Genomic offset modeling for climate-smart seed conservation in red spruce
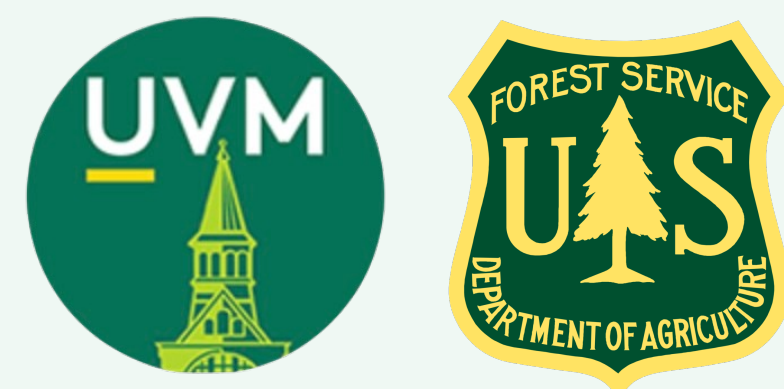
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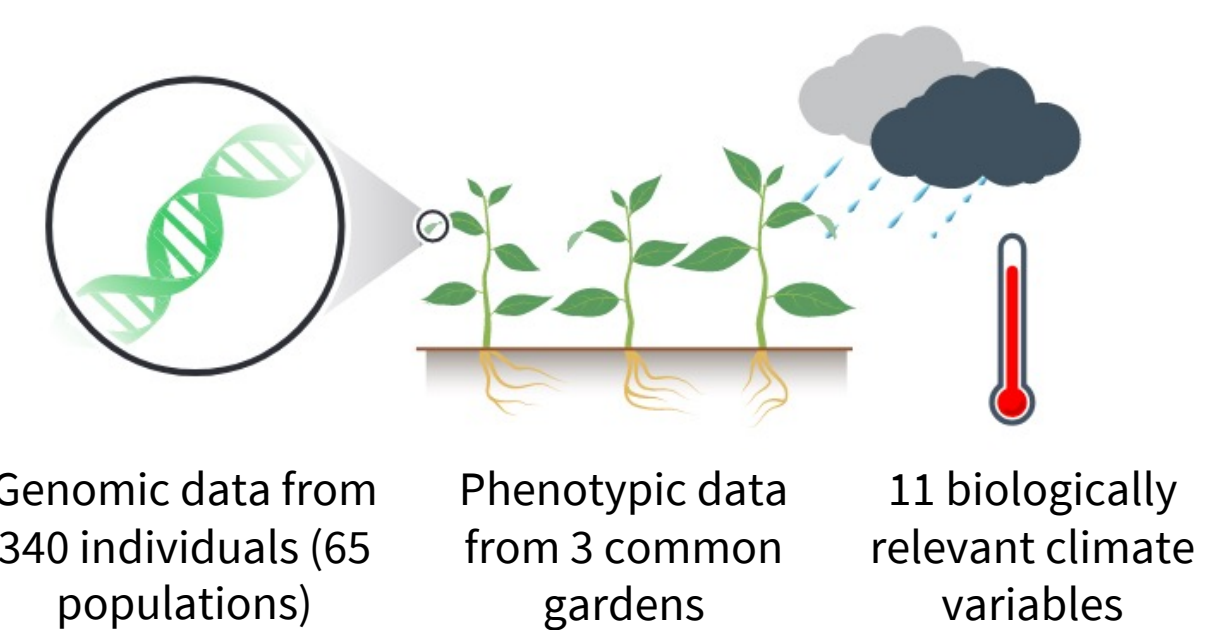
Highlights

