Vegetation: permanent 20 × 20 m forest plots

Version 1.0

This specification was prepared by Kate McNutt in 2012.

Contents

Department of Conservation
Te Papa Atawhai

Synopsis

There are two approaches to monitor long-term changes in forests: spatially extensive small plots that sample landscapes (classically used in forest inventory and forest health studies in Scandinavia, Central Europe, North America and New Zealand); and large plots that sample small scale diversity (exemplified by 50 ha plots in tropical rain forests). Past investigations in New Zealand have used permanent plot data to predict the drivers of change in species-specific rates of mortality, growth and recruitment; species diversity; successional pathways; corroborated patterns of vegetation with environmental site factors (e.g. soil fertility gradients); and effects of animal pest pressures on structure and composition over a range of temporal and spatial scales (Stewart & Burrows 1989; Smale et al. 1995; Allen & Allan 1997; Harcombe et. al. 1998; Bellingham et al. 1999; Allen et al. 2002; Bellingham & Allen 2003; Coomes et al. 2003; Monks et al., 2005; Peltzer et al. 2005; Husheer & Frampton 2005; Bellingham & Lee 2006).

Permanent 20 × 20 m plot data are stored and curated by the National Vegetation Survey (NVS) databank, managed by Landcare Research at Lincoln, Canterbury. Prior investment by government departments (e.g. New Zealand Forest Service and catchment authorities) has led to the development of a comprehensive national network of permanent plots (Lee et al. 2005). By 1993, over 10 000 permanent plots had been established in indigenous forests (NZ Forest Research Institute cited in Allen 1993). To date, data from approximately 45 000 permanent plots are stored in NVS.

Permanently marked 20 × 20 m (400 m^2) plots have emerged as the standard plot size and is currently the most widely applied of all vegetation plot methodologies used in New Zealand and elsewhere. The purpose of a permanently located 20 × 20 m plot is an improved ability to detect change in structure and composition of vegetation communities. Stems of all individuals are identified and counted within the plot. Growth, mortality and recruitment of individuals are derived from repeated measurements of the forest overstorey (tree stems) and understorey (saplings, seedlings). Plots are divided into sixteen 5 × 5 m subplots to increase measurement efficiency and minimise counting errors. Trees are defined as stems that have reached a threshold 2.5 cm diameter at 1.35 m high (diameter breast height—DBH). Growth and basal area of each tree species is calculated from stem diameter measurements. Understorey stem density is determined from complete counts of saplings within a plot. All woody seedlings are counted within 24 (0.75 m^2) permanently marked understorey subplots and assigned into height tiers. Data obtained from seedling subplots is used to calculate seedling densities within the height tiers.

Studies need good sampling designs in order to evaluate the drivers of change, and designs vary in accordance with the study objectives. Previous sampling designs in New Zealand have typically involved systematic placement of plots along randomly orientated transects within catchments, but many different sample designs have been employed.

Practitioners commonly assume trends in data from permanent plots are a direct consequence of animal pest pressures, without taking into account other underlying natural processes driving change. An effective experimental design may include comparative studies between fenced

(exclosure) and unfenced permanently located plots. For example, paired comparisons permit an evaluation of the structural and compositional changes resulting from herbivory. The New Zealand Forest Service established hundreds of exclosure plots in the 1970s and 1980s to assess the impacts of ungulates. These and other exclosure studies have successfully demonstrated the effects of herbivore removal in a range of forest types and contributed to an improved understanding of factors affecting ecosystem processes in New Zealand forests (e.g. Stewart & Burrows 1989; Rose & Platt 1992; Smale et al. 1995; Wardle et al. 2001; Husheer 2005).

However, exclosure plot sampling designs do have their challenges, for example:

- Evaluation of the effects of the partial removal of pest populations is difficult (e.g. Forsyth et al. 2002 for discussions about deer).
- Nested designs of different exclosures are necessary to partition out the effects of multiple pest species on vegetation (Wilson et al. 2006).
- They lack replication (and offer no estimate of error).
- Exclosures are often subjectively located (e.g. Allen & Allan 1997).
- Frequent maintenance of exclosures is required as lapses will confound experimental results if they are left to deteriorate.

The permanent 20 × 20 m plot method is fully described in the expanded and field versions (Hurst & Allen 2007a,b).[1] The expanded protocol includes more information about survey design and sampling than the more compact field version. These revisions address problems with earlier versions (such as incomplete procedural descriptions), and have updated the methodology to bring them in line with common accepted practice. A RECCE plot is nearly always carried out at the same time when measuring a permanent plot. The RECCE plot protocol has also undergone revision—refer to Hurst & Allen (2007c,d) for full details of RECCE plots.

Assumptions

- All individuals within the plots and seedling subplots are observable and counted.
- The precise area (m^2) being measured remains constant between surveys.
- The plot is representative of the vegetation community of interest.

Advantages

- Provides reliable, quantitative measurements of long-term forest processes (e.g. mortality and recruitment).
- Little room for observer bias or subjective assessment of parameters of interest.
- Collects a wide range of data that can be used to meet a variety of monitoring objectives.
- Large existing plot network within New Zealand.
- The NVS databank reliably archives plot data.
- Can be used in combination with other quantitative methodologies for monitoring vegetation change (e.g. transects within ungulate exclosures—Rogers 1991).

[1] Refer to http://nvs.landcareresearch.co.nz/

Disadvantages

- Permanent plots are time consuming and expensive to establish and remeasure.
- Relocation of plot corner pegs, seedling pegs and individual stems can be difficult particularly when there have been significant time intervals between measurement dates.
- Changes observed in plots are frequently assumed to be a direct result from animal pest impacts without consideration of other natural processes that also drive forest change.
- Failure to follow data collection procedures will compromise the comparability of plots between and within surveys, and introduce unknown error.
- Data entry and analysis is time consuming and often overlooked in monitoring budgets.
- If all individuals are not counted, density estimates will be negatively biased.

Suitability for inventory

This method does provide data on species distribution (e.g. presence of threatened or pest plants), but the cost associated with the instalment and measurement of plots at an adequate spatial scale makes it unsuitable for the purposes of inventory. RECCE plots (which are carried out in association with permanent plots) are more appropriate for inventory objectives (Hurst & Allen 2007c,d).

Suitability for monitoring

Permanent 20 × 20 m plots are accepted as the best method available for monitoring structural and compositional change in shrublands and forests over long time periods in New Zealand. Long-term permanent plot data sets with greater than three remeasurement periods permit the analysis of trends at a range of spatial and temporal scales. Temporal trends are best interpreted in combination with other covariate monitoring data on pest animal abundances (e.g. faecal pellet counts) and other habitat and site condition assessments.

Skills

- Training is now compulsory for all DOC staff that establish and measure permanent 20 × 20 m forest plots in the field. Experienced staff (those that have been doing this work for many years) still need to undertake training to demonstrate the required competency. Please refer to DOC's field based courses[2] for more information.
- A high level of botanical skills is essential.
- Specialist skills in data analysis are required.
- A background in plant ecology is essential for the interpretation of data.

