The ForGRAS model is designed to be transparent and flexible so that the user can customize it to meet their specific objectives (Potter and Crane 2010). Using the original model as a starting point, we selected five areas of climate change vulnerability—risk factors—based on our objectives, data availability, and the results of an early peer review. Each of these five risk factors included multiple variables that were used to determine a species' vulnerability score (fig. 2).

The five selected risk factors were based on biological and ecological attributes that are well-established in the

Fire and Climate Change Pressure as Risk Factors

During development and refinement of the Pacific Northwest vulnerability assessment model, we considered adding two risk factors that we ultimately did not include in the final model: (1) effects of future fire regimes, and (2) predicted geographic shifts in species distributions resulting from climate pressure.

The five risk factors that we chose for the model were based on consensus regional climate change projections that are widely accepted and relatively conservative (i.e., increases in temperature and summer drought conditions; Littell et al. 2010). The fire and climate pressure risk factors would have required additional assumptions, and therefore uncertainty, beyond those necessary for the other five risk factors.

Although future wildfire regimes—for example, area burned per year—can be modeled using temperature and precipitation projections, incorporating wildfire as a risk factor would require:

- Assumptions regarding the frequency and intensity of wildfire (and the extent of future wildfire suppression) across the range of habitats that each tree species occupies at a given point in the future; and
- For each tree species, quantification of whether its existing ecological adaptations to fire would be sufficient under this predicted future fire regime. For example, will a species' bark thickness and foliar flammability affect its vulnerability under a future fire regime differently than they do at present?

It should be noted that wildfire effects *are* incorporated in the Pacific Northwest vulnerability assessment model inasmuch as the reproductive capacity risk factor is designed to quantify a species' capacity to regenerate following large-scale disturbance.

Climate change pressure is a risk factor in the original ForGRAS model; its variables are based on the differences between the current distribution of a species and its predicted future distribution according to climate envelope models (Hargrove et al. 2010, Rehfeldt et al. 2006). After initially including this risk factor in the Pacific Northwest assessment model, concerns were raised during the peer review process over the uncertainty associated with the future species distributions predicted by the climate envelope models. After further consideration, we decided to exclude this risk factor from the analysis. Climate change pressure, as a potential risk factor, is described in detail in appendix E of Aubry et al. (2011).

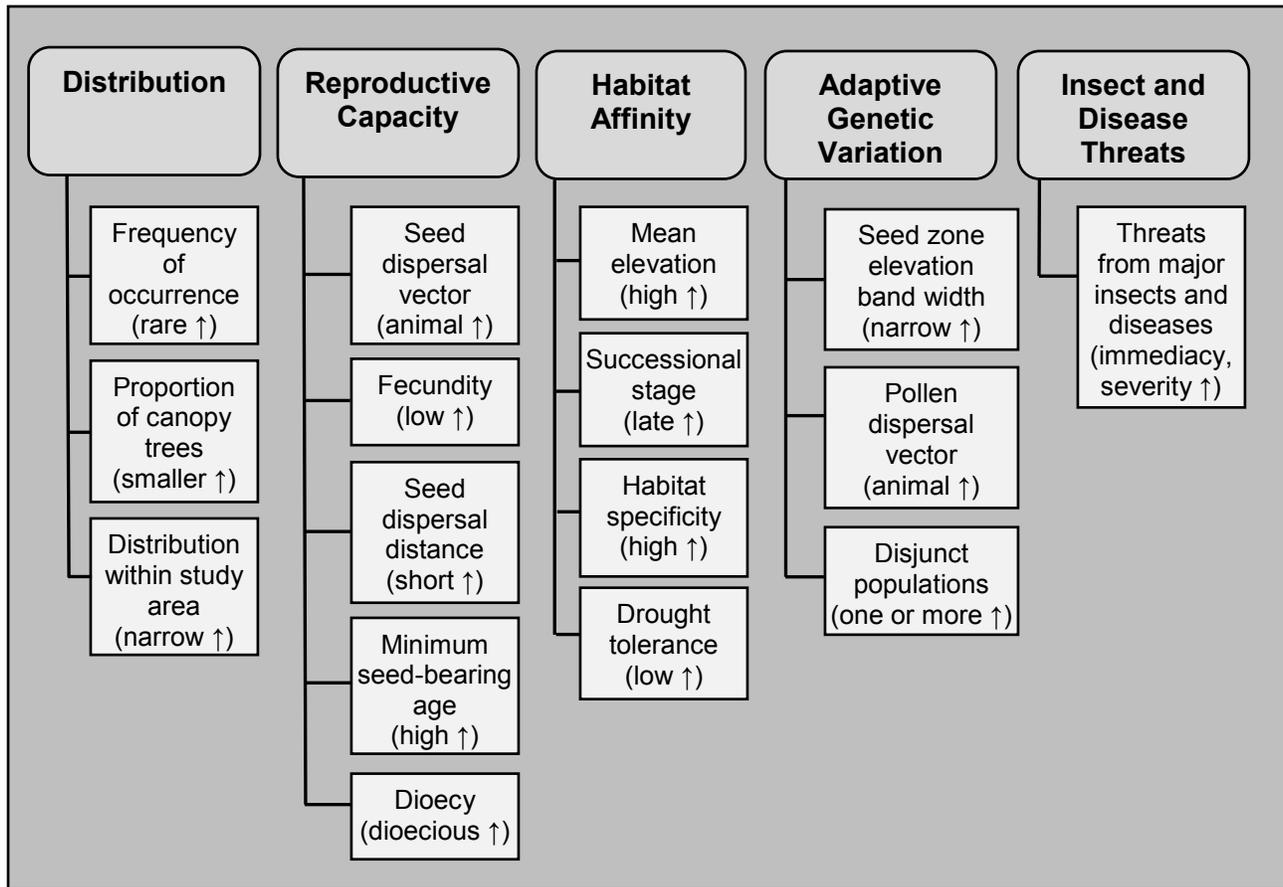


Figure 2. The five risk factors of the Pacific Northwest ForGRAS vulnerability assessment model and the variables used to quantify each risk factor. For each variable, the characteristic that *increases* a species' vulnerability is shown in parentheses

scientific literature, or, in the case of the insect and disease threats risk factor, on information provided by local experts. We chose *not* to include projected future shifts in the distribution of species' habitats as a risk factor (appendix E, Aubry et al. 2011). We included this risk factor initially, but removed it after an early peer review underscored the uncertainties of such models and the lack of agreement among scientists on the assumptions on which those models are based. We also considered but did not use the effects of future fire regimes as a risk factor (see box on Fire and Climate Change Pressure as Risk Factors).

Step 3: Collect Data and Calculate Risk Factor Scores

The process of rating the vulnerability of each tree species requires information from a variety of sources. In the Pacific Northwest assessment, the types of data collected fell into three categories: (1) life history traits expected to influence a species' resistance and resilience to the effects of anticipated climate change, (2) distribution data, and (3) data on forest insect and disease threats that were provided by U.S. Forest Service, Pacific Northwest Region Forest Health Protection Program. The sources of data used to

rate variables within each of the five risk factors are shown in table 2.

The tree species' vulnerability scores for each of the five risk factors are calculated using a Microsoft Excel spreadsheet model. This spreadsheet model is available online at www.ecoshare.info/projects/ccft in two versions: one containing no data and one populated with the data from the Pacific Northwest vulnerability assessment. For each risk factor, the model calculates a score ranging from 0 to 100, with a higher score indicating greater vulnerability. The details of how each risk factor is scored are described later in this guide, in the sections devoted to each risk factor.

Step 4: Calculate Overall Scores and Rank Species

After calculating a score from 0 to 100 for each species for each risk factor, the model calculates an overall score for each tree species by averaging its score across the five risk factors. Species can then be sorted and ranked according to this overall vulnerability score.

In the Pacific Northwest vulnerability assessment, we weighted the five risk factors equally, based on the assumption that we did not know which factors would become most important under future climate scenarios. However, users of this vulnerability assessment system may find it desirable to weight risk factors differently or to calculate the overall species' scores by using a method other than a simple average. Some examples of alternative methods of calculating the overall vulnerability score for each species are:

- **Use risk factor weightings**—Weight the risk factors according to how important each is considered to be. This is based on the assumption that, in a given study

ForGRAS Terminology

Risk factor—An aspect of vulnerability to climate change that is quantified by a set of variables. The Pacific Northwest application of ForGRAS used five risk factors.

Risk factor score—For each tree species, the ForGRAS model calculates a vulnerability score for each risk factor. The model first calculates a raw risk factor score; it then scales this raw score so that the species scores range from 0 (least vulnerable) to 100 (most vulnerable).

Variable—Each risk factor has multiple variables to quantify that aspect of vulnerability to climate change.

Rating—Each variable has a rating, in most cases a value between 0 and 100.

Overall vulnerability score—For each tree species, an overall climate change vulnerability score is calculated by averaging the five risk factor scores.

area, one predicts certain risk factors to be more important than others. For example, if the distribution and insect and disease threats risk factors are deemed twice as important as the other three factors, one would apply the following steps to determine the overall vulnerability score for each species:

1. Assign a weighting factor to each of the five risk factor scores. In this example, the distribution and insect and disease threats risk factors would each be assigned a multiplier of 2, because they were deemed twice as important as the other factors; the other three risk factors would each be assigned a multiplier of 1.