- Climate change is disrupting local adaptation and shifting gene-environment relationships.
- When choosing seed for restoration projects, local is not always best. We should select seed likely to be adapted to the target location's future climate.
- We used genomic offset modeling to select red spruce seed sources for a climate-smart seed orchard in the Green Mountain National Forest.
- There is a tradeoff between adaptation to future climates throughout New England and ability to survive current conditions at the orchard site.
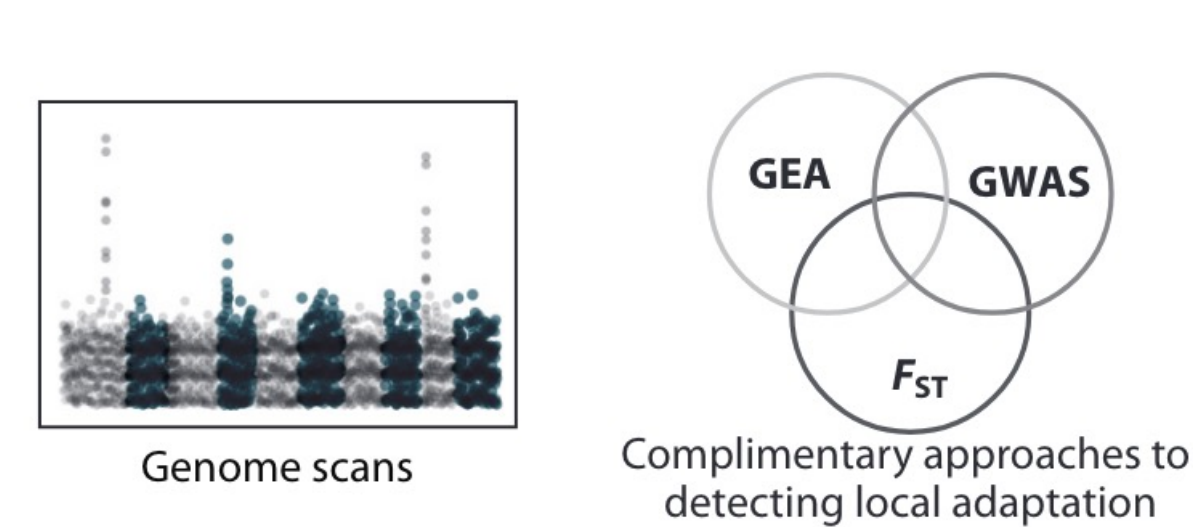
Abstract

Red spruce (*Picea rubens*) is highly vulnerable to climate change and has been a target of significant conservation efforts, including assisted migration. Although restoration has historically followed a "local is best" paradigm, climate change is disrupting local adaptation and shifting prior gene-environment relationships. Our team has mapped climate-adaptive diversity across the