[2] http://www.doc.govt.nz/getting-involved/get-trained/field-based-courses/20-x-20-plots-and-reconnaissance-descriptions/

Resources

- Four people are necessary to set up and collect data. A team of three is possible in some situations. Plot measurement can take as little as 4 hours in simple forest types, but can take substantially longer in species rich forests or when remeasuring plots (as opposed to establishing new ones). The time taken also largely depends on the experience of the field teams and length of time between plot remeasurements. Generally, the longer the period of time between remeasurement, the longer it takes to relocate and measure plots. You need to allow extra time to prepare equipment prior to fieldwork, such as cutting seedling and corner pegs to length, preparing permolat and organising datasheets from previous measurements.
- Standard field equipment includes: maps, datasheets, clipboard, compass, pens, pencils, GPS, compass, binoculars and flagging tape. Specialist equipment specific for permanent plots includes: DBH tape, two 50 m tape measures (or four 30 m tape measures), six 30 m tape measures, one 1 m retractable tape measure, seedling subplot string (0.49 m radius), 24 seedling pegs bent at tops, 4 corner pegs, tree tags with numbers in sequential order, metal detector, dynotape maker, altimeter, clinometer, flat head galvanised nails (include longer nails for tree ferns), hammer, permolat for seedling pegs and corner marking, plant collection bags, labels and plant identification books. Hurst & Allen (2007a,b) have a full list of equipment for field teams.
- Take a copy of the most up-to-date plant species codes from Landcare Research with you into the field.[3]
- For correct standards and procedures for archiving and retrieval of permanent plot datasheets and electronic data, consult the DOC standard operating procedure (SOP) 'National Vegetation Survey (NVS) databank data entry, archiving and retrieval standard operating procedure' (docdm-39000).
- For previously measured plots, it is essential to have copies of Hurst & Allen (2007a) manual, pre-printed stem diameter datasheets from earlier measurements, plus photocopies of the original datasheets. Datasheets from previous measurements are available free of charge. Users must request data using a NVS data request form or by emailing nvs@landcareresearch.co.nz. Complicated data requests may incur fees. Please allow up to 4 weeks for requests to be processed.[4]
- There are a number of ways in which the NVS website can be used to identify and locate particular vegetation surveys or search for data: broad-scale maps can be viewed to see listings of survey names within each DOC conservancy; a search can be conducted for a particular survey name, person, or known geographical area; or interactive maps can be viewed that show NVS plot locations and species distributions.[5]
- Adequate budget needs to be set aside to ensure unknown species are collected, identified and correct species names and codes are updated on the plot sheets before data entry.

[3] Refer to 'NVS plant names and maps' at http://nvs.landcareresearch.co.nz/
[4] Refer to 'Requesting data' at http://nvs.landcareresearch.co.nz/
[5] Refer to 'Interactive plot location maps' at http://nvs.landcareresearch.co.nz/

Minimum attributes

These attributes are critical for the implementation of the method. Other attributes may be optional depending on your objective. For more information refer to 'Full details of technique and best practice'.

DOC staff must complete a 'Standard inventory and monitoring project plan' (docdm-146272).

All datasheets can be accessed from Landcare Research.[6]

The minimum attributes to record for permanent plots are listed on two datasheets: the stem diameter/sapling datasheet and the seedling plot datasheet. On the front page of each it is mandatory to record the plot identifier, survey, catchment, date, measurer and observer.

For permanent plot **stem diameter/saplings,** the attributes to record are:

- Subplot
- Stem species (using the standard six letter species code)
- Tag number
- Stem diameter
- Sapling species (using the standard six letter species codes available from http://nvs.landcareresearch.co.nz)
- Sapling count

For permanent plot **understorey subplots,** the attributes to record are:

- Seedling peg number
- Species (using the standard six letter species code)
- Seedling count per height tier

Optional attributes:

- A RECCE plot is usually completed at the same time. See the method description 'Vegetation: RECCE plots' (docdm-359575) for more information.
- Under the revised protocol, Hurst & Allen (2007a) discuss the merits of measuring the height of tree ferns and collecting additional ancillary data on other biota (e.g. non-vascular species, invertebrates), coarse woody debris (CWD), environmental variables (e.g. soil), and habitat condition variables (e.g. browse scores for ungulate damage). Data on canopy damage from possum browse has been collected in some studies (e.g. Urlich & Brady 2005).

Data storage

- It is standard to deposit all original datasheets in NVS.
- For correct standards and procedures for archiving and retrieval of permanent plot data, consult the 'NVS databank data entry, archiving and retrieval standard operating procedure' (docdm-

[6] Refer to 'Manuals, sheets and tools' at http://nvs.landcareresearch.co.nz

39000). The SOP describes the protocols for submitting and retrieving permanent plot data from NVS.

- Permanent plot data can now be entered using NVS Lite, an interface where plot data can be entered by staff into fields and electronically submitted to Landcare Research. NVS Lite is available from Landcare Research.[7] DOC staff must request for NVS Lite to be loaded onto their computer from DOC's network administrator. Otherwise, you must budget for data entry costs by Landcare Research.
- Never take original datasheets into the field. Store copies of datasheets in a safe location.
- Complete a metadata sheet when submitting data to NVS. Refer to 'Depositing data' at http://nvs.landcareresearch.co.nz/ for copies of metadata forms, though submitters are encouraged to use the more complete 'NVS metadata sheet' (docdm-53429).
- For more discussion on data collection, common problems and storage protocols, refer to the discussion documents Wiser et al. (1999), Newell & Baldwin (2000), Hurst et al. (2006), or contact the NVS databank administrator direct.

Analysis, interpretation and reporting

The approach to data analysis depends on the objectives of the monitoring programme. Always seek statistical advice from a biometrician or suitably experienced person prior to undertaking any analysis. The time and resources that are needed to undertake analysis of permanent plot data are substantial, but they are routinely underestimated. Advanced data handling and analytical skills are necessary to process and interpret this data. Inadequate training in the analysis packages is thought to be an impediment to routine analysis of plot data (Richardson et al. 2005).

Before any analyses are undertaken, it is critical that data errors are identified and corrected. Various data checking and validation programs are run when data are archived into the NVS databank, whether data are submitted using NVS Lite or through other avenues (see 'Data storage'). Should any errors be identified, or corrections made, to permanent plot data supplied by NVS, it is important to lodge any corrections back with the NVS databank to ensure that the most up-to-date copy of the data is archived. Contact the NVS databank administrator for advice on lodging data corrections with NVS.

For permanent plot data, analysis programs exist that have been specifically tailored to analyse overstorey data (tree stems) using PC-DIAM (Hall 1994a) and understorey data (saplings and seedlings) using PC-USTOREY (Hall 1994b). Like any analysis package, these programs require training and expertise to use proficiently. The programs use data entered in a standard ASCII text file format and run under MS-DOS. If these programs are to be used, then data must be obtained in the appropriate file format from the NVS databank. The PC analysis programs are available for DOC staff on request from DOC's network administrator. Manuals for the PC packages (Hall 1994a,b) can be obtained free-of-charge from Landcare Research, and these outline the file formats needed and the various summary statistics and analyses available. The programs are rather clunky and lack flexibility, but there are firm plans by Landcare Research to develop an updated set of analytical tools as part of the ongoing upgrade of the NVS databank and NVS Lite. It

[7] Refer to 'Depositing data' at http://nvs.landcareresearch.co.nz/

is anticipated that summaries will be capable of visualising the data summary results. This will include, as a minimum, the ability to graph relationships between variables calculated by the summaries (e.g. stand basal area, species diversity, stand density by plot or across plots).

