

Date: 12/06/2018
Reference: GCFF TN021

Technical Note

Overcoming GPS error to locate exceptional individual trees in the forest

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Summary: A new approach to tree breeding is under development. Wide-scale tree phenotyping will utilise remote sensing to detect, characterise, and rank individual trees. Genomic DNA collected from exceptional trees will be then analysed to identify parents for future selective breeding. The positional error of GPS devices under forest canopy conditions is of the order of +/- 4 to 5m, making location of selected trees in the forest unreliable. This study evaluated consumer grade GPS, tablet, and mobile phone devices. The tablet and phone devices were used to display current GPS position on a map created from the remotely sensed data. The use of GPS positioning alone was insufficient, however a combination of both GPS and the map enabled the reliable location of target trees. The approach warrants further testing and development, and is likely to lead to an operational solution to the problem of locating individual trees in the forest.

Introduction

The ability to identify exceptional trees in forest stands will enable the development of elite breeds, along with the matching of breeds to sites, and the optimisation of stand management. Such objectives will support the development of precision forestry for the New Zealand planted forest estate. The concept is to phenotype individual trees, sample their DNA, determine their parents from forest and breeding databases, and then selectively breed from the parents producing the exceptionally good progeny, and demote or eliminate parents producing exceptionally inferior progeny and creating elite breeds.

The approach is reliant on the ability to detect and characterise (phenotype) individual trees using remote sensing. By phenotyping individual trees across entire stands, a forest can be treated as a massive genotype by environment (GxE) experiment.

Observed phenotypes, such as total tree height, Diameter at Breast Height (DBH), and Total Stem Volume (TSV), represent the combined effects of the genotype and the local growing environment. A tree with a large DBH likely reflects the combined effects of superior genetics and favourable growth conditions. Individual tree phenotypic data, along with stand records including planted seedlots (or clones) and silvicultural treatments, can provide the basis for segregating the effects of genetics and environment on individual tree growth. Tree performance can be assessed to take into account the growing environment, including climatic and other site factors, as well as management practices. In this way, the performance of exceptional trees could be linked to favourable (and unfavourable) genetics, sites, and silvicultural regimes. One of the strengths of this approach is the potential evaluation of the full range of current operational tree breeds, growing sites, and management practices in the national forest estate.

The role of remote sensing

The ability to carry out phenotyping of individual trees across large areas is reliant on remotely sensed data. The use of airborne laser scanning (ALS) data is being increasingly adopted for use in forest inventory internationally and in New Zealand, using so-called area-based methods to estimate averages across 25 by 25 m patches for stand characteristics such as Mean Top Height (MTH) and biomass [1, 2]. This methodology is revolutionising forest inventory practices, however these area-based methods are not capable of identifying exceptional trees.

Recently developed tree-based Calibrated Individual Tree Crown (CITC) methods enable the detection and characterisation of individual trees using operational ALS data [3-5]. Crown metrics extracted from detected trees have been shown to correlate well with individual tree total height, DBH, and TSV [3]. This capability to phenotype key characteristics of individual trees, using remotely sensed data collected across entire stands or even forests, is the critical factor to enabling the identification of exceptional trees. The CITC methods were recently evaluated in another GCFE project (RA2.1 Comparison of conventional ALS and UAV LiDAR) utilising point cloud data collected from a laser scanner and a colour camera mounted on an Unmanned Aerial Vehicle (UAV). The ability to utilise these potentially lower cost, and more easily deployed, remote sensing methods offers additional options for tree-based phenotyping. Application of tree-based methods for phenotyping trees, using remotely sensed data, provides the opportunity to establish New Zealand as a world leader in the development of tree phenotyping and precision breeding.