range of red spruce, integrating population genomics with spatial models to identify stands most likely to experience a disruption in climate adaptation. This allows us to predict which trees should be moved where to maximize fitness under future climates. Here, we combine genomic and climate data to model genomic offsets, a measure of climate maladaptation, in order to select 15-20 red spruce stands from which to collect scions and graft them onto root stock for future out-planting into a seed orchard site in the Green Mountain National Forest. We will identify 50-100 total genotypes, adapted to a range of future climate conditions anticipated in the northeast by the end of the century. Our objective is to conserve climate-adaptive genetic diversity in red spruce and produce at-scale quantities of seed for restoration plantings under future climate change.
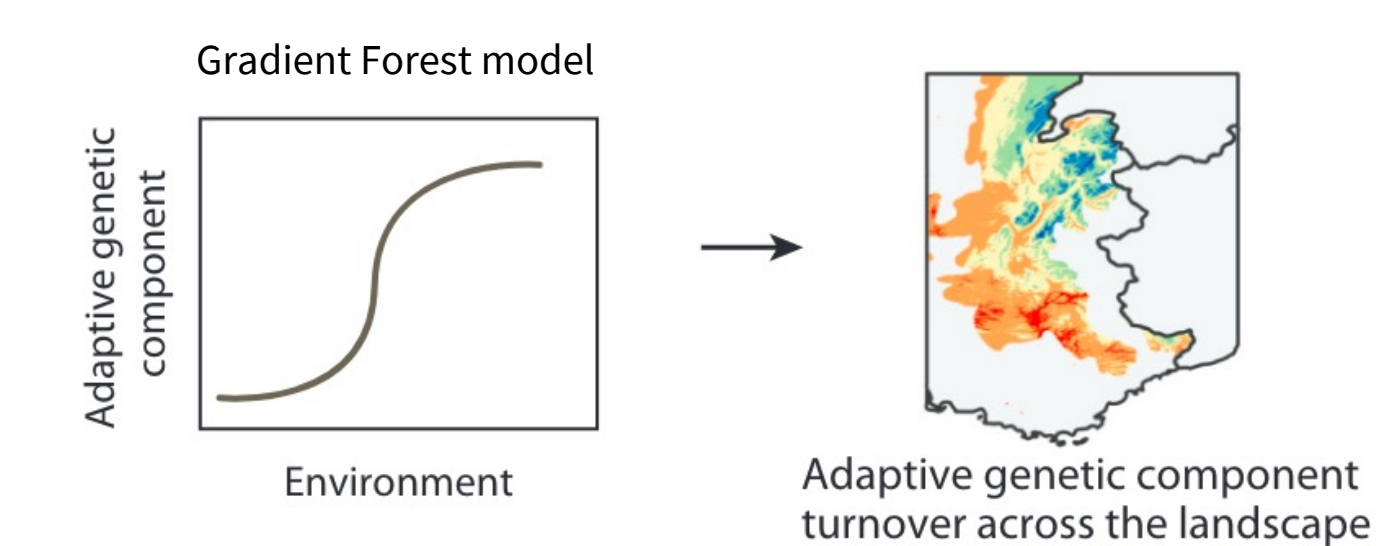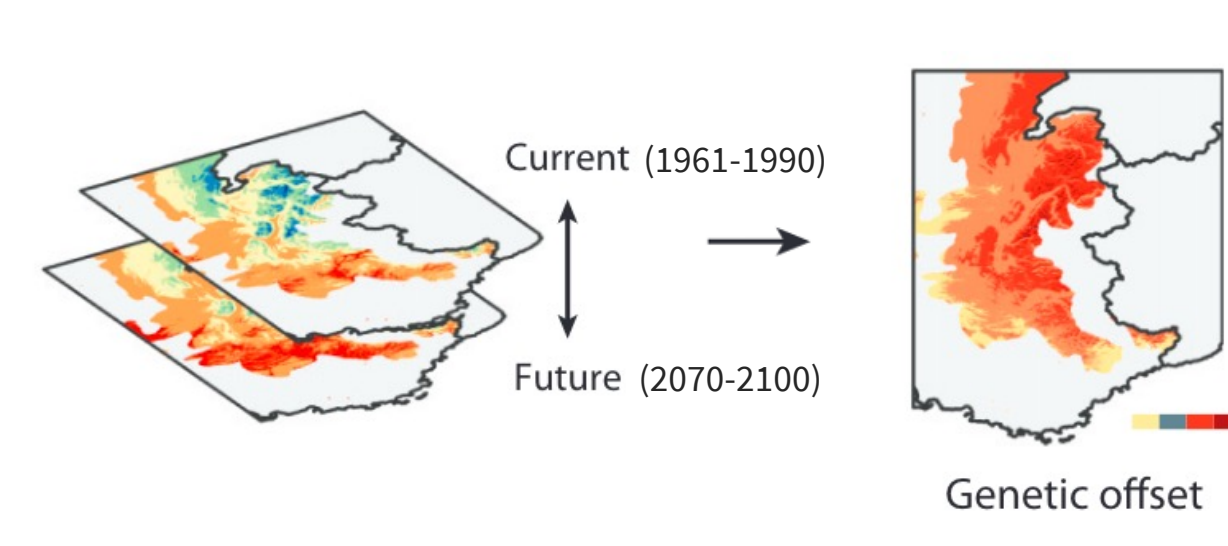
Genomic Offset Modeling