Data from NVS can be made available to users in several other formats (including MS Excel) that can be imported into the PC analysis packages. Analyses of data can be run in statistics programs such as R, S-Plus, SPSS, etc.

Overall analytical approaches

The effects of ungulate browsers on forest succession and composition can be investigated using a number of comparative approaches. Data can be assessed for structural differences between paired ungulate exclosure and adjacent non-fenced plots. Where possible, exclosure plots should be paired for analysis but plots can be pooled when they are in simple or similar forest types (Stewart & Orwin 1986). Stem and sapling density can be compared between palatability classes (e.g. 'high', 'medium', 'low', 'non-palatable'). Further insights may be gained by testing for differences in the density of seedlings at increasing height tiers to identify if imbalances exist. ANOVAs test for differences in plot composition between measurements (Husheer 2005).

Overall trend analyses can similarly identify natural processes of regeneration and recruitment that in turn create compositional changes. Structural changes in forests can be inferred from differences in basal area and mortality rates of structurally important tree species. Analysis of trends in species richness within and between forest types may infer changes in the spread and distribution of particular species, such as plant pests (Wiser et al. 1998).

Tree population demographics

Population dynamics of tagged tree stems of species can be assessed using the summary statistics in Hall (1994a). Species mortality and recruitment rates can be calculated from the proportion of tagged stems that have died and been recruited (expressed as an annual percentage). Mean annual growth rates of species are calculated (mm per annum) from assessments of individual species across plots.

Overstorey summary statistics

Other summary statistics in Hall (1994a) include calculation of the basal area of species (m^2 per hectare), and density (numbers of individuals per unit area). Paired *t*-tests test for significance. Statistical summaries can also draw age-size class distribution graphs to pinpoint structural gaps of tree stems within a population. Alternatively, MS Excel can be used to calculate density, and spreadsheets can be imported into more user friendly statistical analysis packages such as SPSS.

Understorey data

PC-USTOREY analyses the differences in the abundance and growth of saplings and seedlings. In Hall (1994b), the summary statistics function can calculate and compare the density of saplings and woody seedlings, e.g. to compare density between palatability classes or between paired exclosure and unfenced plots. Paired *t*-tests then can test for significance. Alternatively, MS Excel can be used to calculate density, and spreadsheets can be imported into more user friendly statistical analysis packages such as SPSS.

Repeated measures

Repeated measures data analysis using mixed models are needed when data has been collected over three or more sample dates. Repeated measures analysis is challenging using the PC programs, especially if the user has not been trained.

Regression techniques can be used to test for factors that may explain variation in tree, sapling or seedling densities, such as indices of pest abundance (e.g. faecal pellet counts) or environmental variables (e.g. light, altitude) (Bellingham & Allan 2003; Husheer 2005). They can run in statistical packages such as R, SPSS, etc. Mixed model analyses are specialised, and it is recommended that advice be sought from suitably experienced individuals. Training courses and guidance on repeated measured analysis using mixed models has been the recent focus of DOC and it is anticipated they will be advanced through ongoing development work.

Classification and ordination

Analysis of compositional patterns and changes as a function of other factors (e.g. environment) falls into two main groups of analysis: classification and ordination. Both approaches are complementary because stands can be classified and then ordination applied (Mueller-Dombois & Ellenberg 2002). Classification (or clustering) groups individual plots by their compositional similarities and dissimilarities, and is useful when describing compositional patterns. Ordination techniques attempt to explain compositional patterns as a function of other variables, usually environmental (e.g. altitude, soil fertility). It assesses the degree of association within and between plant communities and their environment. A large range of software is available for implementing a myriad of classification and ordination techniques. Many analyses of this type are best undertaken using specialised software packages (e.g. PC-ORD, Canoco, R (specialised packages exist), Decorana, TWINSPAN). Analysts interested in such approaches should consult the large literature on these topics, including the reference material listed below and relevant websites.[8] Only TWINSPAN is available through the PC suite of packages. Detrended Correspondence Analysis (DCA) groups similar plots together and TWINSPAN analysis can explore the factors that drive differences between the groups (e.g. Husheer 2005).

[8] e.g. http://ordination.okstate.edu/index.html

Useful reference material on classification and ordination to consult include:

Lepš, J., Šmilauer, P. 2003: Multivariate analysis of ecological data using Canoco. Cambridge University Press, Cambridge.

Gauch, Jr., H.G. 1982: Multivariate analysis in community structure. Cambridge University Press, Cambridge.

Økland, R.H. 1990: Vegetation ecology: theory, methods and applications with reference to Fennoscandia. *Sommerfeltia Supplement 1*: 1–233.

Jongman, R.H.G.; ter Braak, C.J.F.; van Tongeren, O.F.R. 1987 (Eds): Data analysis in community and landscape ecology. Pudoc, Wageningen. (Now available in a 1995 edition by Cambridge University Press.)

Legendre, P.; Legendre, L. 1998: Numerical ecology (second English edition). Elsevier, Amsterdam. 853 p.

ter Braak, C.J.F.; Šmilauer, P. 1998: CANOCO reference manual and user's guide to Canoco for Windows: software for canonical community ordination (version 4). Microcomputer Power, Ithaca, New York. 352 p.

Case study A

Case study A: dieback in New Zealand *Nothofagus* forests

Synopsis

This case study is a useful example where data from permanent plots was evaluated in conjunction with indices of animal pest populations to understand the drivers of compositional and structural changes in mountain beech forest.

Objectives

- To determine the susceptibility of stands to canopy dieback and the long-term effects of dieback on mountain beech forest.

Sampling design and methods

- Two hundred and fifty permanent 0.04 ha plots were established in 1970–71 in the Harper-Avoca catchments, Canterbury. Plots were 200 m apart along transects that were chosen based on a restricted random design. Transects were restricted to begin in valley bottoms, usually along streams, and often terminated at the treeline. By 1985, all plots had been remeasured six times.

- Deer pellet count surveys were used to monitor the trends in red deer populations over several decades in the Harper-Avoca. Red deer were probably present for 40 years prior to the first pellet count survey in 1956. Original pellet count transects surveyed the main habitat types along altitudinal gradients (Hickling 1986).
- The valley received two major snowfall events, one in 1968 and the second in 1973, causing mechanical damage to the forest canopy and subsequently ongoing death of mature trees due to pathogens.

Results

- Mean plot basal area was calculated from the diameter measurements (PC-DIAM) and mean seedling density (15–135 cm tall) based upon seedling counts in subplots (PC U-STOREY—Hall 1994b). Mountain beech seedlings 15–135 cm in height increased fourfold from 1971 to 1985 (Allen et al. 2003). Initially, the results from an analysis of seedling densities (indicator for regeneration) and frequency of pellet counts (indicator for deer abundance) appeared counterintuitive, as an increase in the density of seedlings occurred during a period of time when the frequency of deer pellets also increased. In later years, a negative relationship was found between beech regeneration and deer density.