Site and competition effects

An observed tree phenotype, such as DBH, represents the combined effects of genetics and environment, which confounds tree selection. With selections based solely on observed DBH, breeders cannot be certain what percentage of the growth characteristics were inherited and what percentage was the result of a good site. A large tree may occur due to “the dead cow effect” – benefitting from an exceptionally fertile microsite. Equally, a tree of superior genetics may be growing relatively poorly, due to unfavourable local microsite, or competition effects.

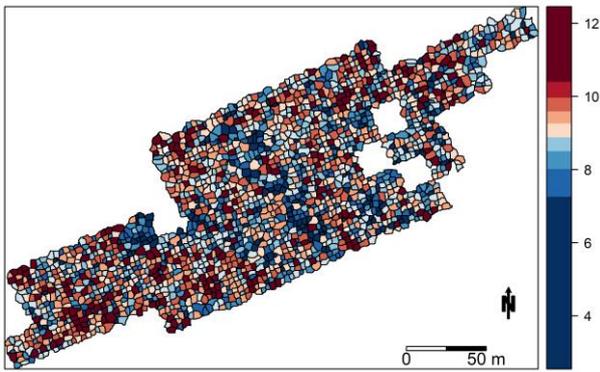
Methods are under development within the GCFE programme to utilise tree-based phenotyping to quantify and tease apart genetic and environmental effects on tree growth [6]. Supplementary funding, in the form of the “tree level phenotyping extension” was made available to accelerate and extend the scope of the research. This extension was used to carry out a deeper investigation of tree-based spatial modelling methods. This led to the formulation of a novel spatial modelling approach allowing the quantification and segregation of competition, site, and genetic effects from remotely sensed phenotypic data. This methodology is only at a proof-of-concept stage, but

already shows strong potential to help solve the riddle of confounded GxE effects in phenotypic observations. The ability to extract a cleaner genetic signal from phenotypic data is a critical requirement for the selection of exceptional trees, or more exactly - trees of exceptional genetics, for the development of superior breeds.

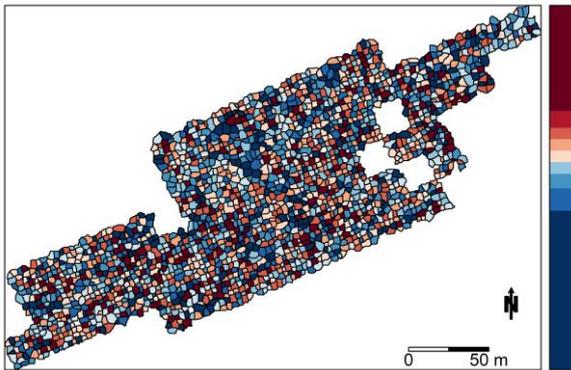
Use of a genetics trial

A study was carried out to evaluate the ability of the newly formulated spatial models to quantify genetic performance. The study utilised phenotypic data from a forest genetics trial which had known parentage for each tree. Phenotypic data took the form of conventional ground measurements, and crown metrics derived from ALS data collected over the trial. Ground measurements used in the study were height and DBH, and remote-sensed crown metrics representing tree height and crown size were highly correlated with the respective ground measurements.

The trial area was crossed by several shallow gullies, which were apparently affecting tree growth, due to Dothistroma and waterlogging. The trial also had trees missing from the original planting grid, creating gaps in the layout, which had allowed some variation in competition effects on tree growth to develop. These factors created variations in tree phenotype, resulting from different combinations of genetics, site, and competition. The trial therefore provided a useful scenario for evaluating the recently developed spatial models. The models were applied to the phenotypic data from the trial, and estimates of genetic performance of trees obtained, after removing the effects of site and competition (Figure 1). Trees were then ranked on those corrected performance values, and the top and bottom 1% were selected as candidate exceptional trees.



a. Observed phenotype - tree height



b. Tree height corrected for environmental effects

Figure 1. New methods correct phenotypic data for environmental effects before selection of exceptional trees. Scale represents variation from mean height.

