An analysis of the Fiji National Forest Inventory 2006 and Permanent Sample Plot measurements 2010-2018

Part 1 : Fiji National Forest Inventory 2006

Prepared under contract for the Ministry of Forestry, Fiji

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SUMMARY

The 2006 national forest inventory (NFI) established 1023 clusters, each nominally of 5 plots, randomly located in forests on the larger forested islands of Fiji, being Viti Levu, Vanua Levu, Kadavu, Taveuni, Gau, Koro and Ovalau. The plots comprised an outer circular plot of 400 m² on which trees of 20 cm and above dbh were measured, and an inner plot of 100 m² recording trees over 5 cm dbh. The plots were arranged in a cross-shaped cluster at the end of 40 m 'arms' (Figure 1, p 8). In all 5010 plots were assessed. A total of 899,398 ha of forest were surveyed. Although various reports have been based on the data, in particular the REDD+ Forest Reference Level (FRL) analysis, it has not hitherto being comprehensively analysed.

In this work, the data was cross-checked for validity. Stand structure and diameter class distributions appear as expected and there were no gross outliers in the diameter data. Height measurements were for bole height only, and therefore height-diameter functions based on PSP measurements were used. However, these also may not be reliable. They were used in the FRL as the basis for biomass estimates, and for reasons of compatibility, the practice is followed here also. A comparison with other height-diameter curves is made which shows however that the values are probably too low, but without field allometric research, it is not possible to be certain.

The data was analysed using the R statistical system. The key data sets, comprising the tree measurements, plot and cluster details, and maps of plot locations, have been bundled into a single directory called FFIDE, available as a zip file from https://bio-met.co.uk/proj/fiji/FFIDE.zip. The R survey package was used to analyse the data as a single-stage cluster design. An app called FFIDE was written using R shiny to surface various aspects of the data. The code is listed in an Annex and explained in the text. It allows subsets of the data to be selected by combinations of forest class, altitude range, island, province or district. The sample statistics for any selected subset (mean, standard error, confidence interval, intra-cluster correlation coefficient [ICC]">https://bio-met.co.uk/proj/fiji/FFIDE.zip. The R survey package was used to analyse the data as a single-stage cluster design. An app called FFIDE was written using R shiny to surface various aspects of the data. The code is listed in an Annex and explained in the text. It allows subsets of the data to be selected by combinations of forest class, altitude range, island, province or district. The sample statistics for any selected subset (mean, standard error, confidence interval, intra-cluster correlation coefficient [ICC]">survey area, volume and above-ground biomass. The frequency distribution of plot values is shown as a histogram, and a box plot allows the data distribution to be partitioned by forest type, altitude class, island, province or district. Full stand tables of species by size class are shown for any selected variable (stocking, biomass, volume, basal area), with cumulative size class distribution. The stand table can also be searched, sorted or sub-setted by species. FFIDE is accessible online at fifte.shinyapps.io/ffide. The online version does not gi

Using FFIDE, the species distributions by forest types are reviewed. There are several dominant species common to all forest types. *Myristica, Endospermum, Calophyllum, Cleistocalyx* and *Parinari* account for about 30% of stocking and canopy cover. Overall, 289 species are recognised. FFIDE shows species abundance curves and tables, which may support conservation programmes.

Forest areas are derived from published sources. Overall in 2006 there were 899,398 ha of natural forest, of which 670,300 ha were lowland (below 600 m altitude) and 229,098 ha upland forest. The lowland forest is subdivided into 414,738 ha of closed forest type, and 255,562 ha of open forest.

Overall mean and total parameters, with confidence interval are tabulated by forest classes (lowland closed and open forest, upland forest). It is found that the structural differences in terms of diameter distribution, volume, basal area and biomass are not large enough to be statistically significant, although the lowland closed forest has the highest stocking by a small margin. Biomass per ha in 2006 was 144.12 t/ha ±2.7% overall, with a total stock for natural forest of 129.62 million tonnes (Mt).

Recommendations for future inventory work are detailed including a specific research program on tree height-diameter allometry, proper allowance for data analysis concurrent with field work, imagery analysis using Sentinel or similar 10-m resolution combined SAR and optical multi-period data, analysed concurrently and in coordination with field work for ground-truthing and supervised classification, concurrent data checking with re-measurement of doubtful plot data, use of coded notes regarding tree and measurement quality, and use of tablets for field data collection. It is noted that this report is the first of 2 parts, with the second to follow being for PSP data analysis, growth and yield estimates and models.

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Acknowledgements

The Consultant would like to thank the members of the Fiji REDD+ unit and Ministry of Forestry who have provided data, information and guidance to support this work, in particular Narendra Chand as principle coordinator, and also Timoci Lagataki, Viliame Tupua, Ilai Tulele, Leone Batigai and Semi Dramibaka.