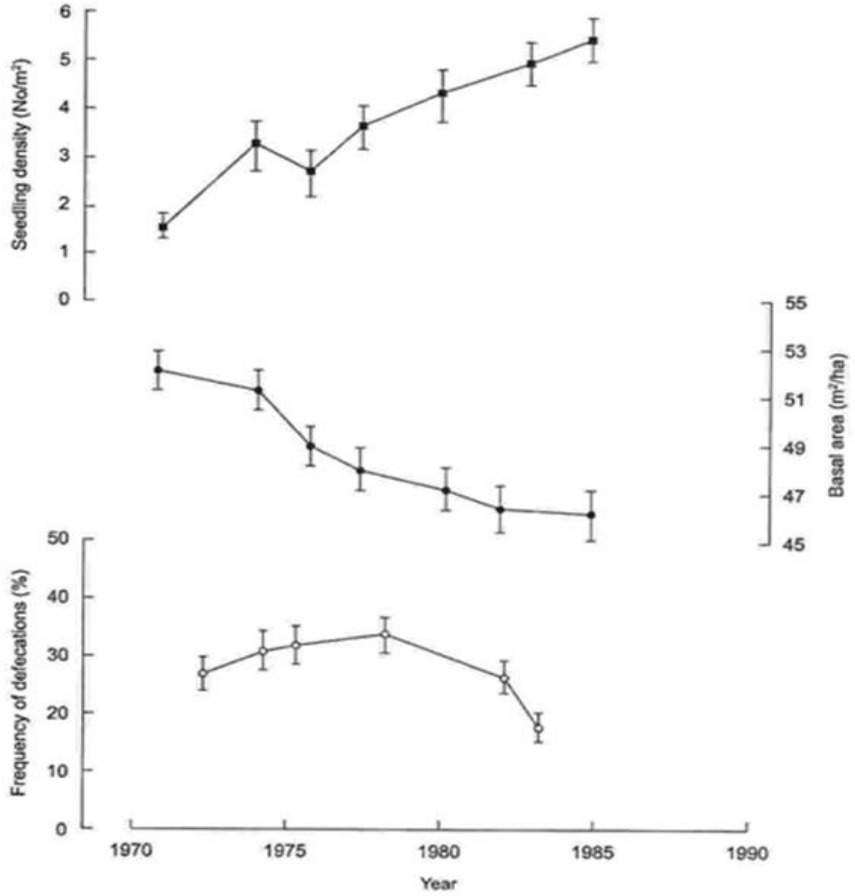

Figure 1. Relationships between deer density, tree basal area, and seedling density between 1970 and 1985 in the Harper-Avoca Catchment, Canterbury.

Limitations and points to consider

- The relationship between forest regeneration and deer densities only becomes apparent when tree basal area is included in the analysis.
- Basal area declined from 52 m^2 to 47 m^2 between 1970 and 1985.
- There was a strong inverse relationship between seedling density and tree basal area.
- Changes in basal area were related to mechanical damage incurred and subsequent dieback of canopy trees from the snowfall events.
- Seedling recruitment responded favourably to the subsequent increase in light from canopy gaps.
- This example demonstrates that caution is needed when assuming there is a direct causal relationship between animal pest densities and forest regeneration. Collecting complementary data on pellet counts proved useful to help interpret the regeneration patterns in forest plots in the Harper-Avoca.

References for case study A

Allen, R.B.; Bellingham, P.J.; Wiser, S.K. 2003: Forest biodiversity assessment for reporting conservation performance. *Science for Conservation 216*: 16. Department of Conservation, Wellington.

Hickling, G. 1986: Red deer population surveys in the Harper-Avoca Catchment 1956–1983. *FRI Bulletin No. 107*. Protection Forestry Division, Forest Research Institute, Christchurch.

Case study B

Case study B: the effects of red deer on tree regeneration in Aorangi Forest, Wairarapa

Synopsis

This case study uses analyses of tree stem densities to compare regeneration in unfenced (experimental control) with paired fenced plots in Aorangi Forest (Haurangi Forest Park) southern Wairarapa. Permanent 20 × 20 m plots were established in Aorangi Forest between 1981–1987 by Joe Hanson (then for New Zealand Forest Service) and all plots were remeasured in 2004. The case study pays special attention to the data analysis that was undertaken.

Aorangi Forest, southern Wairarapa, was highlighted in the 1960s and 1970s as an area where high deer and goat populations had a conspicuous effect on forest regeneration (Jane & Pracy, 1974). Feral goats, red deer and pigs reached high population densities in Aorangi Forest by the 1890s. In the early part of the 20th century, government funded deer cullers were the primary means of controlling deer, followed by commercial hunting from the 1960s until commercial hunting was restricted in Aorangi Forest in the 1980s.

Figure 2. New Zealand Forest Service file photograph of open understorey in the 1960s.

Currently, Aorangi Forest is generally considered to be an area where recreational deer hunting, and non-target kills from aerial 1080 poisoning aimed at controlling brushtail possum populations, limit deer populations. This is thought to be sufficient management so that regeneration of deer and goat palatable plants maintains forest diversity. Culling operations were undertaken by adjoining land owners, until government-funded culling was undertaken by the Department of Internal Affairs in 1939. In 1956, the New Zealand Forest Service took over culling operations until 1971. Following the formation of the Department of Conservation in 1987, limited culling of goats has occurred. Records were available for numbers of deer and goats killed during each annual culling season (July to June) between 1928 and 1999 (Fig. 3).

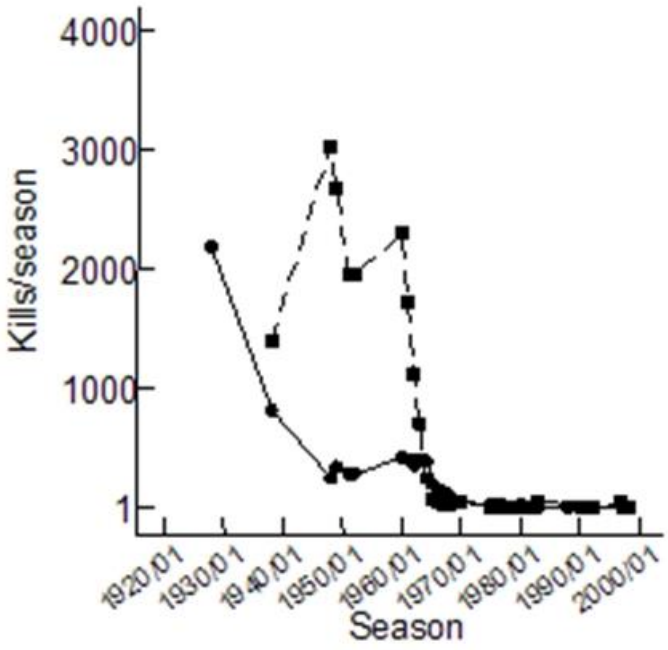

Figure 3. Numbers of deer (●) and goats (■) killed during summer culling seasons between 1928/29 and 1998/99 in Aorangi Forest.

Objectives

- To analyse data from paired fenced and unfenced permanent plots to determine whether the large decrease in deer and goat populations has restored regeneration of highly palatable plants.
- To determine whether there are differences in densities of palatable plants between fenced and unfenced plots. If the effects of ungulates are negligible there should be no difference in densities.
- To show if completely removing ungulates from Aorangi Forest can alter tree species composition (balance of species), or if changes in species composition induced by browsers are irreversible.