2. Multiply each risk factor score by its weighting factor.
3. Average the risk factor scores to create an overall vulnerability score.
4. To ensure that the overall vulnerability scores for all species

range from 0 to 100, the overall vulnerability score calculated in step 3 must be multiplied by the number of risk factors and then divided by the sum of the multipliers. In this example, one would multiply the

Table 2. Major sources of data used to rate climate change vulnerability within five risk factors in the Pacific Northwest climate change vulnerability assessment

Risk factor	Data source	Application of data
Distribution	Forest Inventory and Analysis (FIA) annual inventory Phase 2 data	FIA data were used to calculate each species' frequency of occurrence and the proportion of the canopy trees that it composed
	Other sources listed in table 1	Distribution maps were created using all data sources available; these maps were used to assess the geographic distribution of a species' occurrences
Reproductive capacity	The Woody Plant Seed Manual (Bonner and Karrfalt 2008)	Information used to rate fecundity and seed-bearing age
	Regional compilations of tree data (Klinka et al. 2000)	Information used to rate fecundity and seed dispersal distance
	Comprehensive tree species guides and literature reviews (e.g., Burns and Honkala 1990, Fischer et al. 1996)	Information used to rate seed-dispersal vectors, seed dispersal distance, and dioecy
Habitat affinity	Forest Inventory and Analysis (FIA) annual inventory Phase 2 data	Used to calculate mean elevation of occurrences
	Regional compilations of tree data (Arno and Hammerly 2007, Klinka et al. 2000)	Information used to rate successional stage, habitat specificity, and drought tolerance
	Comprehensive tree species guides and literature reviews (e.g., Burns and Honkala 1990, Fischer et al. 1996)	Information used to rate successional stage, habitat specificity, and drought tolerance
Adaptive genetic variation	Forest tree seed zone manuals (e.g., Randall 1996, Randall and Berrang 2002) and other sources in the scientific literature	Information used to determine width of seed zone elevation bands
	Comprehensive tree species guides and literature reviews (e.g., Burns and Honkala 1990, Fischer et al. 1996)	Information used to rate pollen dispersal vector
	All sources listed in table 1; tree distribution maps of Little (1971, 1976)	Data used to identify disjunct populations
Insect and disease threats	Major insect and disease threats rated by experts at U.S. Forest Service Pacific Northwest Region Forest Health Protection Service Centers	Data used to quantify the vulnerability of each tree species to insect and disease threats

See Aubry et al. (2011) and Devine et al. (2012)

- score by 5 and then divide it by 7 (i.e., $2+1+1+1+2$).
- **Base overall score on each species' most vulnerable factors**—This method is based on the assumption that a species' overall climate change vulnerability is best described by averaging only those risk factors that make it most vulnerable (i.e., the risk factors with the highest scores). For example, using a “top three” approach, the three risk factors with the highest vulnerability scores would be averaged to create the overall vulnerability score for each species. These top three factors would likely differ among species. This approach assumes that, if a species has certain risk factors making it highly vulnerable, those vulnerabilities should be emphasized in creating its overall vulnerability score. Likewise, it also assumes that it is irrelevant to the final score if the other two risk factors have very low vulnerability scores. Examples of the “top three” analysis are given in appendices 2 through 6 of Devine et al. (2012). Overall vulnerability scores also could be calculated using the top one, two, or four risk factor scores.
 - **Use the limiting factor approach**—This approach is based on the assumption that a selected risk factor is important enough that a species' overall vulnerability score should be no lower than its score for that risk factor. For example, if the insect and disease threats risk factor were determined to be of particular importance (i.e., a limiting factor), one would:
 1. Calculate each species' overall vulnerability score by averaging the five risk factor scores (or using another method, if desired).
 2. Compare each species' overall score to its score for the insect and disease threats risk factor.
 3. Select the higher of these two scores.

A broader approach is to apply several calculation methods (such as the three described above), as well as a simple average of the risk factor scores, to evaluate how the overall species' scores and rankings are influenced by the different methods. This approach can be used to gauge the sensitivity of the overall model to the assumptions of the various calculation methods.

CHAPTER 3. RISK FACTOR: DISTRIBUTION

The distribution risk factor quantifies a species' prevalence and distribution throughout the study area. Species with narrow distributions are considered more susceptible to genetic degradation or even extinction, given pressures associated with long-term change in climate (Willi et al. 2006; Potter and Crane 2010). This risk factor is composed of three variables selected to describe a species' distribution: frequency of occurrence, proportion of canopy trees, and distribution within study area.

Required Data

To rate tree species for this risk factor, the Forest Inventory and Analysis annual inventory Phase 2 data are required for the study area. These data are used to calculate ratings for the frequency of occurrence and proportion of canopy trees variables for each species. The distribution within study area variable can also be rated using only the FIA dataset, although we found that our precision, and our confidence in the ratings, increased when we supplemented the FIA dataset with data from some of the other sources listed in table 1. If these other data sources are not available, Little's range maps are a useful resource (Little 1971, 1976). Figures 3 through 6 illustrate the differences in coverage among four of the major data sources used in the Pacific Northwest vulnerability assessment western Washington study area (Aubry et al. 2011). Figures 3 through 5 show all sample plot locations, regardless of which species were found on the plots; figure 6 shows the locations of specimen collections only for species in the Pacific Northwest vulnerability assessment.

Procedures used for acquiring and processing data from major data sources are in appendix 1.

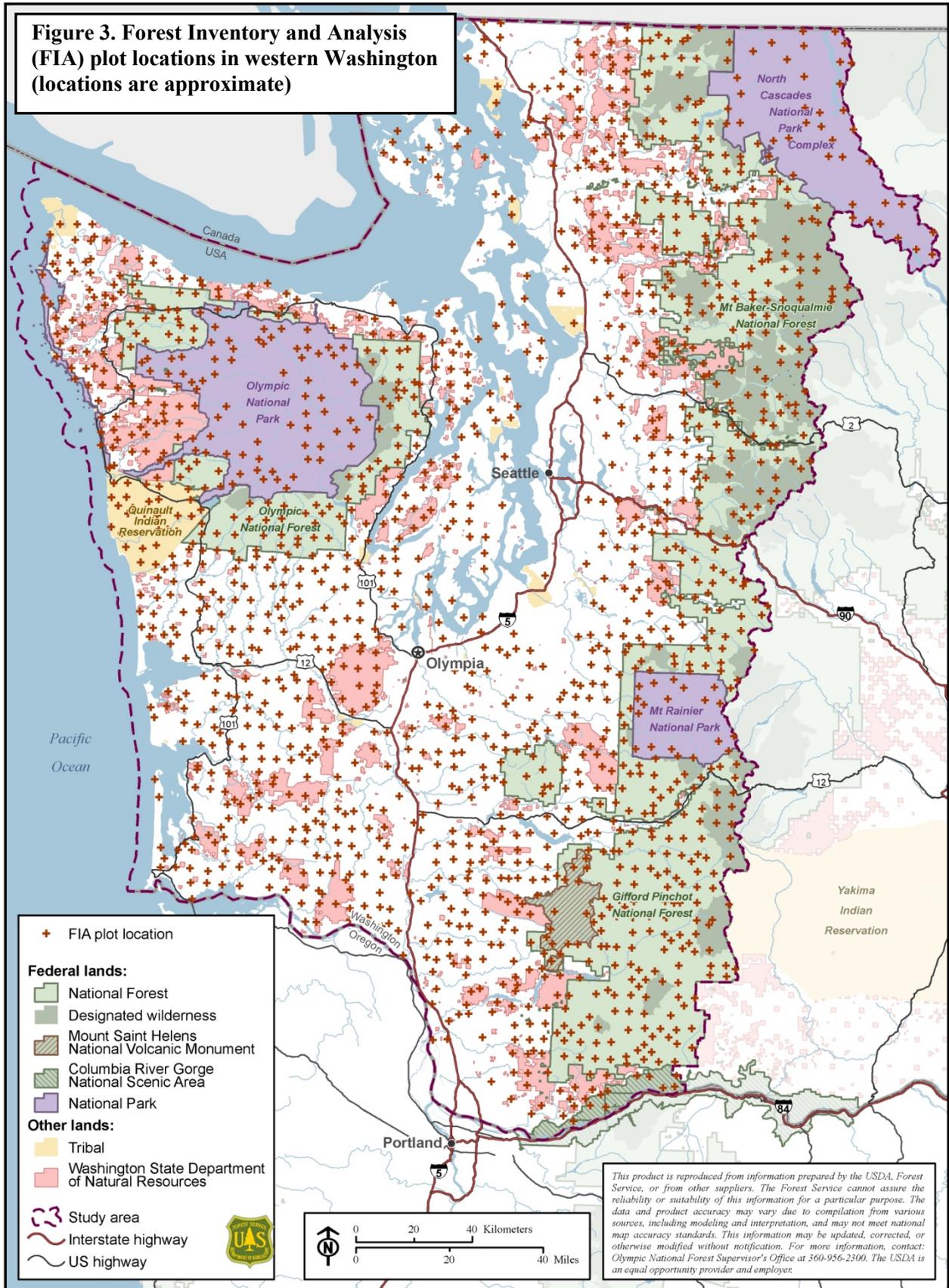
Rating the Variables

Frequency of occurrence—This variable is calculated as the percentage of FIA plots on which a given species occurred as a live tree. The vulnerability rating ranges from 0 (for the species occurring on the most plots) to 100 (for the species occurring on the fewest plots), with values for all other species assigned proportionally, according to the percentage of plots on which each occurred. The procedure for calculating this variable is described in appendix 2 (assuming the FIA data acquisition and processing described in appendix 1 have already been completed).

Proportion of canopy trees—The dominant and co-dominant canopy trees are generally the trees with the greatest vigor and reproductive capacity; thus, a species with a high degree of canopy dominance is assumed to be more likely to maintain its presence. For each of the plots on which a species occurred, we calculated the percentage of all canopy trees (i.e., a tree coded by FIA as dominant, co-dominant, or open-grown) that the given species represented; then we averaged this percentage across these plots. We calculated the vulnerability rating in the same manner as the frequency of occurrence variable, with the species composing the lowest percentage of canopy trees receiving the highest vulnerability rating (100) and the species with the highest percentage of canopy trees receiving the lowest vulnerability rating (0). The full procedure for calculating this value is described in appendix 2.

Distribution within study area—Although the frequency of occurrence variable describes the number of plots on which a species occurs, it does not describe the distribution of the plots within the study area. This variable, distribution within study area, is rated according to how the occurrences are distributed. Because this rating is qualitative, the user should examine the

Figure 3. Forest Inventory and Analysis (FIA) plot locations in western Washington (locations are approximate)