1 Acquire data
Genomic data from 340 individuals (65 populations)
Phenotypic data from 3 common gardens
11 biologically relevant climate variables

2 Investigate genomic basis of local adaptation
Genome scans
Complimentary approaches to detecting local adaptation
GEA / GWAS / F_{ST}

3 Generalize gene-environment relationship
Gradient Forest model
Adaptive genetic component
Environment
Adaptive genetic component turnover across the landscape

4 Measure shift in genomic optimum
Current (1961-1990)
Future (2070-2100)
Genetic offset

5 Validate predictions
Testing the decrease in fitness associated with an increasing genetic offset in controlled environments
Linking population trend surveys and predicted genetic offset
Genotyping biological specimens to look for genetic changes between historical and contemporary climates
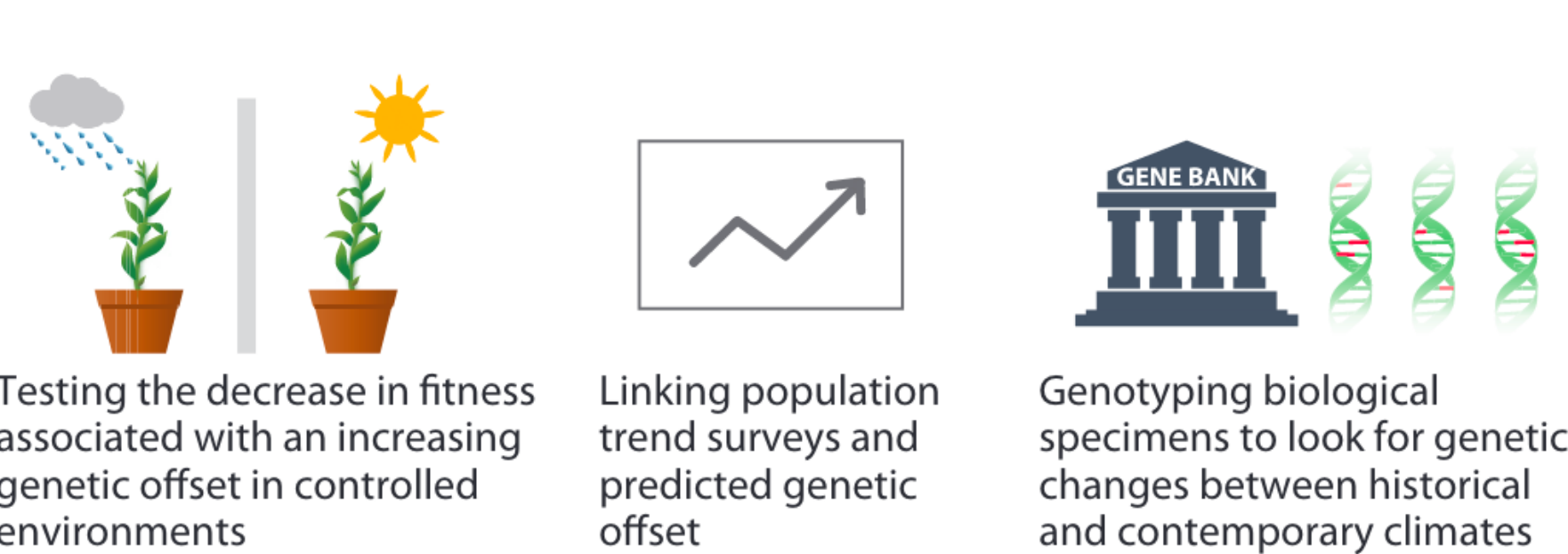
Donors: 4,712 current red spruce localities in greater New England are candidates for the seed orchard.

Recipients: 27,216 gridded cells across greater New England represent possible locations of future restoration plantings under climate conditions for the years 2070-2100.

We want to choose genotypes that have minimal genomic offset with as many potential future sites as possible. However, these trees must also be able to survive current conditions at the seed orchard. The seed orchard will also serve as a means of validating the genomic offset model predictions.

Fig. 1. Adapted with permission from Capblancq, *et al.* 2020. Genomic Prediction of (Mal)Adaptation Across Current and Future Climatic Landscapes. *Annu. Rev. Ecol. Evol. Syst.*