Sampling design and methods

- Paired fenced and immediately adjacent unfenced plots were established annually over 7 years (1981–1987) in each of the seven main river catchments in Aorangi Forest. Fences were 2.2 m high and were designed to exclude all ungulates. Because of limited resources and practicalities of establishing fences at steep sites, representative, and randomised sampling was not possible. Sites were subjectively located to be representative of forest in that catchment and where a fence could be established around plots. This meant that each of the four main forest associations in Aorangi Forest was sampled. These are beech tree associations (*Nothofagus fusca*, *N. menziesii* and *N. solandri*), and a low-altitude association of hīnau (*Elaeocarpus dentatus*), rewarewa (*Knightia excelsa*), māhoe (*Melicytus ramiflorus*), māpou (*Myrsine australis*) and kaikōmako (*Pennantia corymbosa*).

- Methods for stem measurement followed the same protocols used for other permanent plot surveys in New Zealand (Allen 1993), except that trees ≥ 2 cm diameter at breast height (DBH) were individually tagged and measured. Note that this DBH threshold differs from that recommended by Allen (1993) (recommends 3 cm DBH), and Hurst and Allen (2007a) (recommend 2.5 cm DBH). At five paired plots sites, plot size was 20 m × 20 m, but at two sites, paired plots were 15 m × 20 m due to fencing constraints imposed by terrain. Paired plots were remeasured in May and June 2004 and data entered into text files.

Results

Raw data

Raw data was carefully checked before analysis was undertaken. If data are in Excel format, errors will likely become apparent during analysis, which will require going back to raw data, making corrections, and then undertaking analysis once again. This is a potentially time-consuming and frustrating process and so it is better to do a good job on data entry and checking first time around. An accurate way to do this is for two people to enter data (one reading and looking, the other punching), then to swap roles during re-check. If data are in a text file format it can be further checked using PC-DIAM and PC-USTOREY (Hall 1994a,b).

Analysis of plot data

Firstly, summarise data plot by plot for each measurement (plots are generally treated as the sample unit or replicate). In this case study, the authors were interested in comparing tree stem densities between fenced and unfenced plots for all species. A species by plot table was constructed from raw data. Pivot tables in Excel can be used to do this. PC-DIAM can be used to summarise data plot by plot.

Secondly, the ‘tapply’ and table functions in the statistical package R can be used to summarise data (see R code below).

When using PC-DIAM or Excel, the output is in text format and requires further checking before entry into a spreadsheet or statistics package for analysis. For the Aorangi data, the Pivot table dialogue box was used (under the Data menu in Excel). The variable ‘Plot’ was dragged into the Row section, the variable ‘Species’ into the Column section and ‘Count of Diam’ into the Data section. The resulting Pivot table was pasted into a worksheet using the paste special (values) command in Excel. Formulae calculated stems/ha from the plot count summaries in the pivot table (i.e. multiply count data by 25 to get stems/ha). The resulting table can be imported into a statistics package such as SPSS for analysis. The species by plot format is suitable for importing into an ordination programme such as VEGAN (Oksanen 2008) or CANOCO (Ter Braak & Smilauer 1998) where multivariate techniques such as Detrended Correspondence Analysis (DCA) can be used. This analysis can be used to summarise species composition so comparisons can be made between fenced and unfenced plots. Other data such as basal area and seedling counts can be summarised in much the same way. Demographic statistics such as tree growth and mortality are

more difficult to calculate, and analysis generally requires programming in a statistics package or database such as R.

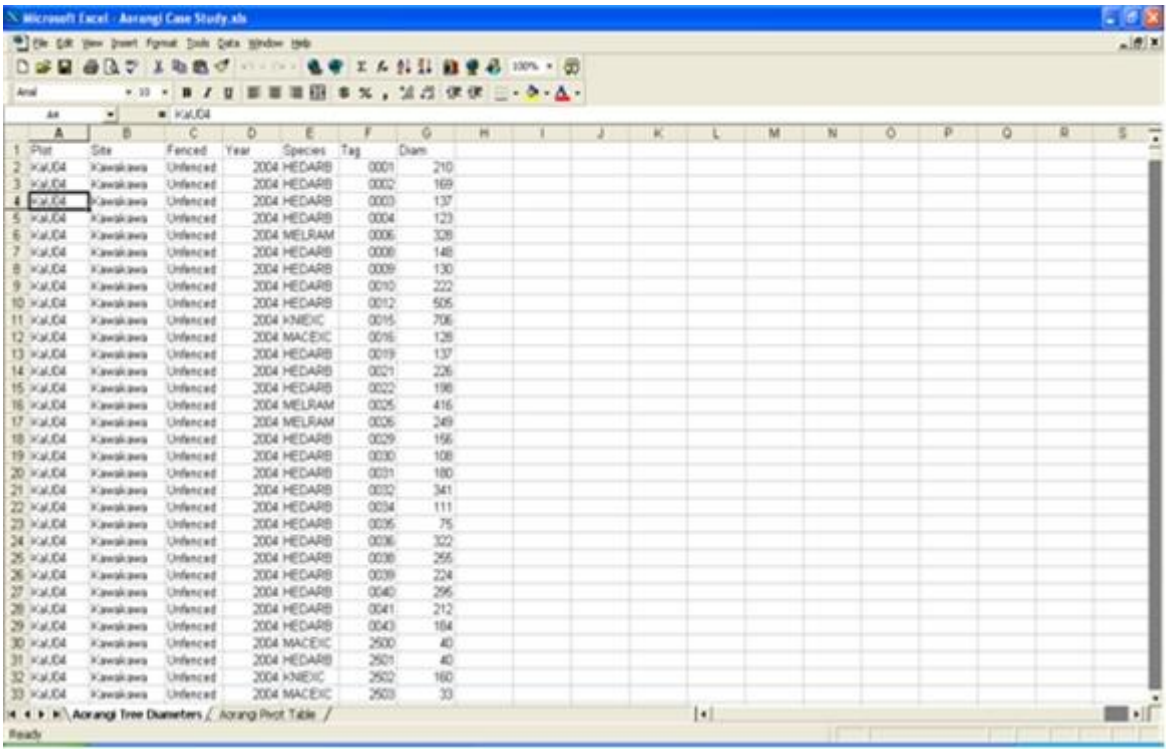

Figure 4. Raw data in Excel.

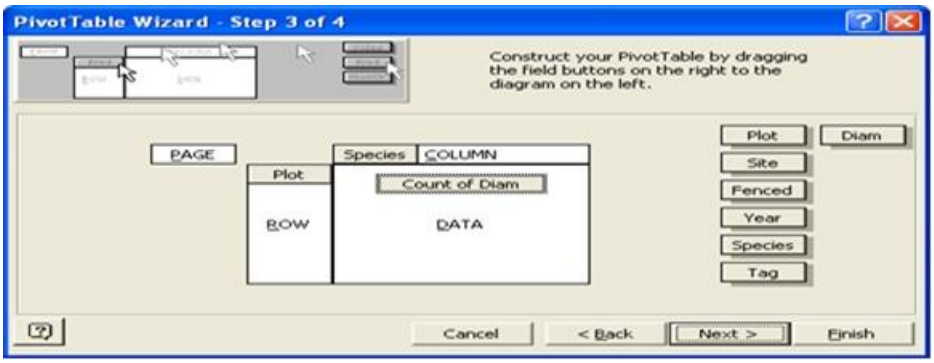

Figure 5. Pivot Table dialogue.