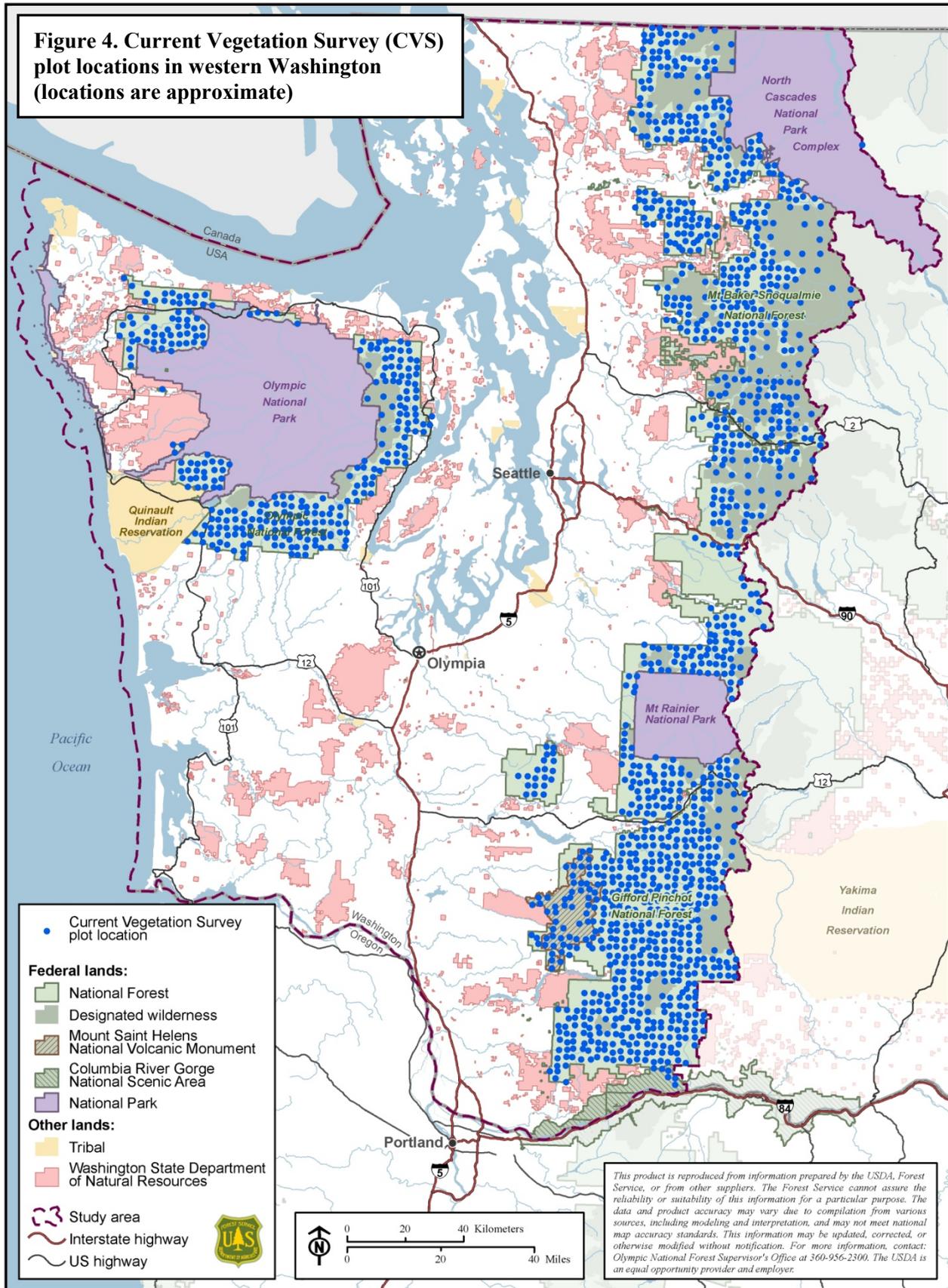


Figure 5. Ecology Core Dataset plot locations in western Washington

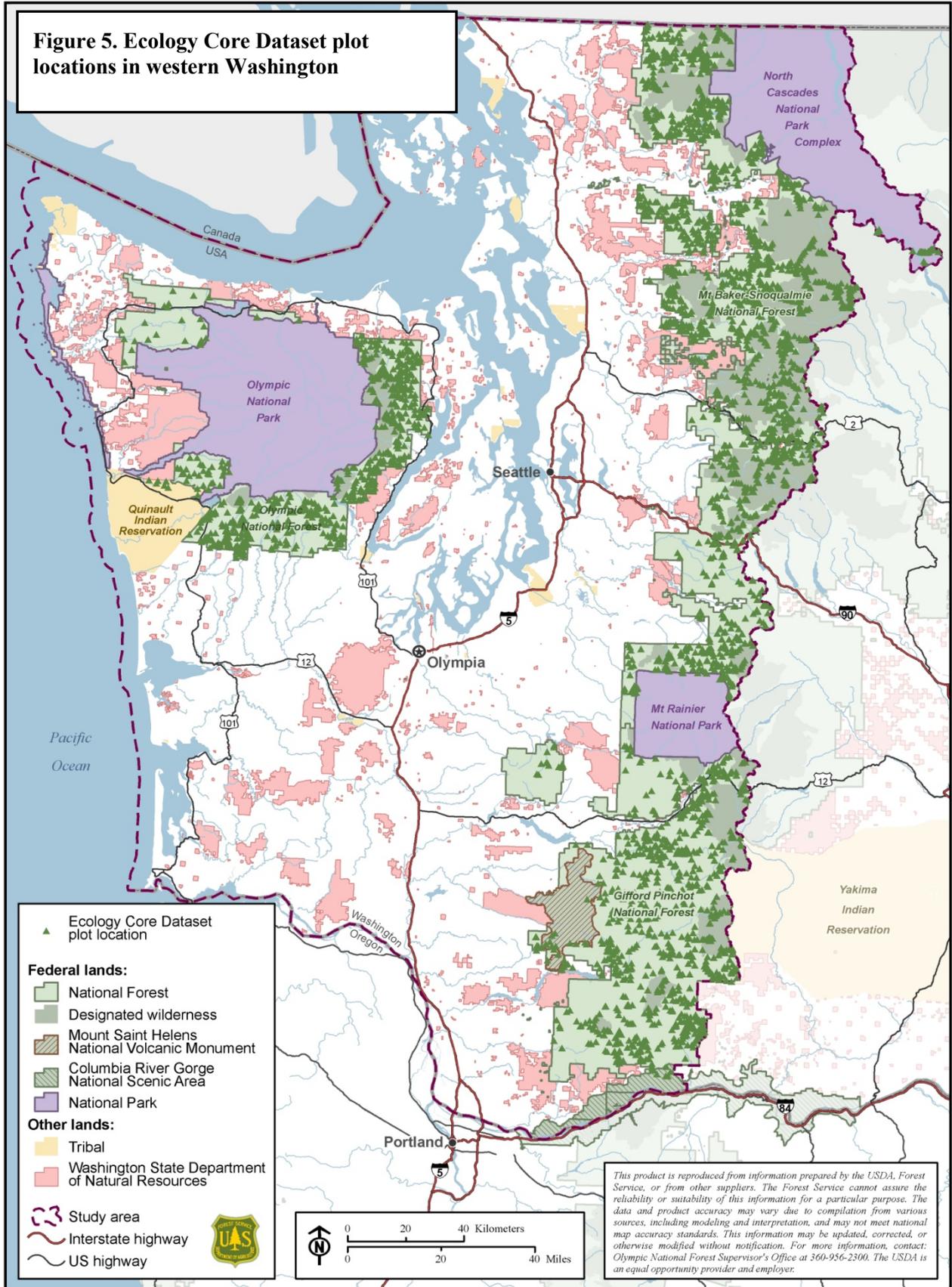
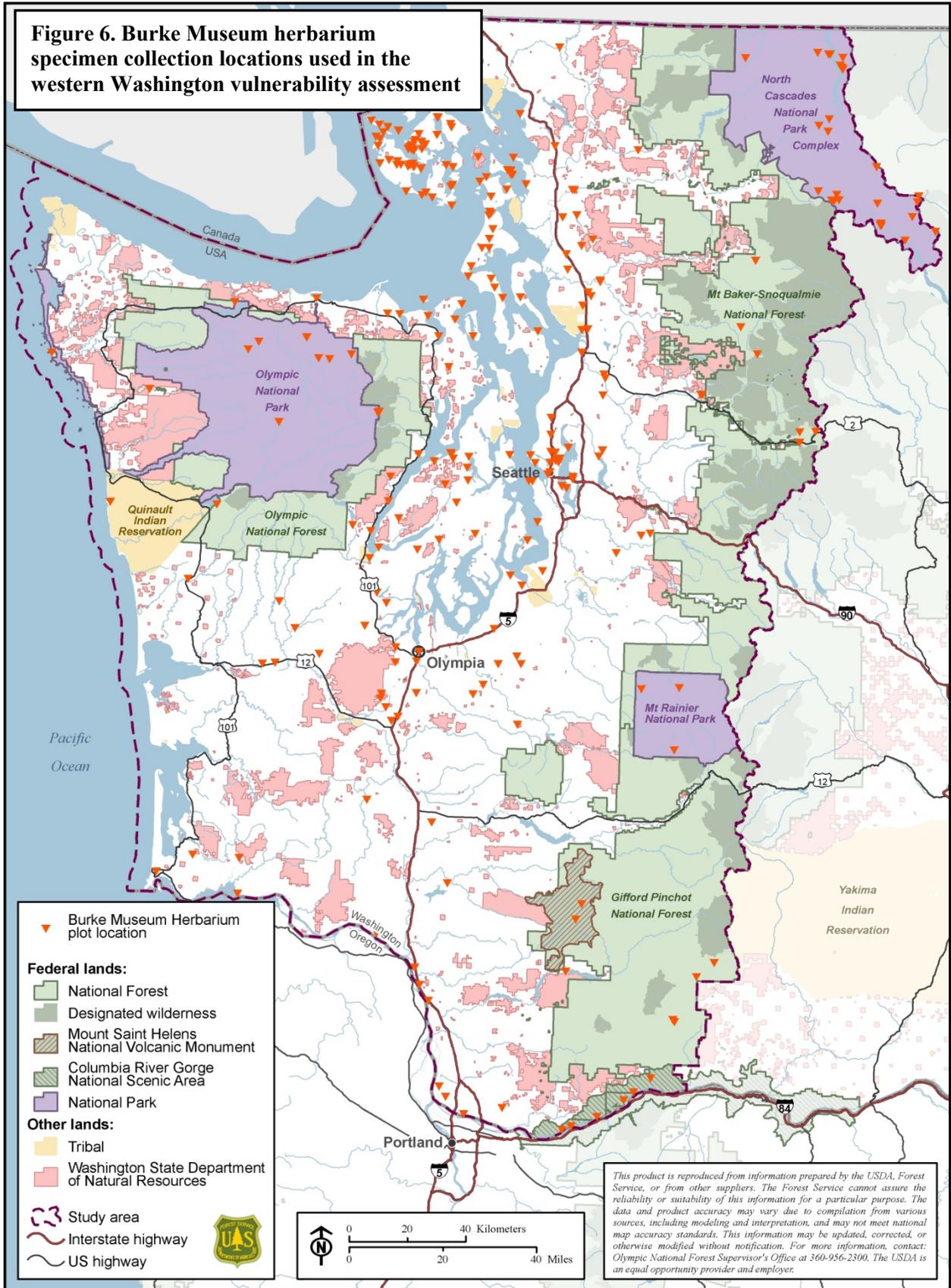


Figure 6. Burke Museum herbarium specimen collection locations used in the western Washington vulnerability assessment



distributions of all tree species before assigning the ratings. We used the following guidelines for rating this variable:

- Wide distribution (species occurs across all of the study area) = 0
- Moderate distribution (species absent from up to half of the study area—e.g., because elevation limits the presence of habitat—but common in the rest of the study area) = 25
- Narrow distribution (species present in less than half of study area, occurring there at a moderate to low density) = 50
- Very narrow distribution (species present only in a small part of the study area) = 75
- Rare (species occurs on only a few plots) = 100

Risk Factor Score

The ForGRAS model calculates a raw distribution factor score by averaging the scores of the three variables. It then scales this score so that the tree species with the lowest score is assigned a risk factor score of 0 and the species with the highest score is assigned 100. The purpose of this scaling is to make the species scores within each risk factor range from 0 to 100, thereby giving each risk factor the same influence on the overall vulnerability score.