Locating exceptional trees

The CITC method detects and characterises individual trees using a high resolution (20 cm) image, called a canopy height model (CHM), which is derived from ALS data. The ALS data has a global spatial horizontal error of the order of 10 cm. Accurate locations (of the order of 20 cm) were therefore available for the selected exceptional trees.

The problem to overcome was how to locate the selected trees on the ground. The CITC methodology detected trees and assigned locations to tree tops. This meant we had tree top locations for our selected trees, giving two problems. The lesser problem was that tree top locations can differ appreciably from tree locations observed on the ground. So when tree locations were being located, we had to take into account any displacement of the tree top.

The greater problem is the inaccuracy of GNSS (Global Navigation Satellite System, commonly referred to as GPS) under tree canopy. An earlier study investigated the issue of GNSS error under mature radiata pine canopy [3]. In a research trial or in an idealised stand, with trees located on a uniform grid, locating individual trees requires positional error less than half the tree spacing (Figure 2). Trees in the trial were planted with spacing of 3.2 by 3.2 m, and accurate tree location in that situation would require positional error less than 1.6 m.

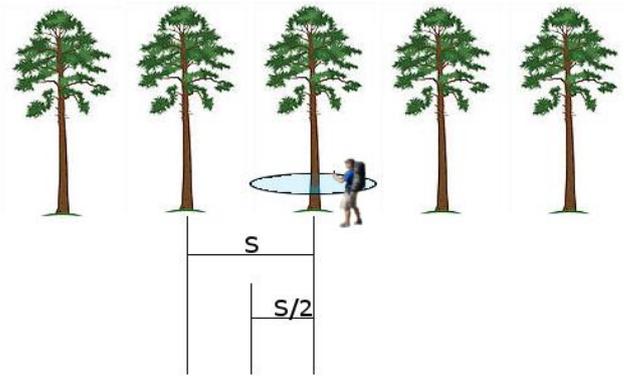


Figure 2. Positional error of $<S/2$ would be required to unambiguously identify trees with a minimum spacing of S .

The earlier study [3] found GNSS error was reduced by using superior (mapping grade compared to consumer grade) GNSS devices, by use of an external antenna, by increasing residency time at the location, and by applying differential correction with post processing. However there are two distinct uses of GNSS devices for determining locations: referred to as mapping and navigation. Mapping refers to situations such as determining locations of trial pegs or inventory plot centres, where residency time, and post processing can be utilised to improve accuracy.

However, locating exceptional trees in the forest requires navigation. Navigation refers to the situation where you need to walk to a given location in the forest. In this scenario you are moving, you have no opportunity to apply corrections, you can only pause periodically and briefly; and the use of an external antenna is often not practical. The earlier study [3] found that mean horizontal GNSS error in that situation was 4.6 m and 3.7 m for Garmin 64S and Trimble Geo7X devices respectively. It was clear that GNSS error greatly exceeded the level required to locate exceptional trees at the trial site (<1.6 m) and we also noted that this was mean error, momentary errors during navigation can and do range much higher than that.

Creation of a tree map

A novel solution was devised to aid identification of exceptional trees. The approach utilised an accurate tree map, with the identified exceptional trees marked on it. The map was based on the same CHM image used for tree detection and was therefore accurately georeferenced. Tree crowns were clearly evident in the image, and were emphasised by drawing over the delineated tree crown boundaries determined by the CITC method. The exceptional trees were identified by placing a coloured mark on the tree tops, along with an identifying label. Target tree locations and identifying labels were also exported into a shapefile.

The map and the shapefile were used to evaluate two approaches to locating target exceptional trees in the forest. The shapefile was loaded into a consumer grade GPS device, a Garmin 64st, and the map was loaded into an offline mapping application (Avenza), on an Apple iPad and an Android mobile phone (see Figure 3).



a. Navigating to waypoint using Garmin 64st



b. Tree map on iPad



c. Tree map on Android mobile phone

Figure 3. GNSS devices tested for locating exceptional trees in the forest.