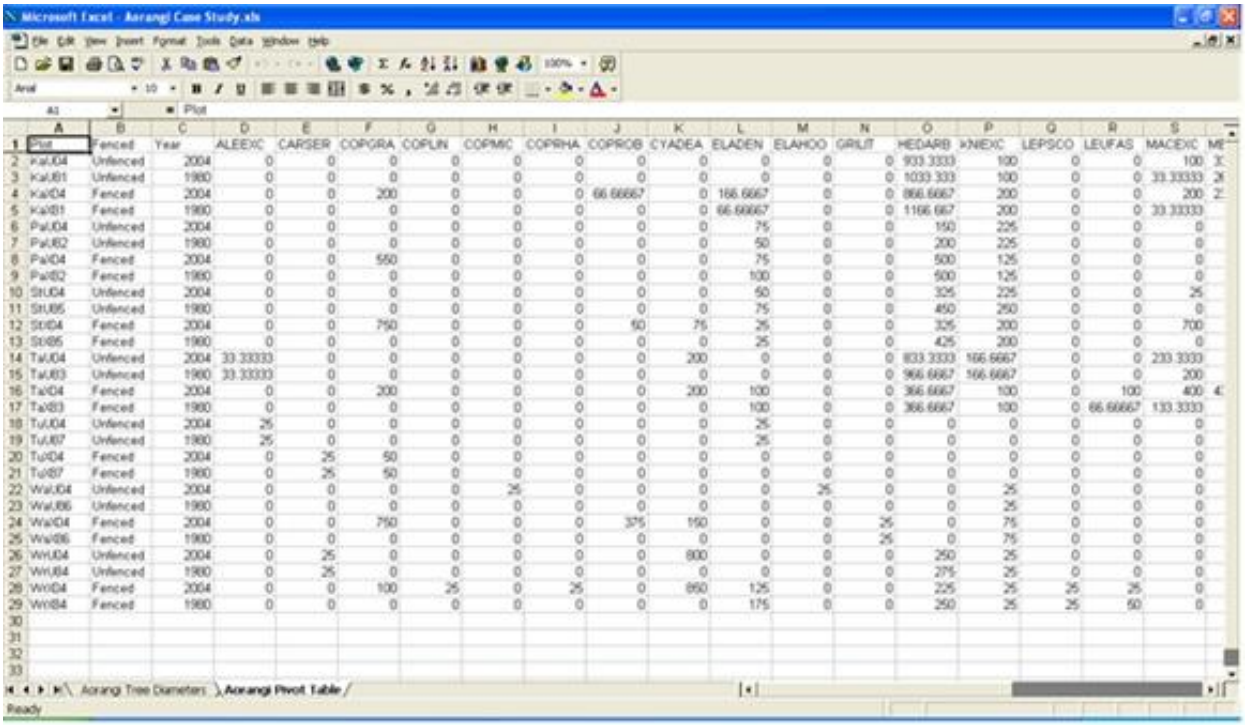

Figure 6. Summarised Pivot Table.

```
# Tree stem data collected from paired exclosure plots from Aorangi Forest, NZ
Forest Service
# Plots were established in the 1980s by Joe Hanson and re-measured in 2004 by
Sean Husheer New Zealand Forest Surveys
# Species codes are first three letters of genus and first three letters of
species
# Note how data has no special formatting. This is important. Data must be
clean.

Plot      Site          Fenced        Year    Species      Tag    Diam
KaU04     Kawakawa      Unfenced      2004    HEDARB       1      210
KaU04     Kawakawa      Unfenced      2004    HEDARB       2      169
KaU04     Kawakawa      Unfenced      2004    HEDARB       3      137
KaU04     Kawakawa      Unfenced      2004    HEDARB       4      123
```

Figure 7. First ten rows of data file used for analysis in R.