CHAPTER 4. RISK FACTOR: REPRODUCTIVE CAPACITY

The reproductive capacity risk factor quantifies a species' capacity to migrate and regenerate in openings created by disturbance. Species that are limited in their production of seed or in seed dispersal are considered more vulnerable, given an expectation of an increase in large-scale disturbances under a changing climate (Littell et al. 2010). The variables in this risk factor are: seed dispersal vector, fecundity, seed dispersal capacity, minimum seed-bearing age, and dioecy (breeding system).

Required Data

To rate the variables in the reproductive capacity risk factor, several sources of data are required:

- *The Woody Plant Seed Manual* (Bonner and Karrfalt 2008). This publication, available freely online, is the most comprehensive single source of data for information on tree seeds and seed production. It summarizes all available information on tree species of the U.S.; therefore, it is applicable to the tree species of any study area in the country.
- Literature reviews and guides to tree species. *Silvics of North America* (Burns and Honkala 1990) and the *Fire Effects Information System* database (Fischer et al. 1996) are excellent compilations of biological and ecological data on U.S. tree species. Both are free online.
- Regional guides to tree species. For the Pacific Northwest assessment, *The Distribution and Synopsis of Ecological and Silvical Characteristics of Tree Species of British Columbia's Forests* (Klinka et al. 2000) was a useful source of information for this risk factor. It

includes tables that summarize reproductive information for each tree species.

Rating the Variables

Seed dispersal vector—Tree species that depend primarily on animal seed dispersal vectors are potentially vulnerable to climate change because behavior of animal species could be altered by changes in annual climate patterns. Tree species not adapted to long-distance dispersal of propagules, such as those with seeds dispersed primarily by gravity or those reproducing vegetatively, are also vulnerable.

- Species with wind or water dispersal vectors are assigned a vulnerability rating of 0.
- Species with animal dispersal vectors, seed dispersed by gravity, and species with minimal seed production (e.g., those reproducing primarily vegetatively) are assigned a rating of 100.

Fecundity—Fecundity is defined as the capacity to reproduce. For each species, gather information on the typical interval between seed crops, the interval between *large* seed crops, sound seed percentage, seed germination capacity, and how long seed can retain viability in the forest floor. Assign vulnerability ratings to species based on their fecundity relative to the other species in the assessment:

- Assign a rating of 0 to species with high fecundity.
- Assign a rating of 50 to species with medium fecundity.
- Assign a rating of 100 to species with low fecundity.

Seed dispersal capacity—For this variable, rate species according to the distance to which seed is typically dispersed. Often, values in the scientific

literature are based on the maximum distance to which the *majority* of seed (e.g., 90 percent) is dispersed; these are the values that should be used to rate this variable. For some tree species, information on seed dispersal distance is lacking; thus, values must be interpolated using dispersal distance values of other species within the same genus that have the most similar seed size, weight, and structure.

- Assign a rating of 0 for a dispersal distance of greater than 0.5 mi.
- Assign a rating of 50 for a dispersal distance of 400 ft to 0.5 mi.
- Assign a rating of 100 for a dispersal distance of less than 400 ft.

Minimum seed-bearing age—This variable is based on the premise that species that produce seed at a younger age have a shorter generation time and thus can more rapidly adapt to environmental change, migrate, and reproduce after large-scale disturbances. Migration rate is important for facilitating natural regeneration, given potential geographic shifts in suitable habitat. The age at which seed production begins for a given species can be variable; thus, for consistency, we recommend using the values given in *The Woody Plant Seed Manual* (Bonner and Karrfalt 2008), which describe minimum seed-bearing age under good growing conditions.

- Assign a rating of 0 for a minimum seed-bearing age of less than 10 years.
- Assign a rating of 50 for a minimum seed-bearing age of 10 to 20 years.
- Assign a rating of 100 for a minimum seed-bearing age of greater than 20 years.

Dioecy—Species with more complex breeding systems, for example, dioecious species which have separate male and female individuals, are at higher risk of extinction (Vamosi and Vamosi

2005). For this reason, we assigned these species a higher vulnerability rating.

- Species that are always or usually monoecious were assigned a rating of 0.
- Species that are always or usually dioecious were assigned a rating of 100.

Risk Factor Score

The ForGRAS model calculates a raw reproductive capacity factor score by averaging the scores of the five variables. It then scales this score so that the tree species with the lowest score is assigned a risk factor score of 0 and the species with the highest score is assigned 100.

CHAPTER 5. RISK FACTOR: HABITAT AFFINITY

The habitat affinity risk factor rates the degree to which a tree species' habitat affinities are expected to increase its vulnerability to projected changes in climate. For example, a species with a high level of drought tolerance is better-suited to warmer summer conditions with high evaporative demand, compared to a species with low drought tolerance. Thus, in the Pacific Northwest assessment, drought-tolerant species were assigned lower vulnerability ratings, given projected increases in summer temperatures during the 21st century (Littell et al. 2010). Four variables were selected for the habitat affinity risk factor: mean elevation, successional stage, habitat specificity, and drought tolerance.

Required Data

Several sources of data are used to rate the four variables in the habitat affinity risk factor:

- To rate the mean elevation variable, use FIA annual inventory data for the study area. A detailed description of the data preparation and analysis process appears in appendices 1 and 3.
- To rate the other three variables (successional stage, habitat specificity, drought tolerance), use information from literature reviews (e.g., Burns and Honkala 1990 and Fischer et al. 1996) and regional tree species guides (e.g., Arno and Hammerly 2007 and Klinka et al. 2000).

Rating the Variables

Mean elevation—Species with habitat limited to higher elevations are considered more vulnerable to climate change because the extent of their

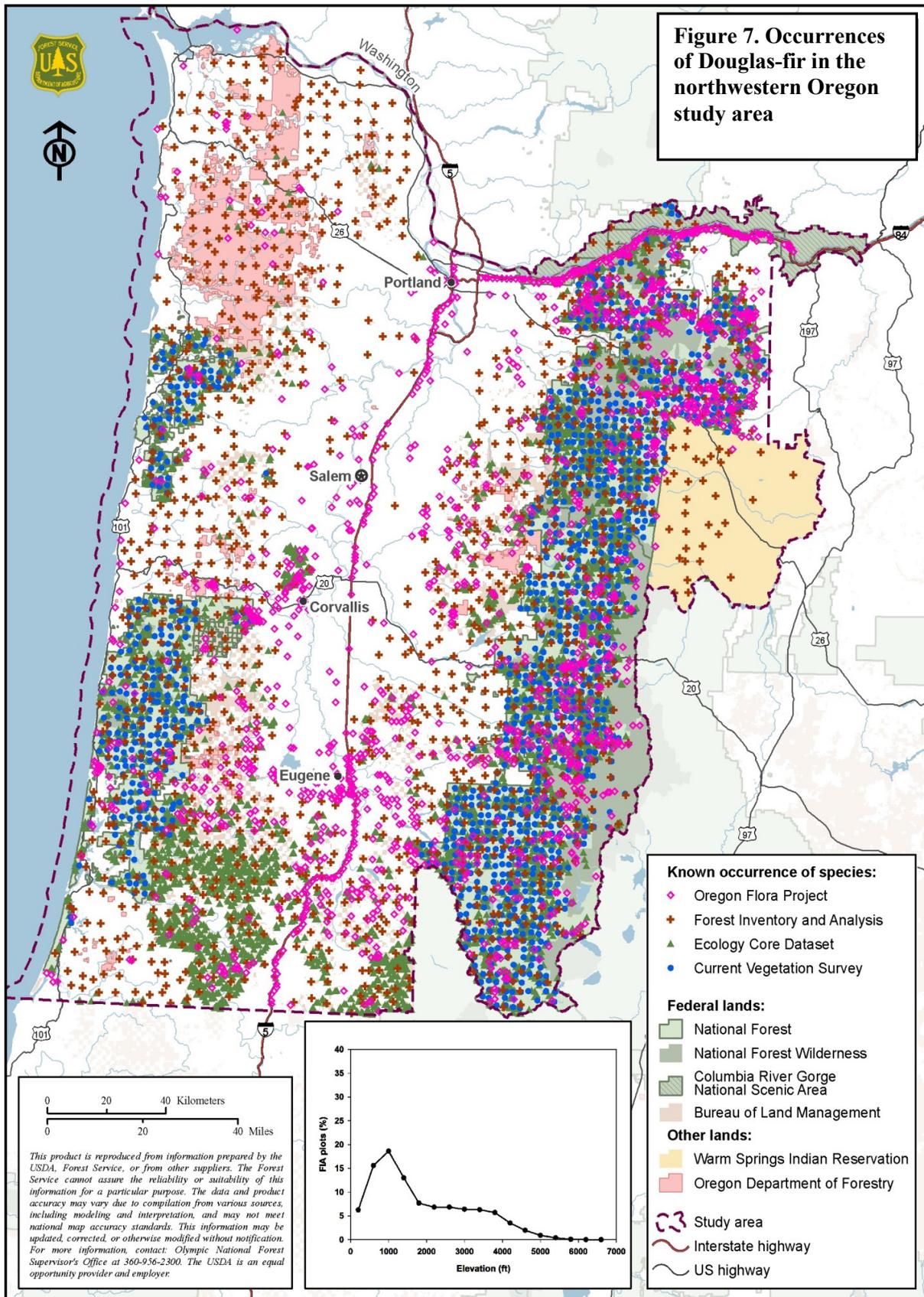
habitat and their pathways of migration become increasingly limited under long-term warming (Parmesan 2006). For each species, calculate the mean elevation of all FIA plots on which that species occurs within the study area (appendix 3). The ForGRAS model will then calculate a rating for each species ranging from 0 (the species with the lowest mean elevation) to 100 (the species with the highest mean elevation), with values for all other species assigned proportionally, according to where their mean elevations fall between these two extremes.

Although not necessary for rating this variable, graphs illustrating the distribution of species occurrences by elevation can be useful in understanding spatial patterns in habitat. An example of this type of graph is shown near the bottom of figure 7; instructions for creating an elevation graph appear in appendix 3.

