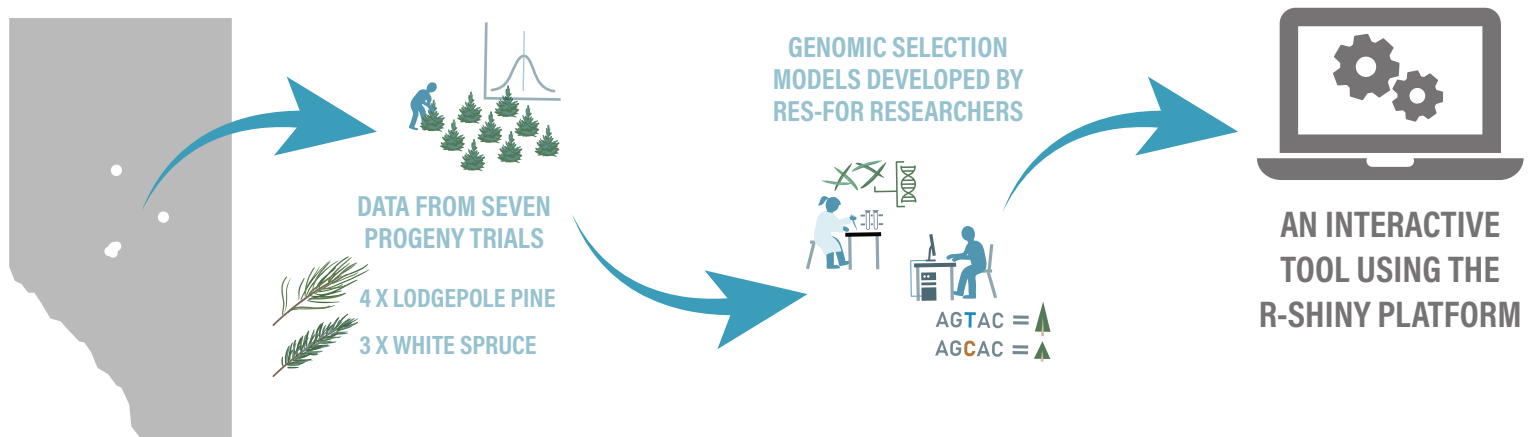# The RES-FOR Interactive Selection Tool

Oct 2021

Successful reforestation relies on healthy and resilient seedlings. **Genomic selection has emerged as a tool to generate well-adapted seedlings in a much shorter time frame compared to conventional tree improvement methods.** Using predictive models that identify associations between genomic information and phenotypic traits of interest, breeders can precisely identify the best trees to use in their seed orchard. **However, genomics data is complex to manage and making genomic selection accessible to tree improvement professionals has been a challenge. The RES-FOR Interactive Selection Tool is designed to bridge that interface.**

DATA FROM SEVEN PROGENY TRIALS

4 X LODGEPOLE PINE

3 X WHITE SPRUCE

GENOMIC SELECTION MODELS DEVELOPED BY RES-FOR RESEARCHERS

AGTAC = ▲
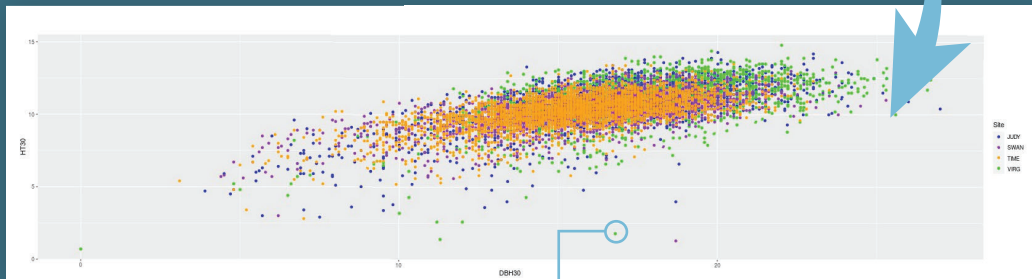AGCAC = ▲

AN INTERACTIVE TOOL USING THE R-SHINY PLATFORM

The RES-FOR project has created an easy-to-use, interactive selection tool to help tree improvement professionals make genomics-informed breeding decisions for their program. Rather than select on a few traits at a time, users can select on a wide variety of traits and explore how different selection choices will impact the following generation of trees.

Visualize Site and Trait Relationships
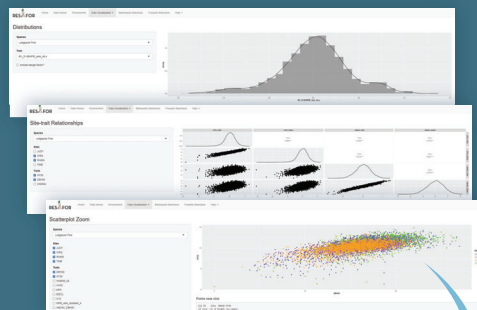
Users can explore the RES-FOR project data and visualize relationships between breeding values for traits of interest. The tool can display informative plots, including trait distributions, scatterplots, and correlations within and between progeny sites.