R code for analysis:

```
# Summarise Aorangi Excl Plot Data
dat <- read.csv ("C:\\Temporary\\Aorangi\\Aorangi Case Study.csv", header=TRUE, skip =5)
dat <- as.data.frame(table(dat$Plot, dat$Species)) # summarise data plot by plot and spp x spp
names(dat) <- c("Plot", "Species", "Count") # apply names to variables

# calculate tree stem density/ha and transform data
# Tauanui and Kawakawa were 300 m2, all other pairs 400 m2

dat$Area <- ifelse(dat$Plot == "KaU04" | dat$Plot == "KaX04" | dat$Plot == "KaU81" | dat$Plot == "KaX81" |
dat$Plot == "TaU04" | dat$Plot == "TaX04" | dat$Plot == "TaU83" | dat$Plot == "TaX83", 10000/300,
10000/400 )
```

```
dat$Count <- dat$Count * dat$Area

# produce a spp x plot table using loops
nplot <- length(table(dat$Plot)) # what number of plots
nspp <- length(table(dat$Species)) # what number of species
splot <- matrix(0, nrow=nplot, ncol=nspp) # produce a matrix of 0's of length plots and width species
rownames(splot) <- levels(dat$Plot) # give row names plots
colnames(splot) <- levels(dat$Species) # give column names species

plots <- dat$Plot # matrix py takes the form of py from data frame dat
species <- dat$Species
count <- dat$Count

for(i in 1:nrow(dat)) {
r <- which(rownames(splot)==plots[i])
c <- which(colnames(splot)==species[i])
splot[r, c] <- count[i]
}
rownames(splot) <- levels(dat$Plot) # give row names plots
splot <- splot[,-c(1)] # subset removes columns 1 to 2
summary(splot)

# Undertake DCA
library(vegan)
ord <- decorana(splot)
plot(ord, display = "site")
unclass (ord)
ord$rproj <- ord$rproj[,1:2]
names(ord$rproj) <- c("Plot", "DCA1", "DCA2") # apply names to variables
typeof (ord$rproj)
dcascores <- as.data.frame (ord$rproj)
dcascores$Plot <- rownames(dcascores)
plot.sp <- as.data.frame (splot)
plot.sp$Plot <- rownames(plot.sp)
summary.dat <- merge(plot.sp, dcascores,by=c("Plot"), all.x=TRUE, all.y=TRUE)

# SUMMARISE DATA
summary.dat$Site <- substr(summary.dat$Plot, 1, 2)
summary.dat$Fenced <- substr(summary.dat$Plot, 3, 3)
summary.dat$Year <- substr(summary.dat$Plot, 4, 5)
summary.fenced <- summary.dat[which(summary.dat$Fenced == "X"), ]
summary.unfenced <- summary.dat[which(summary.dat$Fenced == "U"), ]
summary(summary.fenced)
summary(summary.unfenced)

# Produce summary tables
dat$Fenced <- substr(dat$Plot, 3, 3)
dat$Year <- substr(dat$Plot, 4, 5)
dat <- dat[which(dat$Year == "04"), ]
sem <- as.data.frame(tapply(dat$Count, list(dat$Species, dat$Fenced), function(x)sqrt(var(x)/length(x))))
sem <- round(sem, 1)
names(sem) <- c("Unfenced SEM", "Fenced SEM") # apply names to variables
sem$Species <- rownames(sem)
means <- as.data.frame(tapply(dat$Count, list(dat$Species, dat$Fenced), mean))
means <- round(means, 1)
names(means) <- c("Unfenced Mean", "Fenced Mean") # apply names to variables
means$Species <- rownames(means)
summary.tab <- merge(means, sem, by=c("Species"), all.x=TRUE, all.y=TRUE)
```

```
summary.tab <- summary.tab[ , c("Species", "Fenced Mean", "Fenced SEM", "Unfenced Mean", "Unfenced SEM")]

# Append DCA scores to the table
# DCA 1
dcascores$Fenced <- substr(dcascores$Plot, 3, 3) # Identify fenced plots
dcascores$Year <- substr(dcascores$Plot, 4, 5)
dcascores <- dcascores[which(dcascores$Year == "04"), ] # select from 2004 only
dca.sem <- tapply(dcascores$DCA1, dcascores$Fenced, function(x)sqrt(var(x)/length(x))) # Calculate SEM in tabular form
names(dca.sem) <- c("Unfenced SEM", "Fenced SEM") # apply names to variables
dca.means <- tapply(dcascores$DCA1, dcascores$Fenced, mean) # calculat means
names(dca.means) <- c("Unfenced Mean", "Fenced Mean") # apply names to variables
dca.means <- as.matrix(dca.means)
dca.sem <- as.matrix(dca.sem)
dca.sum <- as.data.frame(t(rbind(dca.means, dca.sem)))
dca.sum <- round(dca.sum, 3)
dca.sum$Species <- "DCA Axis 1"
dca1.sum <- dca.sum[ , c("Species", "Fenced Mean", "Fenced SEM", "Unfenced Mean", "Unfenced SEM")]

# DCA 2
dca.sem <- tapply(dcascores$DCA2, dcascores$Fenced, function(x)sqrt(var(x)/length(x)))
names(dca.sem) <- c("Unfenced SEM", "Fenced SEM") # apply names to variables
dca.sem <- as.matrix(dca.sem)
dca.means <- tapply(dcascores$DCA2, dcascores$Fenced, mean)
names(dca.means) <- c("Unfenced Mean", "Fenced Mean") # apply names to variables
dca.means <- as.matrix(dca.means)
dca.sum <- as.data.frame(t(rbind(dca.means, dca.sem)))
dca.sum <- round(dca.sum, 3)
dca.sum$Species <- "DCA Axis 2"
dca2.sum <- dca.sum[ , c("Species", "Fenced Mean", "Fenced SEM", "Unfenced Mean", "Unfenced SEM")]
summary.tab <- rbind(summary.tab, dca1.sum, dca2.sum)

# UNDERTAKE A SERIES OF Paired T TESTS
t.test(summary.fenced$COPGRA, summary.unfenced$COPGRA, paired = T)
t.test(summary.fenced$PITEUG, summary.unfenced$PITEUG, paired = T)
t.test(summary.fenced$COPROB, summary.unfenced$COPROB, paired = T)
t.test(summary.fenced$ELADEN, summary.unfenced$ELADEN, paired = T)
t.test(summary.fenced$PENCOR, summary.unfenced$PENCOR, paired = T)
t.test(summary.fenced$MYRAUS, summary.unfenced$MYRAUS, paired = T)
t.test(summary.fenced$OLERAN, summary.unfenced$OLERAN, paired = T)
t.test(summary.fenced$MACEXC, summary.unfenced$MACEXC, paired = T)
t.test(summary.fenced$KNIEXC, summary.unfenced$KNIEXC, paired = T)
t.test(summary.fenced$MELRAM, summary.unfenced$MELRAM, paired = T)
t.test(summary.fenced$HEDARB, summary.unfenced$HEDARB, paired = T)
t.test(summary.fenced$DCA1, summary.unfenced$DCA1, paired = T)

t.test(summary.fenced$DCA2, summary.unfenced$DCA2, paired = T)
```

Statistical tests

- Husheer (2005) used paired *t*-tests to test for differences in tree stem density between fenced and unfenced plots in 2004. A paired *t*-test requires additional formatting, but the pivot table associated with this case study can be imported into SPSS as it is and a more straightforward (but less powerful) two group *t*-test applied to individual species. When data are imported into

SPSS, use the select pull down to select only rows from 2004. In the *t*-test pull down, use the variable 'Fencing' as a grouping variable, insert the variables for species and run the test on as many species as you wish. Alternatively, R can be used to restructure data prior to analysis for paired *t*-tests.

- Husheer (2005) found that only palatable species that showed significant differences in tree stem density between fenced and unfenced plots was *Coprosma grandifolia*. Over the two decades between plot establishment and remeasurement, mean stem density increased by 40 times inside fenced plots.
- There were no significant differences between paired fenced and unfenced plots in tree stem density for the other 12 common tree species.
- DCA scores, which are a statistical index of diversity and composition, also did not show differences between paired plots. The package VEGAN in R can be used to produce DCA summary scores.

Limitations and points to consider

- Using paired *t*-tests, Husheer et al. (2005) concluded that deer populations were sufficiently large in Aorangi Forest to consistently prevent regeneration of *Coprosma grandifolia*, though not low enough to preclude the regeneration of less palatable species at some sites. Other permanent plot and exclosure plot studies in New Zealand have shown that palatable plant species will generally not regenerate unless deer populations are maintained at very low densities (e.g. Husheer 2007). The conclusion of this study was that successful native forest management will probably only occur in New Zealand where deer populations are maintained at very low levels over several decades. A problem inherent in this case study is the relatively low number of plots available (seven paired plots) for analysis. Vegetation data in permanent plots are often highly variable. In this Aorangi case study, high variability among fenced plots resulted in the absence of a statistically significant difference between tree stem densities in fenced and unfenced plots for *Coprosma robusta* and *Pittosporum eugenioides,* even though both species were completely absent from unfenced plots. With sufficient sample plots, data could be subjected to statistical modelling to partition the variation due to environmental conditions or other factors such as herbivore browse.
- Permanent plot data invariably contains zero counts where some species are absent from most plots. Strongly skewed over-dispersed Poisson type distributions preclude the use of many traditional statistical techniques. The high number of zeros in permanent plot data means that only a few multivariate ordination techniques are suitable as well. DCA is a good example of a multivariate analysis technique which performs well with data encountered in permanent plots.
- Aorangi Forest's exclosure plot network makes up an important part of New Zealand's > 150 currently viable 20 × 20 m paired plots that were established between the 1950s and 1990s. Over 500 were established, but most have not been remeasured or maintained. While the exclosure plot network DOC has inherited will continue to provide information on what forest recovery would have been like had deer been maintained at low densities over the past 3 decades, responses to more contemporary deer control will be less clear with the current network. Relatively few fenced 20 × 20 m plots have been established since 1987, and with the

demise of commercial deer hunting current effects may be quite different to historical effects of deer.

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Full details of technique and best practice

- The permanent 20 × 20 m plot method is fully described in the expanded and field versions (Hurst & Allen 2007a,b).[9] The expanded version provides guidance on sampling regimes and more background on the development of the method.
- The corners of a permanent 20 × 20 m plot are permanently marked with four corner pegs and further subdivided into sixteen 5 × 5 m subplots using perpendicular tapes running across the plot every 5 m (Fig. 8).