Successional stage—Species adapted to late successional stages generally have greater within-population genetic diversity than species of early successional stages (Hamrick et al. 1992) and thus are assumed to be more vulnerable to loss of genetic diversity (Myking 2002, Potter and Crane 2010). We based the successional stage variable ratings on the successional stage at which a tree species typically becomes a significant component of the forest canopy:

- Significant canopy component in early successional stages only = 0.
- Significant canopy component in early and late successional stages = 50.
- Significant canopy component in late successional stages only = 100.

Habitat specificity—Habitat specificity represents the specificity of a given species' habitat requirements relative to the other tree species in the study area. A species with high habitat specificity is assigned a high vulnerability



rating because it is considered more vulnerable to habitat loss associated with climate change than a species adapted to a broad range of habitats. Because ratings are based on habitat specificity relative to the other tree species, one must consider the range of habitats of each of the species in the study area. Habitat specificity is rated qualitatively, as low, medium, or high:

- Species with low habitat specificity are assigned a rating of 0. These species occur in a habitat type that is very common within the study area or in a range of habitats that, when combined, represent a substantial portion of the study area.
- Species with medium habitat specificity are assigned a rating of 50. These species may be limited to a certain elevational range that represents only a portion of the study area or they may have other habitat requirements that prevent them from becoming widespread.
- Species with high habitat specificity are assigned a rating of 100. These species are limited to very specific habitat within the study area. It is possible that, within a study area, no species have this level of habitat specificity. For example, in the western Washington study area, none of the group 1 tree species (i.e., major canopy trees) were rated as having high habitat specificity (Devine et al. 2012).

Drought tolerance—Projected increases in summer temperatures are likely to be associated with greater evaporative demand, even if no substantial change occurs in summer precipitation. Thus, tree species with low drought tolerance have a higher level of vulnerability to projected increases in summer temperature in regions such as the Pacific Northwest where summer moisture is generally growth-limiting (Littell et al. 2010). Drought tolerance is rated as low, medium, or high. Ratings are assigned

relative to the other tree species within the study area; therefore, drought tolerance information for all species must be examined before ratings can be assigned.

- Species of high drought tolerance are assigned a vulnerability rating of 0.
- Species of medium drought tolerance are assigned a vulnerability rating of 50.
- Species of low drought tolerance are assigned a vulnerability rating of 100.

Risk Factor Score

The ForGRAS model calculates a raw habitat affinity risk factor score by averaging the scores of the four variables. It then scales this score so that the tree species with the lowest score is assigned a risk factor score of 0 and the species with the highest score is assigned 100.

CHAPTER 6. RISK FACTOR: ADAPTIVE GENETIC VARIATION

The adaptive genetic variation risk factor describes a tree species' ability to adapt to a changing climate using three variables: elevation band width of seed zones, pollen dispersal vector, and the presence of disjunct populations. This risk factor is based on elements that describe genetic diversity, gene flow, and population structure. Genetic variation in traits related to local adaptation is critically important in assessing vulnerability to climate change. We chose to use seed zone elevation band width (within the study area) as a surrogate for adaptive genetic variation. Species with one or no elevation bands are considered generalists with wide climatic tolerances, whereas species with several narrow elevation bands are considered specialists, highly adapted to their local environment, with specific climatic requirements. Gene flow occurs through the movement of pollen and seed; species that are insect-pollinated are more vulnerable to climate change because of the required interaction with another organism whose behavior may be influenced by a changing climate. Some tree species with disjunct populations are considered to have elevated vulnerability to climate change because loss of the genetic variation represented by the disjunct population could negatively affect the climate change vulnerability of the species as a whole.

Required Data

- Local forest tree seed zone manuals (e.g., Randall 1996, Randall and Berrang 2002) provide specific information on seed zone elevation band width for many tree species. For some tree species,

particularly non-commercial species, data on elevation band width are absent from the manuals and therefore must be extracted from other sources in the scientific literature. In a few cases, data are not explicitly available in the literature, and values must be interpolated by a geneticist, by using data from closely related species.

- Tree species guides and literature reviews (Burns and Honkala 1990, Fischer et al. 1996) provide data on pollen dispersal vectors.
- To identify disjunct populations, use the species distribution maps created in the distribution risk factor (chapter 3) in conjunction with range-wide maps (available online at: <http://esp.cr.usgs.gov/data/atlas/little/> and in publications such as Little (1971, 1976)). The tree distribution maps created with documented occurrences provide greater fine-scale accuracy for the study area (fig. 8), whereas the range-wide maps are necessary to evaluate the location of disjunct populations relative to a species' full distribution.

Rating the Variables

Elevation band width of seed zones—Seed zone band width is defined as the range in elevation within which maladaptation due to seed movement is minimized. Species with narrow elevation band widths are highly adapted to their local environment, with specific climatic requirements, and are thus considered more vulnerable to climate change.

- Species with no seed zone elevation bands (i.e., seed may be moved across the species' full elevational range without maladaptation) are assigned a rating of 0.

Figure 8. Recent documented occurrences, and Little's (1971) distribution data, for Rocky Mountain juniper in western Washington. Note that the mapped recent occurrences show additional populations



- Species with seed zone elevation bands greater than 1,500 ft wide are assigned a rating of 33.
- Species with seed zone elevation bands 1,000 to 1,500 ft wide are assigned a rating of 67.
- Species with seed zone elevation bands less than 1,000 ft wide are assigned a rating of 100.

Pollen dispersal vector—Tree species that depend on insects, rather than wind, for pollination (and therefore gene flow) have a potentially increased vulnerability to climate change. Changes in climate could affect behavior of pollinators and influence tree phenology; thus, gene flow could be negatively affected if the interaction between trees and pollinators are altered.

- Primarily wind-pollinated tree species are assigned a vulnerability rating of 0.
- Primarily insect-pollinated tree species are assigned a vulnerability rating of 100.

Disjunct populations—A tree species is assigned a high vulnerability rating if the potential loss of a disjunct population is deemed likely to impact the climate change vulnerability of the species as a whole. For example, if a study area includes a disjunct population that is known to be genetically distinct, or if the disjunct population represents the edge of the species' distribution, the loss of this population could represent loss of adaptive genetic variation for the species as a whole.

- If the study area does not include a disjunct population that either (a) represents the edge of the species' distribution, or (b) is known to be genetically distinct, then assign a rating of 0.

- If the study area includes a disjunct population that represents the edge of the species' distribution (e.g., the species' southernmost or easternmost occurrence), assign a vulnerability rating of 100. Or, if a disjunct population in the study area is known to be genetically distinct, even if it does not represent the edge of the species' distribution, it should also be assigned a rating of 100.

Risk Factor Score

The ForGRAS model calculates a raw adaptive genetic variation risk factor score by averaging the scores of the three variables. It then scales this score so that the tree species with the lowest score is assigned a risk factor score of 0 and the species with the highest score is assigned 100.

CHAPTER 7. RISK FACTOR: INSECT AND DISEASE THREATS

This risk factor quantifies insect and disease threats that presently affect a tree species or are expected to exacerbate the negative impacts of climate changes on tree survival, growth, or vigor. For each tree species, as many as five of the most important threats are rated according to the immediacy and severity of the threat.

Required Data

Data for this risk factor are ideally provided by experts in forest entomology and pathology. In the Pacific Northwest assessment, data were provided by personnel from the Forest Service Forest Health Protection Service Center (i.e., field office) that served the area in which each study area was located. We provided the pathologists and entomologists at the service center with a list of tree species and a detailed description of the overall objectives and the rating system. The service center personnel then listed and rated each of the major insect and disease threats for each of the tree species.

Rating the Variables

In the Pacific Northwest vulnerability assessment, Service Center personnel identified the most important insect and disease threats for each tree species (to a maximum of five threats per tree species). They rated two variables for each threat: severity and immediacy.

Severity—Severity is defined as the present impact of a threat. Potential ratings range from 1 to 10:

- Minor mortality, usually of already-stressed trees = 1
- Moderate mortality in association with other threats = 3
- Moderate mortality of mature trees = 5
- Significant/complete mortality in related species = 6
- Significant mortality of mature trees = 8
- Complete mortality of all mature trees = 10.

Immediacy—The immediacy of each threat is rated on a scale of 1 to 3:

- Potential to reach region of interest = 1
- Present in region = 2
- Present in region and climate change appears to be a contributing factor in increases in distribution and impact = 3.

Risk Factor Score

For each tree species, the ForGRAS model calculates a score for each threat by multiplying the threat's severity and immediacy values. The model next calculates the tree species' raw risk factor score by summing all of the threat scores for that species. It then scales all of the tree species' raw scores so that the tree species with the lowest score is assigned a risk factor score of 0 and the species with the highest score is assigned 100.

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APPENDIX 1: DATA RETRIEVAL AND PREPARATION

This appendix contains a description of the steps followed to retrieve and prepare tree distribution data for the Pacific Northwest vulnerability assessment. It includes the major data sources used: FIA, CVS, Regional Ecology Program Core Dataset, the Burke Museum herbarium, and the Oregon Flora Project. When applying the ForGRAS model to other regions (i.e., areas outside Washington and Oregon), available sources of data will differ; however, the descriptions of these processes should provide a useful starting point.

Determine Tree Species List and Associated Codes

Before extracting data from various sources, it is helpful to compile a comprehensive list of species names and synonyms, and their associated species codes. Different sources may use different names and/or codes to represent the same species; sometimes multiple codes are even used within the same dataset (table 3). The online USDA Plants Database (www.plants.usda.gov) lists many pseudonyms and associated codes but should not be solely relied upon, especially if searches are based on species codes. For example, the Plants Database code for *Acer macrophyllum* (bigleaf maple) is ACMA3, but searching the Ecology Core Dataset (which uses codes but not species names) for “ACMA3” will result in zero selections because the Ecology Core Dataset code is “ACMA” (without the “3”). Searching for FRPU (not FRPU7, as listed in the Plants Database) will result in a partial selection of *Frangula purshiana* (cascara) because many of the species’ records in that dataset are coded RHPU, an older synonym. Other agencies, such

as the USDI National Park Service, may use a completely different coding system, in which case it might be more appropriate to base searches on species names, where included, or on multiple fields. It is useful to run a frequency on the search field (code or name) in each shapefile to obtain a list of all choices within each dataset.

Data Sources

The ForGRAS model, as applied in the Pacific Northwest Vulnerability Assessment, can be run using only data from the FIA annual inventory. However, the Pacific Northwest Assessment included data from several secondary sources as well. The most frequently used of these secondary sources were CVS, Ecology Program Core Dataset, the Oregon Flora Project, and the Burke Museum herbarium. These secondary data sources were not used to calculate the quantitative variable ratings for the model; rather, they were used to improve the precision of the distribution maps and better our understanding of species’ distributions. In the case of less-common tree species, the FIA annual inventory often did not full capture the full distribution, and the secondary data sources proved highly useful. A drawback of using the secondary sources is that it can be time-consuming to process and compile the data, particularly for large study areas. If a model user chooses not to acquire secondary data (i.e., only uses FIA data), it is recommended that the user augment their data with Little’s range maps (Little 1971, 1976).

