

RES-FOR HIGHLIGHT #5

May 2020

“Spatial Analysis”

a good opportunity to revise genetic evaluations

Overview

Progeny test trials are typically large and located throughout the deployment region established for a tree improvement program. These trials are often established on heterogeneous sites to mimic future reforestation sites. However, to maximize the information from these trials, including a precise genetic evaluation, these trials should provide performance information without confounding factors such as soil fertility, moisture availability, and terrain variation (i.e., spatial variation). The magnitude and direction of the spatial variation should, in theory, be accounted for before (*a priori*) trial establishment. However, progeny test designs can only account for the obvious, identifiable causes of site variation and this is accomplished through a statistical term called “blocking”. However, unknown sources of variation often confound the results which can lead to the incorrect identification of superior trees. Therefore, ‘after-the-fact’ (*a posteriori*) analysis is often needed to adjust for these unknown factors and this is known as “spatial analysis”. In the RES-FOR¹ project, three mature (>30-year-old) progeny tests from one of Alberta’s first generation white spruce (*Picea glauca* (Moench) Voss) breeding programs were established across a range of sites. Previous analyses based on an *a priori* blocked design, offered a good opportunity for reanalysis using an *a posteriori* spatial approach.

Objective

To compare the performance of the classical *a priori* block design with the *a posteriori* bidimensional autoregressive spatial model on 30-year-old height and diameter measurements.

Methods

Data from 150 half-sib open-pollinated families from three progeny trials associated with the Region D1 first generation white spruce breeding program were used for analysis. The experimental design employed a random complete block design with six-tree family row plots and six blocks per site. Total height and diameter at breast height (1.3m) were measured at year 30 (HT30 and DBH30, respectively). Two individual-tree models were evaluated. Both models included a fixed effect of genetic group to account for the means of the different origins of parents, a random plot design effect, random additive genetic effects (breeding values), and random errors. The standard *a priori* block model also included random block effects, while the *a posteriori* spatial approach included a random autoregressive correlated residual at the individual level.

Results

As an example, Figure 1 displays the estimates of the block effects for the block model (left), and the estimated surface for the spatial model (right) for HT30 at the Red Earth progeny test site. The fit of the *a priori* block model is expectedly abrupt as block effects are parameters for a categorical variable. On the other hand, the estimated surfaces with the spatial model shows continuous spatial variation resulting in a more accurate modeling of environmental variability. Note also that the environmental

¹RES-FOR = Resilient Forests: Climate, pests & policy – genomic applications (Genome Canada 2015 LSARP)

variability accounted for in the *a priori* block analysis is in the opposite direction to that shown in the *a posteriori* spatial analysis, based on HT30. Additionally, the *a posteriori* analyses, using a multiple-trait multiple-site mixed model, showed that differences between the *a priori* standard (without spatial consideration) and *a posteriori* spatial analyses were evident by the change in ranking of 132 of the top selected trees (Figure 2).

Figure 1. Heat maps showing a comparison of predicted spatial effects from *a priori* (left) block and *a posteriori* (right) spatial analysis for each tree from height at age 30 in the white spruce Red Earth progeny test site.

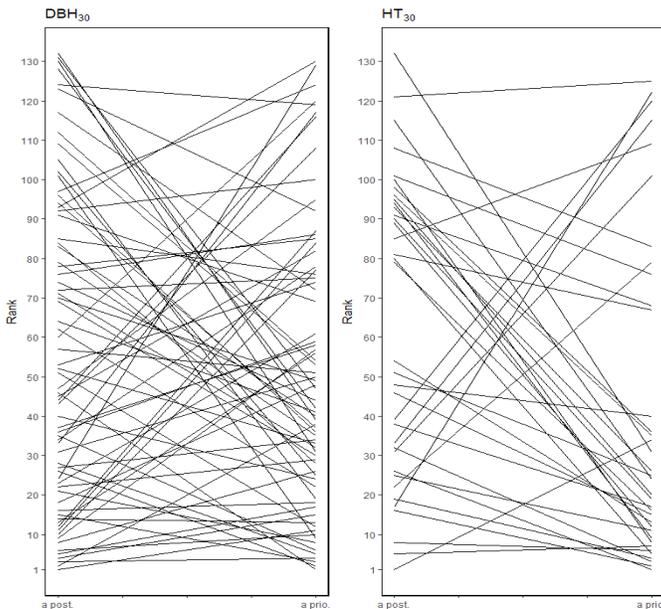
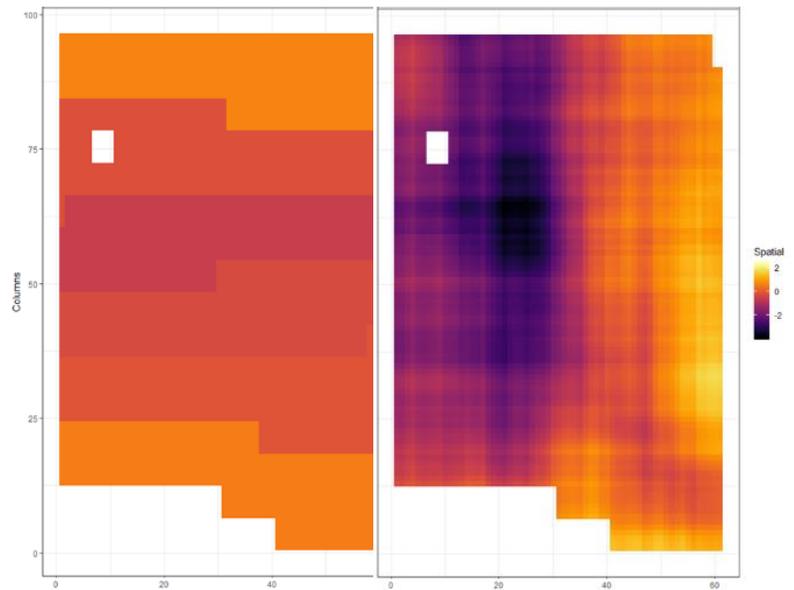


Figure 2. Ranking of the top 132 white spruce trees based on *a priori* (a prio.) blocking and *a posteriori* (a post.) spatial analyses in a multi-site multi-trait genetic analysis. Note change of rank for two traits at age 30 years (diameter at breast height (DBH₃₀, left) and height (HT₃₀, right)).

Conclusions

Precise genetic evaluation is of critical importance before selection of parents for either second-generation breeding or seed orchard establishment. In this example, the spatial model approach captured the complex environmental spatial variation at the progeny test sites and yielded more precise genetic estimates of performance for height and diameter. This analysis allowed for better ranking and selection of superior trees by removing variation not captured through the blocked design, leading to higher and more reliable estimates of improved performance or genetic gain in this program.

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