Background

Red spruce is a conifer found at high elevations in the Appalachian Mountains and northern maritime forests, where it is valued for its timber, wildlife habitat, and ecosystem services. It is most abundant in New England, Nova Scotia, and eastern Quebec, but the range extends as far south as North Carolina, where populations can be found on "sky islands"—isolated patches of suitable habitat left behind on mountaintops in the wake of receding glaciers (Fig. 2). Red spruce is adapted to cool, moist climates with low potential evapotranspiration. The USDA's Climate Change Tree Atlas predicts poor capability for red spruce to persist under future climate change, as well as a substantial reduction in suitable habitat. Hundreds of thousands of seedlings are used in red spruce restoration each year, yet the seed required to meet this demand currently comes from single-tree collections with limited provenance diversity. There is an urgent need to (1) conserve existing genetic resources to maximize the *ex-situ* banking of adaptive diversity, and (2) increase capacity for seed production for large-scale restoration and assisted migration plantings. This project will establish a seed orchard that will produce large quantities of genetically diverse seed exhibiting climate adaptation broadly applicable to reforestation and assisted migration plantings throughout the region.
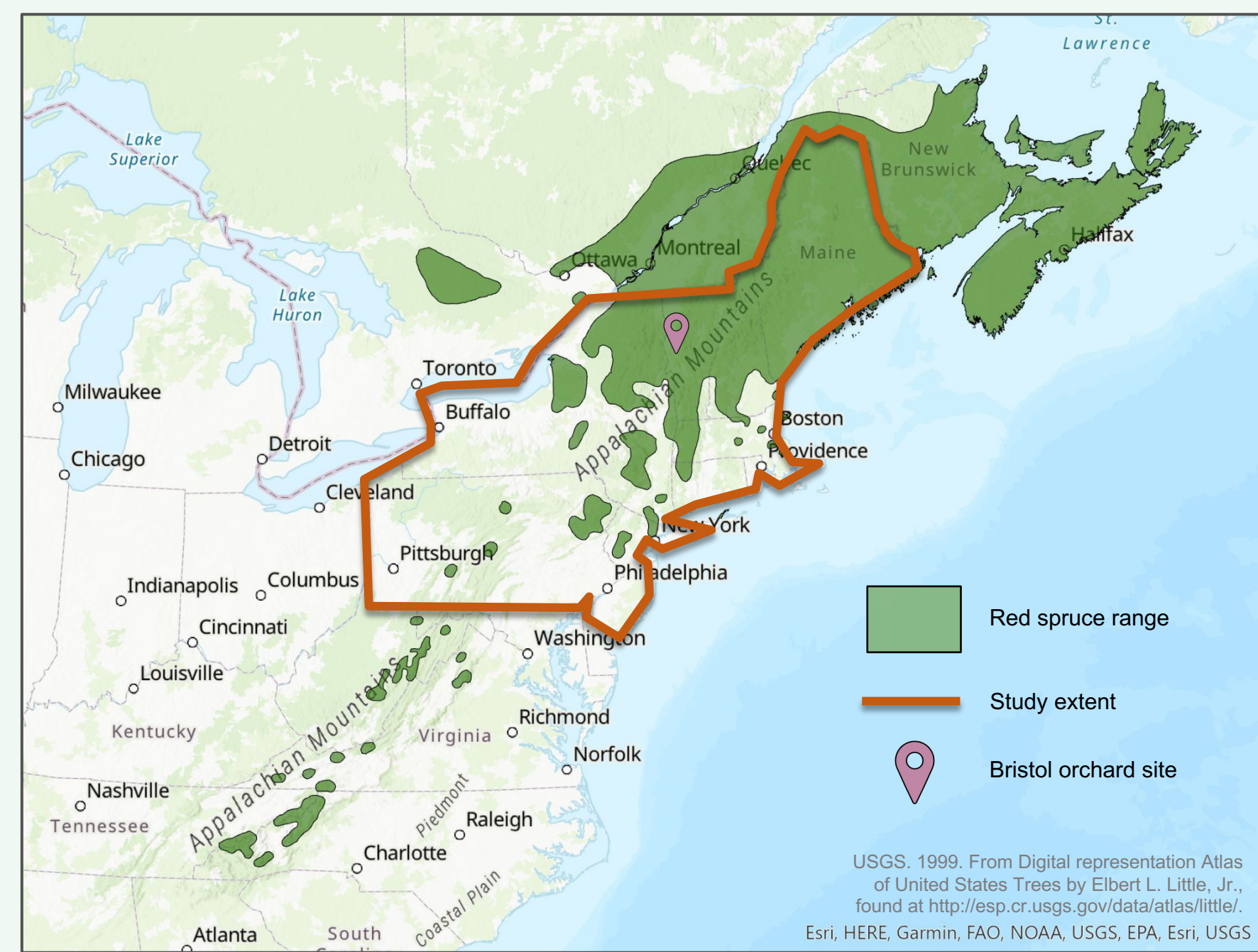

Fig. 2. Map of red spruce current distribution (green) and extent of study (red outline). Site of future seed orchard in the Green Mountain National Forest in Bristol, VT is marked with a pin.