The Garmin device provided navigation functionality in the form of a displayed distance and direction to a selected waypoint (Figure 1a). The Avenza application displayed the provided map and used the devices internal GNSS capability to display the current position as a marker on the map (Figure 1b and 1c).

The ability to locate target trees using the two devices was carried out on the ground at the trial site for a set of 16 target trees. Two operators independently

attempted to locate each tree, one operator using the Garmin and one using the iPad. The use of the Android mobile phone was also evaluated for a few sample trees.

When navigating to a target tree, identification of the general direction to proceed along initially was very clear using either device. Operators were able to walk freely, navigating around and through typical obstacles and hindrances such as thick vegetation, uneven terrain, and fallen trees while maintaining a clear sense of direction towards the target location. The Garmin device and Android phone were marginally superior in this phase as they were held in one hand, while viewing of the tablet screen practically required two hands. Addition of an elastic strap to the back of the tablet would be useful to address this relatively minor issue. The tablet also had a highly glossy screen, causing strong reflections which often made it hard to see, a screen overlay could help.

Once distance to the target tree was approximately 10 m, the effects of GNSS error became apparent. The error seemed to be similar for all three devices, certainly it was not possible to reliably navigate to the target tree using GNSS position alone. The Garmin typically reported the waypoint was reached while also reporting the distance to the waypoint was 8 m. This implied the Garmin had determined a positional uncertainty of 8 m. The displayed current position would move apparently randomly within a region approximately 10 m in radius, preventing navigation any closer to the target tree (see Figure 4).



Figure 4. Random GNSS error when static (blue line).

At this stage, use of the crown map was essential to identify the target tree. The distinctive local configuration of crown sizes and canopy gaps usually enabled quick determination of the target. In a few instances where adjacent candidate trees were similar, it was only necessary to examine a slightly wider area on the map to locate a feature such as a gap to work from to determine the target. Part of the final determination also took into account the tree selection criteria - was it selected as being an exceptionally tall, or short, tree for example. It was also important to recognise that site and competition effects had been taken into account in tree selection.

As the target trees had been selected as exceptional, amongst their immediate neighbours, they generally were quite distinctive, however it was necessary to be aware that a tree ranked top for height might not have the greatest absolute height.

Conclusions

Our study has shown that GNSS error for typical under-forest canopy conditions makes it impossible to reliably locate individual trees with GNSS positioning alone. This confirms findings from prior research. This issue therefore presented a significant barrier to the potential use of remote sensing to locate exceptional trees in the forest.

Our study trialled the use of the Garmin 64st, a consumer grade GNSS device widely used in forestry applications, finding it unsuitable for tree location due to GNSS error. The study also trialled the use of tablet and mobile phone devices. Their internal GNSS capability was likely inferior, or at best comparable, to the Garmin. However, the ability to display a georeferenced map permitted reliable tree location by visual comparison map features with ground observations of trees and gaps. This trial was merely a pilot study, but the approach demonstrated considerable promise. Testing in a range of operational forest conditions is necessary to further evaluate and develop the approach.

The ability to reliably locate exceptional trees in the forest is not simply a minor technical issue. This is a critical requirement for the advancement of a new approach to tree breeding, potentially accelerating breeding programmes by unlocking the considerable genetic knowledge being accumulated through new genomic technologies, and machine learning methods. The novel solution trialled in this study is likely the basis of a future tree location system, thus contributing a critical component for the tree phenotyping platform currently under development.

Acknowledgements

Funding for this research came from the “Growing Confidence in Forestry’s Future” research programme (C04X1306), which is jointly funded by the Ministry of Business Information and Employment (MBIE) and the Forest Growers Levy Trust, with the support of the NZ Forest Owners Association (FOA) and the NZ Farm Forestry Association (FFA). We are grateful to Timberlands Ltd. for supplying the LiDAR dataset and to the Radiata Pine Breeding Company Ltd. for access to the trial site.

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