By plotting two traits, users can compare different environments (shown in different colours). Users can also identify trees that deviate from the overall correlation and which may be of particular interest.
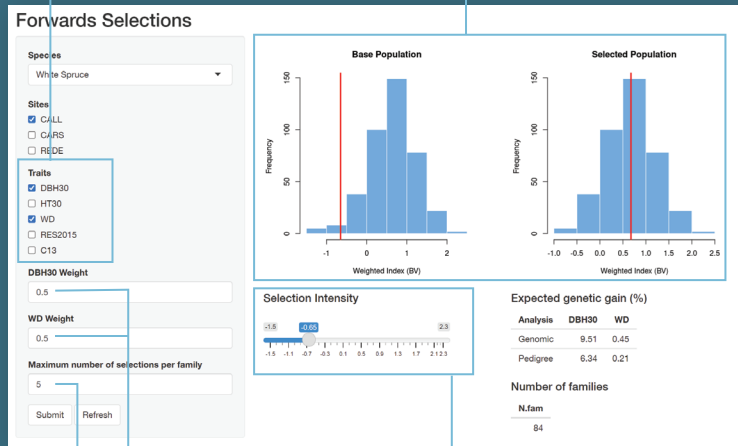
Identify unusual trees that break the overall correlation.

By visualizing the project data, users can better understand the relationships between traits prior to performing selections.

Compare Selections Based on Traits of Interest

Select traits of interest, such as diameter at breast height or wood density.

A distribution of the weighted index is shown for the base and selected populations.

Users can use the tool to make backwards and forwards selections. Based on their custom selection criteria, users will receive a list of the top ranked trees in the population and expected genetic gain.

Forwards Selections

Species
White Spruce

Sites
☑ CALL
☐ CARS
☐ REDE

Traits
☑ DBH30
☐ HT30
☑ WD
☐ RES2015
☐ C13

DBH30 Weight
0.5

WD Weight
0.5

Maximum number of selections per family
5

Submit   Refresh

Base Population / **Selected Population**

Selection Intensity: -1.5 ... -0.65 ... 2.3

Expected genetic gain (%)

Analysis	DBH30	WD
Genomic	9.51	0.45
Pedigree	6.34	0.21

Number of families
N.fam
84

Customize the weighting for each trait based on interest.

Limit how many progeny can be selected from a particular family to reduce inbreeding.

Adjust the slider to see the effect of selection intensity.

Base Population / **Selected Population**

Selection Intensity: -1.5 ... 1.25 ... 2.3

Expected genetic gain (%)

Analysis	DBH30	WD
Genomic	20.67	2.06
Pedigree	16.79	1.27

Number of families
N.fam
28

By changing the selection criteria and generating different rankings, users can design multiple seed orchards that prioritize different traits.

TOP RANKED FOR INSECT RESISTANCE

TOP RANKED FOR HEIGHT
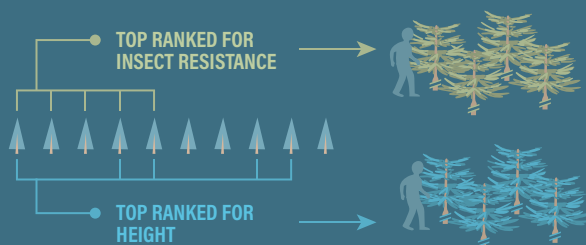
Selections Preview

Family	ID	DBH30	WD	Index
1919	1177	27.53	5.90	2.25
170	1642	27.07	2.66	2.01
188	1569	19.15	10.33	1.97
2101	1258	25.39	3.01	1.
165	1105	22.34	6.06	1.91
188	1383	21.77	6.56	1.91
1586	1296	33.15	-6.18	1.85
1586	1340	30.12	-3.67	1.81
170	1476	23.94	2.76	1.81

See the effect of genomic selection on breeding values.

Ongoing Development

Development is ongoing and new features will continue to be added.

RES-FOR

The tool is pre-loaded with the RES-FOR project data from seven progeny trials in Alberta.

Future plans are for the tool to act as a template where users can upload their own dataset.

USER DATASET

TOP RANKED
RANKING OF RES-FOR PROJECT SEEDLINGS

TOP RANKED
RANKING OF USER PROJECT SEEDLINGS

To learn more about genomic selection, its potential applications in tree improvement, and the history of its use, check out these additional resources available on the RES-FOR website:

Genomic Selection in Forestry
Context of Genomic Technology
How to Use Genomic Selection for Tree Improvement

RES-FOR
https://resfor.ualberta.ca/