Candidates with low landscape-wide genomic offset in the future are least likely to do well in the Bristol site's current climate.
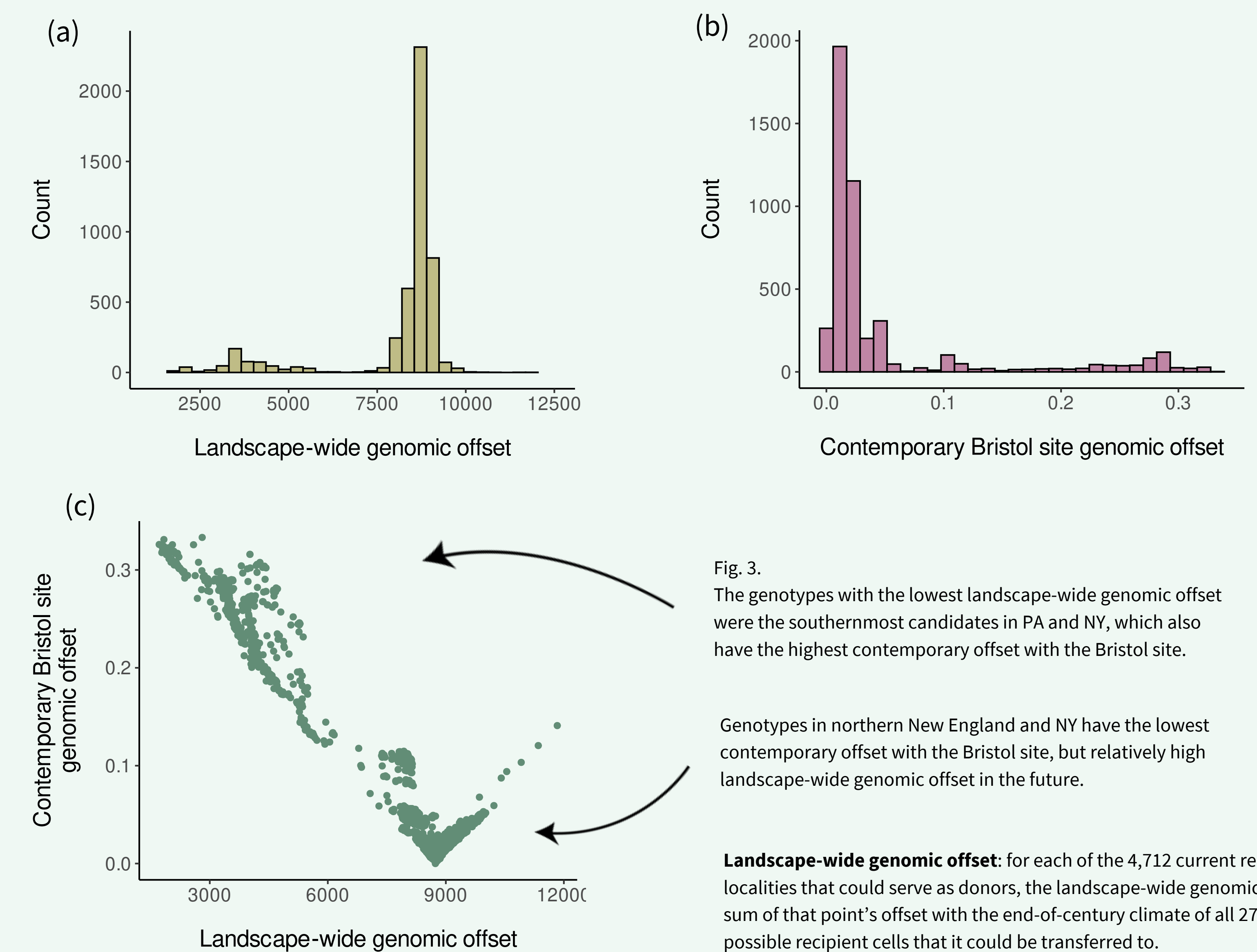
Fig. 3.
The genotypes with the lowest landscape-wide genomic offset were the southernmost candidates in PA and NY, which also have the highest contemporary offset with the Bristol site.

Genotypes in northern New England and NY have the lowest contemporary offset with the Bristol site, but relatively high landscape-wide genomic offset in the future.

Landscape-wide genomic offset: for each of the 4,712 current red spruce localities that could serve as donors, the landscape-wide genomic offset is the sum of that point's offset with the end-of-century climate of all 27,216 possible recipient cells that it could be transferred to.

Summing only the offsets of the best 0.5% recipient sites reduces the tradeoff.