FIA Annual Inventory Data (Available Nationwide)

The FIA dataset is used for vulnerability ratings and for creating maps of species occurrences; the other datasets, described later, are used only for creating maps of occurrences. For the purpose of the ForGRAS vulnerability assessment, the FIA annual inventory dataset is the most important

source of tree distribution data. The FIA annual inventory consists of sample plots on all forested lands, regardless of ownership, at a frequency of one plot per 6,000 acres. This inventory is conducted on a 5- to 10-year cycle (depending on the state) in which 10 to 20 percent of all plots are measured each year. This annual inventory began around 2000 in most states, and for some states operating on a 10-year cycle, the full dataset is not publicly available yet. However, a partial state dataset consisting of at least 70 percent of plots is sufficient for this type of assessment because there is no spatial bias in

sequence of plots measured (i.e., the 70 percent of plots that have been measured are uniformly distributed across the state).

The FIA database is publicly available at the FIA DataMart: <http://apps.fs.fed.us/fiadb-downloads/datamart.html>. The User Manual can be downloaded from <http://fia.fs.fed.us/library/database-documentation/>, and the Field Guide can be found at <http://www.fia.fs.fed.us/library/field-guides-methods-proc/>. To retrieve and prepare an FIA dataset:

Table 3. Examples of variation in tree species codes among data sources used in the Pacific Northwest vulnerability assessment

Scientific name	Working code	Synonyms listed in USDA Plants Database	Dataset			
			Forest Inventory and Analysis	Ecology Core Data	Current Vegetation Survey	NPS
<i>Abies amabilis</i>	ABAM	None.	ABAM	ABAMT, ABAM ¹	ABAM	ABIAMA
<i>Acer macrophyllum</i>	ACMA3	None.	ACMA3	ACMAT, ACMA ¹	ACMA and ACMA3	ACEMAC
<i>Cupressus nootkatensis</i>	CUNO	CHNO, CUNO, XANO4, CANO9 ²	CHNO	CHNOT, CHNO ¹	CUNO and CHNO	CHANOO
<i>Frangula purshiana</i>	FRPU7	RHPU	FRPU7 (in shrub dataset)	RHPUT	None.	None.
<i>Populus balsamifera</i> ssp. <i>trichocarpa</i>	POBAT	POBAC3, POHA15, POTR15, POTRH, POTRC, POTRH2, POTRI	POBAT	POTR2T, POTR2 ¹	POBAT or POTR2	POPBALTRI
<i>Populus tremuloides</i>	POTR5	POAU8, POCE6, POPO12, POTRT, POTRA, POTRC2, POTRI2, POTRM, POTRR, POTRV, POVA11	POTR5	None. (although POTR3 was listed)	POTR5	POPTRE

¹ Code used on the Gifford Pinchot National Forest only.

² Code currently used in USDA Plants Database, which is different from the working code.

- 1) Download the FIADB Microsoft Access database for the state of interest. At <http://apps.fs.fed.us/fiadb-downloads/datamart.html> click on the state abbreviation on the right-hand map of the U.S. Note that the species codes, common names, and scientific names used in the FIA database can be found in Appendix F of the FIA Database User Manual. Unzip the downloaded file if necessary.
- 2) Query this database for plot number, coordinates, and elevation, species codes and names, and tree status of all trees (defined as one inch in diameter and larger). To perform this query, first open Microsoft Access, and then open the database that was just downloaded in step 1. Click on the Create menu, click Query Design on the ribbon, close the window that pops up, and then click the SQL button on the ribbon. In the window that appears, delete “SELECT;” and replace it with the query in the box below (i.e., the capitalized paragraph in the box). Next, click the Run button on the ribbon. The result of the query will appear in a new window. Export the results of this query to an Excel spreadsheet by clicking on the External Data menu; then, within the Export ribbon, click on the Excel button. In the resulting window, name the file, and check the box titled “Export data with formatting and layout.” Click OK.
- 3) In ArcGIS, use the Excel spreadsheet data to create an ArcGIS shapefile (or feature class). FIA coordinates are recorded in decimal degrees, using NAD 83 datum. (Note that these coordinates are “fuzzed” and are accurate at least to within one mile of the actual location. In addition, up to 20 percent of coordinates representing plots on private land have been “swapped” with similar locations within the same county in an effort to protect landowner privacy.)
- 4) *Optional step, only for analyses that include species recorded as shrubs in FIA data:*
Query the FIA database for tree species that may have been recorded in the

SQL Query for selecting FIA trees

```
SELECT DISTINCT PLOT.PLOT, PLOT.LAT, PLOT.LON, PLOT.ELEV, TREE.SPCD,
REF_SPECIES.GENUS, REF_SPECIES.SPECIES, REF_SPECIES.VARIETY,
REF_SPECIES.SUBSPECIES, REF_SPECIES.SPECIES_SYMBOL,
REF_SPECIES.COMMON_NAME, TREE.STATUSCD
FROM (PLOT INNER JOIN TREE ON PLOT.CN = TREE.PLT_CN) INNER JOIN REF_SPECIES
ON TREE.SPCD = REF_SPECIES.SPCD
WHERE ((TREE.STATUSCD)=1);
```

For each plot, this query will list each tree species (live trees only, which is specified by TREE.STATUSCD=1) that exists within the plot (genus, species, variety, subspecies, species symbol, and common name) and the lat/long location and elevation of each plot.) This query DOES NOT select species classified as shrubs.

database as understory vegetation, or “shrubs” (due to having multiple stems instead of single stems, or due to a change in recording protocol). For the Pacific Northwest vulnerability assessment, records containing trees classified as shrubs were selected with the help of FIA personnel from the Forest Service Pacific Northwest Research Station FIA Program. We supplied them with a list of all FIA plot numbers within the study area and a list of all the species in the analysis, and then they created a table that included all plot numbers where each shrub species was recorded. We then imported this table into the FIA database and used it to retrieve the location coordinates and related information for each of those species. For the Washington and Oregon study areas, the tree species classified as shrubs by FIA were Douglas and Rocky Mountain maple, black and Suksdorf’s hawthorn, cascara, golden chinquapin, western chokecherry, and all willow (*Salix*) species. An additional shapefile was created for each of these shrub species, which was then selectively combined with the tree shapefile: only points representing new locations for a species (i.e., those plots where the species was not already represented as a tree) were transferred to the tree shapefile.

- 5) Create maps showing the distribution of each species, incorporating any desired base maps for the study area. Visually inspect the maps for each species and remove from the shapefile any point that is obviously in error. Detecting these errors requires some judgment when locations show a species occurring in areas where it is highly unlikely to occur (example in fig. 9). Such unusual

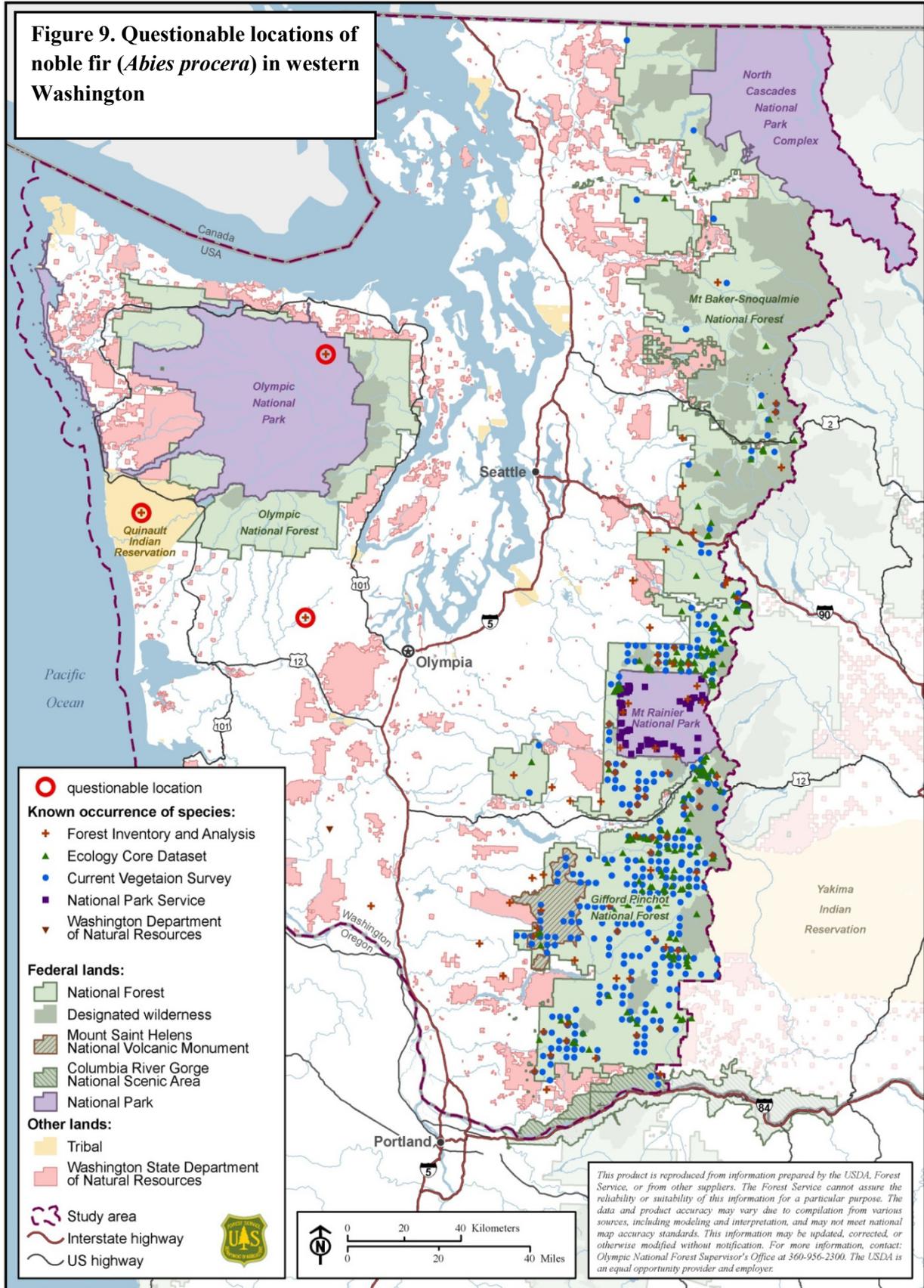
locations are typically the result of error. These errors usually result from data entry mishaps, particularly in older records that were input prior to the inception of software checks. Examples are mistyping species codes (“101” instead of “110”), or mistyping a coordinate.