[9] Refer to http://nvs.landcareresearch.co.nz/

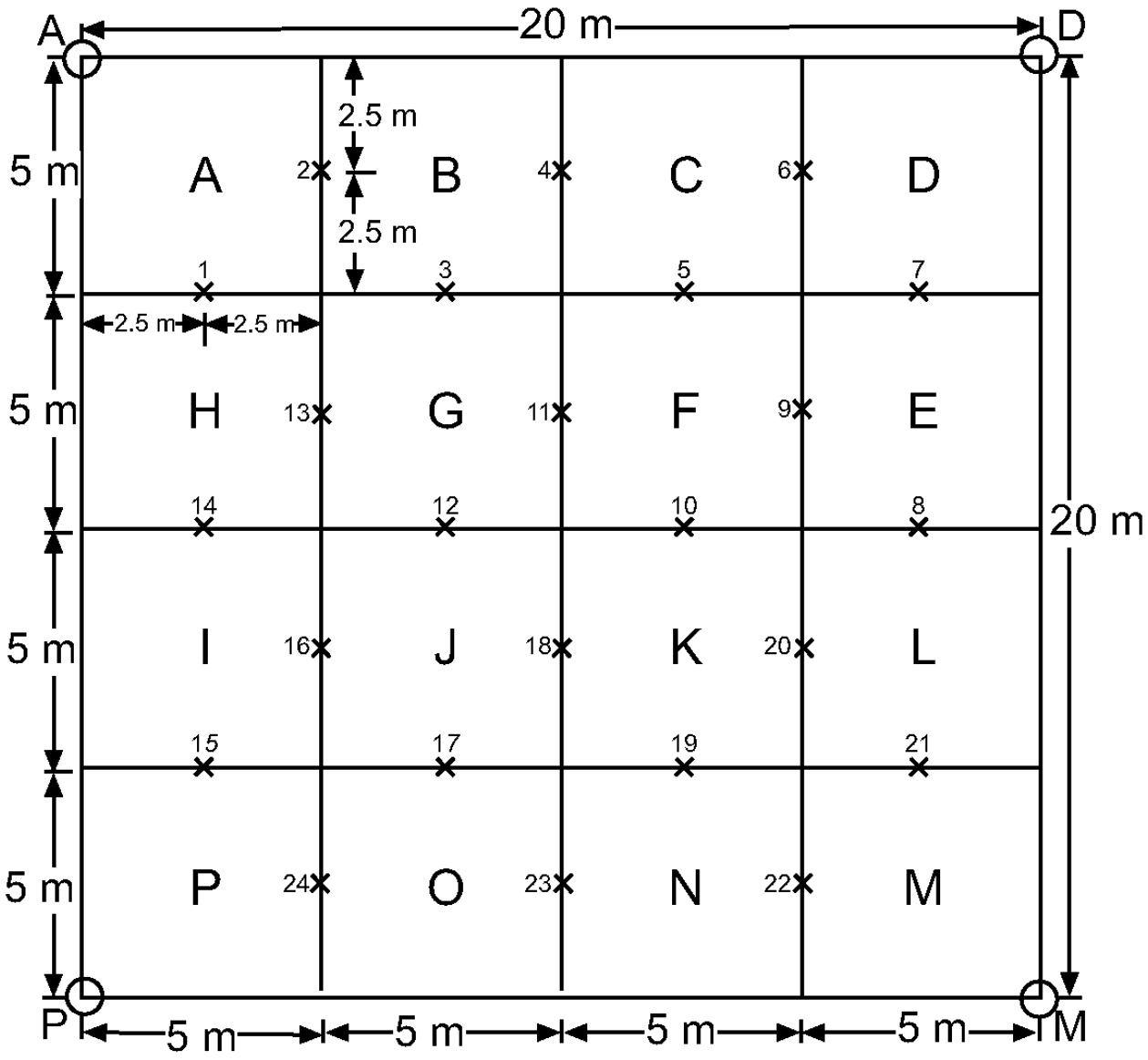

Figure 8. Permanent 20 × 20 m plot layout.

- It is important to make the effort to relocate as many corner pegs as possible during remeasurements for the plot to be orientated and measured correctly. Once the corners (labelled A, D, M, P) have been relocated, run the internal tapes out at 5 m intervals to create sixteen 5 × 5 m subplots (labelled A through to P).
- Move through each subplot sequentially starting at subplot A. Tag and measure the diameter of all live tree stems and tree ferns (> 1.35 m high and > 2.5 cm DBH). Tagging thresholds have varied over the years but the standard is now every stem greater than or equal to 2.5 cm DBH. Diameters are measured 1 cm above the tree tag on the uphill side of the stem if the ground is sloping, and are recorded on the pre-printed stem sheets. Ensure species are correctly recorded using the six letter species code. New stems that have reached the diameter threshold of 2.5 cm DBH must be tagged, measured and added to the datasheet.

- It is very important that all live stems are individually tagged, identified and measured correctly to ensure comparability between surveys. The Hurst & Allen (2007a) manual provides excellent instructions on dealing with plot anomalies such as epiphytes, dead stems, irregularly shaped stems, stems measured incorrectly, misidentified stems, leaning stems and missing stems.
- The understorey is measured from sapling and seedling counts.
- Tally the total number of individual saplings (> 1.35 m high, < 2.5 cm DBH) within each 5 × 5 m subplot, for each species. Do not count lianas. Record sapling counts on a new stem diameter datasheet, and indicate they are sapling counts using the notation < > (e.g. '< A >' denotes sapling counts for subplot A).
- Lay out 24 permanent seedling pegs in a systematic and standardised pattern along the 5 m subplot tape measures as denoted in the manual. Note that layout of seedling pegs has varied over the years and some plots will have alternative designs, but refer to the manual for more explanation of other possible layout patterns. Count the number of live woody seedlings present within a 0.49 m radius of each seedling peg and assign every individual seedling into one of four standardised height tiers. If it is not possible to identify individual seedlings (i.e. non-woody species) record their presence (not count) in the height tiers they occur. Record the presence (not count) of species if they occur in the lowest height tier (< 15 cm). Refer to the manual for guidance on counting seedlings on uneven ground surfaces and other anomalies.
- If the plot methodology is followed properly, all individual stems, saplings (within the plot) and woody seedlings (within the seedling subplots) will be observed and counted. However, this error may be positive or negative as individuals could be accidentally counted twice, or individuals may not be detected at all. If we assume this error is random then it is not really a problem and it just become part of the error of sampling. On the other hand, if individuals are followed inaccurately between measurements it will dramatically affect the calculation of demographics.
- A bounded RECCE description is recorded in conjunction with each permanent 20 × 20 m plot (Hurst & Allen 2007c,d).
- The notation that is required on the datasheets is important to follow. Clear and consistent notation will decrease data entry errors and it saves a lot of time chasing up original recorders and measurers to clarify errors.
- High-quality herbarium specimens are preferably collected away from or adjacent to plots, and should support new plant records.
- It is essential to have a training component for field teams to ensure data quality standards are upheld. Audits should be conducted early on in a survey to prevent inconsistencies and discrepancies with data collection. It is generally left to field teams to uphold good standards and practices.

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Appendix A

The following Department of Conservation documents are referred to in this method:

docdm-39000	National Vegetation Survey (NVS) databank data entry, archiving and retrieval standard operating procedure
docdm-53429	NVS metadata sheet
docdm-359575	Vegetation: RECCE plots
docdm-146272	Standard inventory and monitoring project plan