Candidate points
Cumulative offset < 1.75*
Bristol offset < 0.035*
n = 125

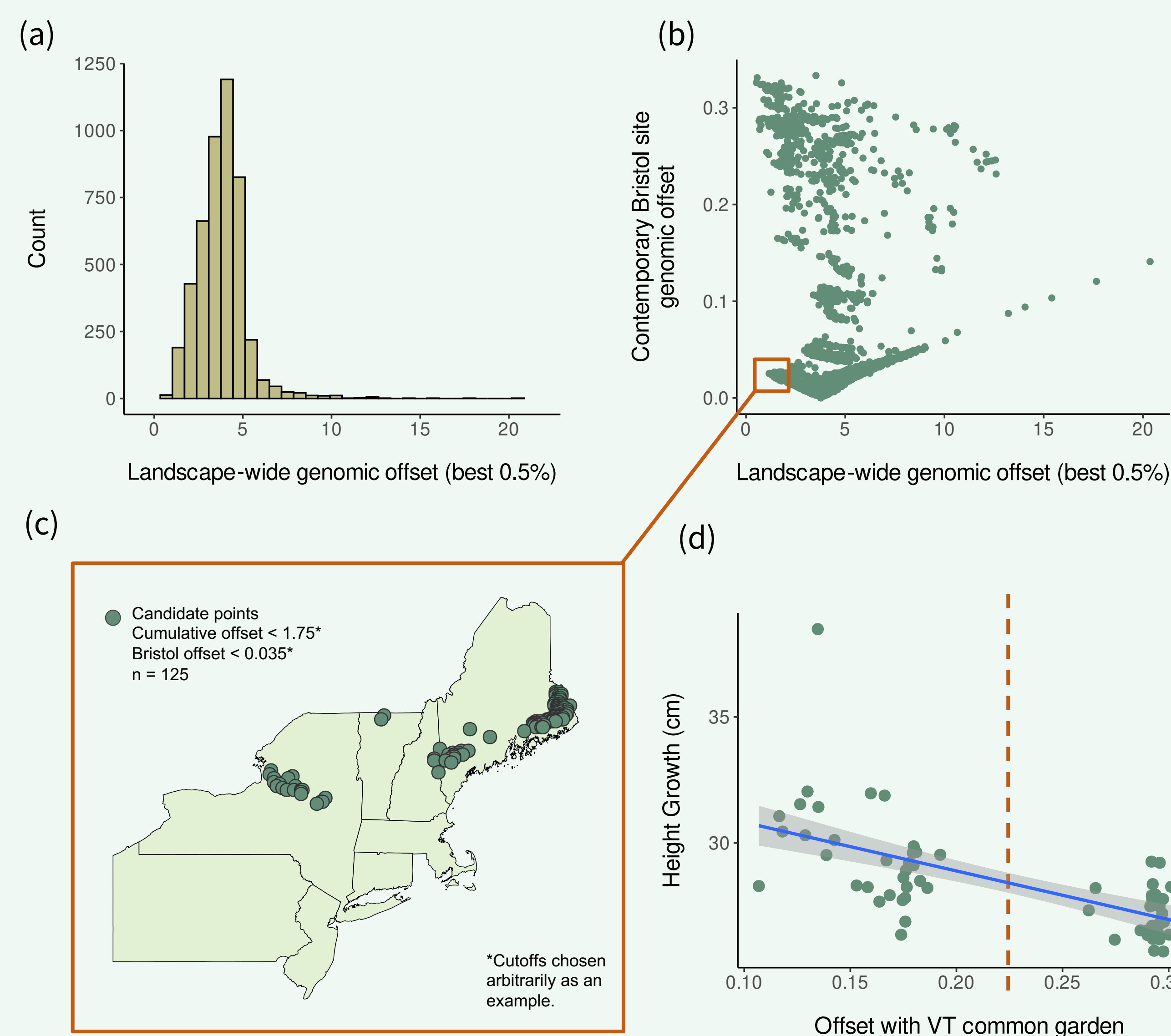*Cutoffs chosen arbitrarily as an example.

Fig. 4. (a) Distribution of landscape-wide genomic offsets for each of the 4,712 candidate donors, summing only their future offsets with the 0.5% of possible recipient locations with which they have the lowest offset (i.e., the best match for future transplantation). (b) All candidate donors plotted by landscape-wide genomic offset (best 0.5% match) and contemporary offset with Bristol orchard site. (c) Map of example set of candidate points chosen from distribution in (b). (d) Genomic offsets of genotypes transplanted into VT common garden and their height growth as a proxy for seedling fitness (dead seedlings scored as zero). Higher offset correlates to lower fitness. Red line indicates proposed threshold for survival at Bristol site.

However, the best recipient sites for these top candidate donors are highly geographically clustered.

Cumulative offset with candidate donors
0 to 5 / 5 to 10 / 10 to 15 / 15 to 20 / 20 to 25 / 25 to 30 / 30 to 35 / 35 to 40 / 40 to 45 / 45 to 50
Candidate donors
Cumulative 0.5% offset < 1.75
Bristol offset < 0.035
n = 125