Current Vegetation Survey Data (Forest Service Region 6 Only)

The CVS dataset is used only for creating species occurrence maps. Compressed dBase files of CVS data for national forests within Oregon and Washington can be downloaded at http://www.fs.fed.us/r6/survey/data_tables.htm. The User Guide can be found at <http://www.fs.fed.us/r6/survey/document.htm>.

- 1) Download and then unzip the data files for each national forest in the area of interest. It is best to unzip each forest’s data into a separate folder, as each forest has multiple data files. For each national forest within the study area, complete the following steps:
 - a. Import the data into Access by first opening Access and creating a new blank database (under the File menu), named for the national forest. Next, go to the External Data menu and select More>dBASE File from the Import & Link ribbon. Import the TREEDATA.DBF for the forest.
 - b. Go again to the External Data menu and select More>dBASE File from the Import & Link ribbon. This time import the PSUDATA.DBF for the same

Figure 9. Questionable locations of noble fir (*Abies procera*) in western Washington



forest. The database will now have two tables, one named PSUDATA and one named TREEDATA.

- c. After steps 1a and 1b have been repeated for each national forest in the study area, there should be a database for each forest, and each database should contain two tables.
- 2) *Repeat this step for each national forest's database:* Query the database for plot number, coordinates, and elevation, and species codes and names. To do this, click on the Create menu, click Query Design on the ribbon, close the window that pops up, and then click the SQL button on the ribbon. In the window that appears, delete "SELECT;" and replace it with the query in the box to the right. Next, in the Query Type group, click on Make Table. Name the table and leave "current database" selected. Click OK. Next, click the Run button on the ribbon. A warning box will appear; click Yes to create the new table. Open the new table in Datasheet View. Click on the left-most column header and then click on Fields tab under Table Tools. The Data Type shown in the ribbon should appear as "Number"; click the next column header. With the exception of the species code column, which should be "Text", all other columns must be set to "Number."
- a. Export this table by clicking on the External Data menu; then, within the Export ribbon group, click on the Excel button. In the resulting window, name the file after the national forest, and check the box titled "Export data

with formatting and layout."
Click OK.

SQL Query for selecting trees in CVS data

```
SELECT DISTINCT TreeData.PSUNr,
TreeData.SPECSCIA,
PSUDData.UTMZone,
PSUDData.Northing, PSUDData.Easting,
TreeData.VegCode,
PSUDData.ELEVATIO FROM TreeData
LEFT JOIN PSUDData ON
TreeData.PSUNr = PSUDData.PSUNr;
```

- b. Open the Excel spreadsheet, and examine the UTM zone data. If multiple zones are represented within a single national forest (i.e., a single spreadsheet), then use cut and paste to separate the records into additional spreadsheets based on UTM zone. Each sheet must include only one UTM zone and should be named according to the forest and the zone.
- 3) Use the Excel spreadsheets to create ArcGIS shapefiles (or feature classes). Coordinates are UTM, NAD 1983, zones 10 or 11. Note that these coordinates are "fuzzed", but most are accurate to within 0.85 mile of the actual location.
 - 4) In ArcMap, add a "Source" field to each shapefile and populate with the forest name, then merge all shapefiles.
 - 5) Add an "ELEV" field to the final shapefile and calculate equal to "ELEVATIO * 100" (the ones and tens

digits for elevation values were not entered in the database).

- 6) Create maps showing the distribution of each species. Visually inspect the maps for each species and remove from the shapefile any point that is obviously in error (as described above in step 5 of the FIA data preparation process).

Regional Ecology Program Core Dataset (Forest Service Region 6 Only)

This dataset is used only for creating species occurrence maps. Zipfiles containing Access databases of USFS Region 6 Ecology Program core dataset are available at <http://ecoshare.info/category/data-sets/>. Data dictionaries are included.

- 1) Download and unzip the Core Data file or files for the study area from <http://ecoshare.info/category/data-sets/>.
- 2) *Repeat this step for each Core Data dataset needed for the study area (e.g., SW Oregon, NW Oregon, etc.):*
 - a. Open the Access database file (i.e., the “.mdb” file) in Access.
 - b. The procedure will involve joining plot number fields from different tables. However, these field must be of the same data type. Verify this first by opening (double-clicking) the table name ending in “VEGETATION_LOADER”. Click on the PLOT_NUMBER column header at the top of the table. Click on the Fields tab under Table Tools at the top of the window. Data Type should be

set to “Number”. Now open (double-click) the table name on the left side of the screen ending in “EXPORT_VU”. Click on the PLOTNBR column header at the top of the table. Click on the Fields tab under Table Tools at the top of the window. Data Type should be set to “Number”. If it is not, change it to “Number”.

- c. Query the database for plot number, coordinates, elevation, and species codes. To perform this query, click on the Create menu, click Query Design on the ribbon, close the window that pops up, and then click the SQL button on the ribbon. In the window that appears, delete “SELECT;” and replace it with the query in the box below (i.e., all of the non-italicized text from the box). Next, click the Run button on the ribbon. The result of the query will appear in a new window. Export the results of this query to an Excel spreadsheet by clicking on the External Data menu; then, within the Export ribbon, click on the Excel button. In the resulting window, name the file, and check the box titled “Export data with formatting and layout.” Click OK.
- 3) Open the exported Excel spreadsheet, and examine the UTM zone data. If multiple zones are represented within a single spreadsheet, then use cut and paste to separate the records into additional spreadsheets based on UTM zone. Each sheet must include only one UTM zone

and should be named according to the area and the zone.

- 4) Use the Excel spreadsheets to create ArcGIS shapefiles (or feature classes). Coordinates for these data are UTM, NAD 1983, zones 10 or 11.
- 5) In ArcMap, delete points that do not represent species of interest. Also delete any points that were created for records that do not have UTM coordinates. Add a "SOURCE" field to each shapefile and populate with the region name.
- 6) Standardize the item names and definitions so that multiple shapefiles can be combined, then merge all shapefiles.
- 7) Create maps showing the distribution of each species. Visually inspect the maps for each species and remove from the shapefile any point that is obviously in error.

SQL query for selecting Ecology Program Core Dataset tree data

This example is from the Program's southwestern Oregon area. Note that the final line of this query excludes understory species.

```
SELECT DISTINCT
FS_R6ECD_ECD_SW_OR_VEGETATION_LOADER.PLOT_NUMBER,
FS_R6ECD_ECD_SW_OR_VEGETATION_LOADER.LAYER,
FS_R6ECD_ECD_SW_OR_VEGETATION_LOADER.SPECIES_CODE,
FS_R6ECD_ECD_SWO_PLOT_EXPORT_VU.AGENCY,
FS_R6ECD_ECD_SWO_PLOT_EXPORT_VU.REGION,
FS_R6ECD_ECD_SWO_PLOT_EXPORT_VU.ELEV,
FS_R6ECD_ECD_SWO_PLOT_EXPORT_VU.UTMZONE,
FS_R6ECD_ECD_SWO_PLOT_EXPORT_VU.UTMEAST,
FS_R6ECD_ECD_SWO_PLOT_EXPORT_VU.UTMNORTH
FROM FS_R6ECD_ECD_SW_OR_VEGETATION_LOADER LEFT JOIN
FS_R6ECD_ECD_SWO_PLOT_EXPORT_VU ON
FS_R6ECD_ECD_SW_OR_VEGETATION_LOADER.PLOT_NUMBER =
FS_R6ECD_ECD_SWO_PLOT_EXPORT_VU.PLOTNBR
WHERE ((Not (FS_R6ECD_ECD_SW_OR_VEGETATION_LOADER.LAYER)="U"));
```

Burke Museum Herbarium Data (Primarily Washington State)

This dataset is used only for creating species occurrence maps. The Burke Museum Herbarium maintains an online database of its specimens, and many of these specimen records include coordinates indicating where the specimen was collected and a date of collection. In the Pacific Northwest assessment, we assumed that locations of herbarium specimens collected within the last 20 years still represent current locations of that species (this timeframe could be longer or shorter based on user objectives). A description of the Burke Museum's online herbarium database is at: <http://biology.burkemuseum.org/herbarium/collections/list.php>. To download and map specimen collection locations:

- 1) Search database by species, genus, family, or other variables:
<http://biology.burke.washington.edu/herbarium/collections/vascular/search.php>. Because data must be downloaded separately for each species or genus, it may be more efficient to acquire data only for those species for which the other data sources provide inadequate coverage. For example, we did not download herbarium data for Douglas-fir or western hemlock, which were well-covered by other data sources, but we did download data for the less-common Rocky Mountain juniper and Oregon white oak. Note that you can narrow the query by state, if desired.
- 2) Download the results of a species search by clicking on the DOWNLOAD tab. Next, click on the "Tab-Delimited Text" option, and save the file.
- 3) To open this saved file in Microsoft Excel, first load Excel, then choose "Open" and specify the saved ".txt" data file. This will automatically launch the Text Import Wizard. The default settings

in the Wizard (i.e., "delimited" data type; "tab" delimiters; "general" column data format) will import the file with proper formatting.

- 4) Save this imported file as an Excel spreadsheet.
- 5) Edit the data as desired, to retain only the records that you want to map. We deleted records that did not include coordinates. (If necessary, for records of rare species that do not have coordinates, you may want to screen digitize points based on written descriptions.) We also deleted records from states outside of the study area and records of specimen collections older than 20 years. Alternatively, some of these criteria can be included in the initial query in step 1.
- 6) Repeat steps 1 through 5 for all species.
- 7) Using Copy and Paste functions, transfer data for all species into a single Excel sheet.
- 8) Prepare spreadsheet by removing spaces from field names and shortening field names to be ArcGIS compatible. Delete any columns that do not contain data needed for mapping or species identification.
- 9) Use the Excel spreadsheets to create shapefiles (or feature classes) after separating records based on coordinate type. Most coordinates are given in decimal degrees, with various datums (some datums are unknown). Some records also have UTM coordinates, while some only have UTM coordinates. Others have only Public Land Survey System locations and/or written descriptions.
- 10) Create maps showing the distribution of each species. Visually inspect the maps and remove from the shapefile(s) any point that is obviously in error, or that

represents an occurrence of a species that is likely planted.