Cumulative offset with candidate donors
0.0 to 3.5 / 3.5 to 7.0 / 7.0 to 10.5 / 10.5 to 14.0 / 14.0 to 17.5 / 17.5 to 21.0 / 21.0 to 24.5 / 24.5 to 28.0 / 28.0 to 32.5 / 32.5 to 35.0
Candidate donors
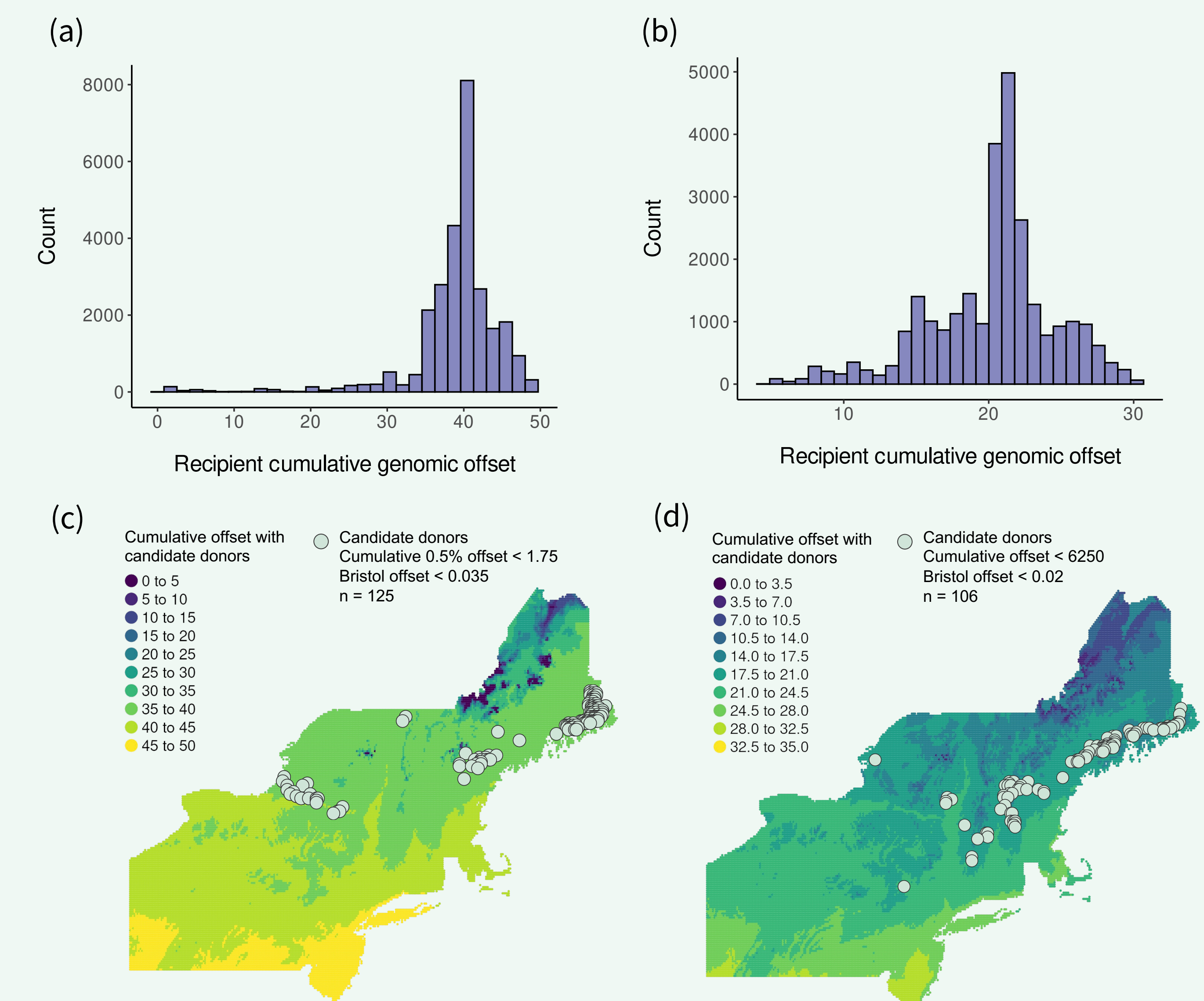Cumulative offset < 6250
Bristol offset < 0.02
n = 106

Fig. 5. (a) For each potential recipient locality, sum of its offset with the 125 candidate donors shown in Fig. 4c. Most recipient locations have high offset for these donors. (b) Recipient cumulative offsets for an alternative set of 106 donors selected based on low landscape-wide genomic offset (not restricted to best 0.5% matches). (c) All possible recipient locations colored by offset with candidate donors from Fig. 4c. Locations with low offset relegated to only a small area in northern Maine. (d) All possible recipient locations colored by offset with candidate donors from Fig. 5b. Geographic spread of acceptable recipient locations is far higher than in Fig. 5c.

Next steps

Incorporate Forest Inventory Assessment data on spruce presence / absence, as well as logistical considerations such as distance from roads and public vs. private land.

Investigate sensitivity of predictions to different climate model scenarios and time points (e.g., 2040-2070).

Examine climate space and geographic space covered by different candidate donor sets. Formalize selection criteria. Scions will be collected in early spring 2024.

To test how different parameter choices affect set of donor points, please visit the dashboard at **bit.ly/spruce-dashboard**

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SCAN ME