Oregon Flora Project (Oregon Only)

This dataset is used only for creating species occurrence maps. The Oregon Flora Project (<http://oregonflora.org/about.php>) makes available the geographic coordinates of herbarium specimen collections and observations of approximately 4,500 vascular plant taxa within the state of Oregon. Data are available through the “atlas” feature at <http://oregonflora.org/atlas.php>. To extract and process data:

- 1) At the web page <http://oregonflora.org/atlas.php>, search for a species by scientific or common name and then click the CREATE MAP button. The resulting map will include a DOWNLOAD RESULTS button. Click this button and choose a location to save the “.csv” data file. Alternatively, the website also allows one to map multiple species at the same time, so it is possible to map and then download data for all species of interest to a single “.csv” file. If this option is chosen, then skip steps 3 and 4.
- 2) Edit the data file as desired using Microsoft Excel or another program, to retain only the records that you want to include on the GIS map.
- 3) Repeat steps 1 and 2 for all species of interest.
- 4) Using Copy and Paste functions, transfer data for all species into a single Excel sheet.
- 5) Prepare spreadsheet by removing spaces from field names and shortening field names to be ArcGIS compatible.
- 6) Use the spreadsheet to create an ArcGIS shapefile (or feature class). Geographic coordinates are given in decimal degrees, with no datum specified (we assumed the datum was NAD 1983).
- 7) Create maps showing the distribution of each species. Visually inspect the maps and remove from the shapefile(s) any point that is obviously in error, or that represents an occurrence of a species that is likely planted.

APPENDIX 2. DATA PROCESSING AND CALCULATIONS FOR THE DISTRIBUTION RISK FACTOR

Frequency of Occurrence Variable (Percent of FIA Plots)

- 1) Prepare the FIA shapefile (the file already processed as described in appendix 1) by completing these steps:
 - a. Determine whether any species is represented by more than one code. Do this by comparing the list of species under assessment to the list of species in the FIA dataset. This requires some familiarity with the species under assessment (and, if applicable, subspecies or varieties).
 - b. If the vulnerability assessment is conducted at the subspecies or variety level, and if these subspecies or varieties are not each represented by a unique code in the FIA dataset, then it is necessary to add an additional field using ArcMap and calculate a unique code for each subspecies or variety. For example, in the Pacific Northwest assessment, PICO represented two varieties in the FIA database: shore pine (PICOC) and lodgepole pine (PICOL). For these varieties, we coded a new field and identified observations as PICOC or PICOL, based on their geographic locations.
- 2) Determine the total number of plots in the study area.
 - a. Clip the FIA shapefile with the study area boundary shapefile. This clipped shapefile will also be used later in appendix 3.
 - b. In ArcMap, select all points in the clipped shapefile. Run the Frequency Tool on PLOT. Note the number of records returned by the frequency operation to obtain the total number of plots within the study area (this is not the same as the highest OID number). Export the results to a textfile to obtain a list of all plot numbers in the study area (this will be used in the next section).
- 3) Calculate the percentage of plots in the study area on which each species occurs.
 - a. In ArcMap, run the frequency tool on the field representing unique species codes (either field SPECIES_SYMBOL from the FIA database, or the field added in step 1b, above).
 - b. Export the frequency results to a text file, and then import the text file to a spreadsheet (the file will be comma delimited; do not import the OID field). To do this using Excel, first open Excel, then choose Open under the File menu. Make sure "All Files" is selected as the file type; this will allow a text file to be opened. Column B of the imported spreadsheet should contain the frequency (number of plots) for each species.

- c. In a new column in the spreadsheet, calculate the percentage of plots on which a given species occurs (e.g., $=B2/totnum \times 100$, where *totnum* is the total number of plots within the study area from step 2b).

Proportion of Canopy Trees Variable

- 1) Download the FIA data for the state in which the study area is located by going to <http://apps.fs.fed.us/fiadb-downloads/datamart.html>, scrolling down to the appropriate state, and clicking on the “TREE.CSV” file. For example, for the state of Oregon, the file is called OR_TREE.CSV. The following steps described how to extract from this TREE.CSV file only the records for plots that are in the study area:
 - a. To extract study area plots only, you will first need the list of FIA plots within the study area. This list was created, as a text file, in step 2c for the frequency of occurrence variable above.
 - b. Next, open a blank database in Microsoft Access. Under the External Data ribbon, choose “Text file”. In the new window that appears, click the Browse button to locate the plot list text file described in the previous step (1a). Click OK. In the next window, accept the Delimited option, and click Next. Comma should be selected; check the box “First Row Contains Field Names” and click Next. In the next window, change the name of the plot field to PLOT_LIST and then click Finish and then Close.
 - c. Under the External Data ribbon, again choose “Text file”. In the new window that appears, click the Browse button to locate the “TREE.CSV” file described at the beginning of step 1 above. Click OK. In the next window, accept the Delimited option, and click Next. Comma should be selected; check the box “First Row Contains Field Names” and click Finish and then Close. Import errors may occur regarding some of the date fields, but these may be ignored because they are not needed for this process.
 - d. Under the Database Tools ribbon, select Relationships. In the window that appears, add the two tables from steps 1b and 1c. Click Close. Click the Edit Relationships button in the Design ribbon. Click the Create New button in the Edit Relationships window. For Left Table Name, select the plot list table created in 1b; for Left Column Name select the PLOT_LIST variable. For Right Table Name, select the tree data table created in 1c; for Right Column Name select the PLOT variable. Click OK. In the Edit Relationships window click Create.
 - e. Under the Create ribbon, click Query Design. In the Show Table window, select each of the two tables from steps 1b and 1c and click Add to add each one. Click

Close to close the Show Table window. In the small window showing the plot list table variables, double-click the PLOT_LIST variable. In the other small window, showing the tree data variables, double click on each of the following variables: STATUSCD, SPCD, CCLCD, and TPA_UNADJ (the last variable is near the bottom of the list). In the lower window, in the STATUSCD column, enter a value of 1 in the Criteria row. In the lower window, in the CCLCD column, enter <4 in the Criteria row. Uncheck the Show boxes in the STATUSCD and CCLCD columns. In the Design ribbon, click Run.

SQL Query for step 1e (an alternative way of completing step 1e, for users familiar with Access)

```
SELECT PLOT_LIST.PLOT, TREE.SPCD,
TREE.TPA_UNADJ
FROM PLOT_LIST INNER JOIN TREE ON
PLOT_LIST.PLOT = TREE.PLOT
WHERE (((TREE.STATUSCD)=1) AND
((TREE.CCLCD)<"4"));
```

- f. Export this query (named Query1 by default): with the query results showing, go to the External Data ribbon and click Excel in the Export group. Choose the location to save the file, and then check the box "Export data with formatting and layout."
- 2) Open the exported file from step 1f in Microsoft Excel. Click on any cell with the numerical data, then go to the Insert

ribbon and click on PivotTable to create a PivotTable. In the Create PivotTable window, click OK.

- 3) In the PivotTable Field List: right-click on PLOT_LIST and select Add To Row Labels, right-click on TPA_UNADJ and select Add To Values, and right-click on SPCD and select Add To Report Filter.
- 4) Near the bottom of the PivotTable Field List window, find the small Row Labels window and left-click on the small arrow to the right of PLOT_LIST. Choose Field Settings. Click on the Layout & Print tab. Check the box that says "Show items with no data." Then click OK. This step assures that the lists of plots in columns A and B are properly aligned; the lists of values in these two columns should always be of the same length after completing this step.
- 5) Two columns appear at the left of the sheet. Column A is a list of Row Labels which is a list of every plot in the study area with a live canopy tree on it. Column B is the sum of the trees per acre (TPA) represented by all live canopy trees on the plot. (Note that each "plot" actually consists of cluster of plots of different sizes. For this reason, the same tree could represent different TPA values depending on which plot or subplot it occurred on. For the purposes of this analysis, we combine data from all of clustered plots.) Click on the B at the top of column B and right-click to choose Copy. Right-click on the C of Column C and choose Paste Special, Paste as Values. Column C is now the total TPA of all species on each plot.
- 6) Column D will be used to calculate the percentage TPA represented by a given species on each plot. In the column D cell to the right of the topmost numerical value in column C (this should be cell

D4) type: “=B4/C4*100” (without quotes). Copy this formula down to the bottom of the column of numbers, except for the final value which is a grand total. *Do not* paste the formula in the Grand Total line.

- 7) In cell E1, type:
=SUM(D:D)/COUNTIF(D:D,">0") and then press enter.
- 8) This is the value that will, in the next step, represent the average proportion of canopy cover for each tree species.
- 9) In the upper left corner of the spreadsheet (cells A1 and B1), there is a small arrow. Click on this arrow and a list of numbers will appear. These numbers are the FIA species codes. You can cross-reference these numerical species codes with species names using the list in appendix F at:

http://www.fia.fs.fed.us/library/database-documentation/historic/ver3/FIADB_user%20manual_v3-0_p2_7_10_08.pdf

Now, the click on the numerical code representing a species of interest. In cell E1, mean proportion of canopy trees represented by this species will appear (as a percentage). Select the code for the next species of interest and that species' percentage will then appear.

APPENDIX 3. DATA PROCESSING AND CALCULATIONS FOR THE HABITAT AFFINITY RISK FACTOR

Mean Elevation Variable

- 1) Locate the FIA shapefile that was clipped to the study area boundary in appendix 2, in the frequency of occurrence variable calculation procedure, step 2a.
- 2) Run the Summary Statistics Tool using the FIA shapefile as the input table, “ELEV” (elevation) as the statistics field, “MEAN” for Statistic Type, and “SPECIES_SYMBOL” (from the FIA database, or the field representing unique species codes) as the case field.
- 3) Open the resulting table, turn off the OID field, and then export the results to a text file.

Creating Elevation Graphs (Optional)

Graphs showing the distribution of species occurrences by elevation are not required for rating any of the variables; however, such graphs

can be helpful in understanding spatial patterns in habitat. To create elevation distribution graphs:

- 1) Elevation records for FIA plots are supposed to be recorded to the nearest 100 feet; however, some records have been recorded to the nearest foot. These can be corrected in ArcMap using the following equation in the field calculator: $\text{ROUND}([\text{ELEV}]/100)*100$. In order to preserve the original elevation records (if desired), create a duplicate of the ELEV field before performing this calculation.
- 2) Run the summary statistics tool using the clipped shapefile as the input table, “ELEV” (elevation) as the statistics field, “COUNT” for statistic type, “SPECIES_SYMBOL” (from the FIA database, or the field representing unique species codes) as the first case field, and “ELEV” as a second case field.
- 3) Open the resulting table, turn off the OID and FREQUENCY fields, and then export the results to a text file.
- 4) Import the text file into a spreadsheet, sum the number of plots in which each species occurs, add a new column for “Plot (%)” and calculate the percentage of plots at each elevation.
- 5) For each species, create a graph of elevation versus percentage of FIA plots and save as a “.jpg”. If desired, import into ArcMAP to include graph on a map.

CLIMATE CHANGE AND FOREST TREES IN THE PACIFIC NORTHWEST:

GUIDE TO VULNERABILITY ASSESSMENT METHODOLOGY



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