Abbreviations

| AGB Above Ground Biomass |
|---|
| AMR Annual Mortality Rate |
| ANOVA Analysis of Variance |
| API Aerial Photo Interpretation |
| BA basal area |
| CO ₂ Carbon Dioxide |
| DBH Diameter at Breast Height (1.3 m) |
| FFIDE Fiji Forest Inventory Data Explorer |
| FRL Forest Reference Level (of REDD+) |
| GIS Geographical Information System |
| ha hectares |
| ICC intra-cluster correlation coefficient |
| IPCC Intergovernmental Panel on Climate Change |
| m ² /ha square metres per hectare |
| m ³ /ha cubic metres per hectare |
| MAI Mean Annual Increment |
| MoF Ministry of Forestry |
| Mt millions of metric tonnes |
| MYRLIN Method of Yield Regulation with Limited Information |
| NFI National Forest Inventory |
| NIR Near Infra Red |
| PNG Papua New Guinea |
| PSP Permanent Sample Plot |
| REDD+ Reducing Emissions from Deforestation and Forest Degradation etc. |
| SOP Standard Operating Procedure |
| t/ha metric tonnes per hectare |
| TOR Terms of Reference |
| URL Uniform Resource Locator |
| VBA Visual Basic for Applications |

Disclaimer

This report presents the author's research, analysis, and findings as an independent consultant. Any errors or omissions are solely the responsibility of the author. The findings and recommendations do not represent any policy, opinion or statistic of the Fiji Ministry of Forestry or any of its officers and should not be construed or referenced as such.

1. Introduction

1.1. Terms of reference and objectives

Parts 1 and 2 of this report covers two related themes : The analysis of Fiji's 2006 National Forest Inventory (NFI), and the analysis of Permanent Sample Plots (PSPs) to measure forest growth and yield over the period 2010-2018, based on biannual re-measurements. The consultant's Terms of Reference (TOR) for this work are given in Annex A. This document, Part 1 of the report, is concerned primarily with the analysis of the 2006 NFI. It does however also use some information form the PSPs, particularly tree height measurements. Part 2 of the report, to be issued separately, covers the growth and yield analysis of the PSPs.

The NFI gives reference information on the condition of the forest at the point in time (2006-07) when the inventory was done. The plots are mainly in native forest, though they include some exotic regrowth. The PSPs cover a period of 8 years forest growth (2010-2018), with measurements at approximately 2-year intervals, and give information on forest dynamics, or change over time. From the PSPs, growth models can be constructed to forecast the future condition and economic value of the forest estate.

Clearly, a considerable period has elapsed since the 2006 NFI. The data has been used in several previous studies to inform the REDD+ forest reference level for Fiji, and for this purpose various focussed analyses have been done (Mundhenk et al, 2019; Weaver & Payton, 2011). These have been presented as internal documents, Excel spreadsheets, and incorporated into other reports. However, a general and systematic write-up of the results has never been completed, and is now required as a reference document for comparison with future inventories.

1.2. Data sets supplied

The consultant was supplied with a directory of files which contained two key Excel documents:

- The NFI 2006 tree measurements, plot and cluster assessments. These were provided in an Excel file called *Fiji NFI 2006_CarbonResults 16Nov2018.xlsx*. This included data from 76,968 trees, 1,023 clusters (of 5 plots each) and 561 species.
- The PSP tree measurements and species lists. These were contained in several files, one for each measurement campaign, as follows:

20200526124328_PSP-ROUND1-2010-2012.xlsx 20200526124328_PSP-ROUND2-2012-2015.xlsx 20200526124328_PSP-ROUND3-2015-2017.xlsx 20200526124328_PSP-ROUND4-2017-2019.xlsx

Additionally, the consultant was provided with GIS shape files for provinces, districts, and plot locations.

1.3. Prior analyses

As noted above, there has been no general analysis of the NFI 2006 published in any form. However, the data has been used in aggregate form (without reference to location, species or forest type) to develop the Forest Reference Level (FRL) scenario for Fiji's REDD+ programme (Mundhenk et al., 2019). An earlier carbon stock assessment, using a simpler and less complete methodology, was also

made by Weaver and Payton (2011). Data on broad forest types and areas, derived from the NFI 2006 field data combined with remote sensing analysis, were provided by MoF to FAO for the 2015 Global Forest Assessment (FAO, 2015). The PSP data has not hitherto been analysed, as far as the author is aware. Mundhenk et al (2019) in Annex B.1 refer to it, discuss some features, but did not include any results in their study.

1.4. Analysis tools used : R and Shiny

For data analysis and presentation in the report the open source statistical language <u>R</u> was used, after consultation with the REDD+ team to confirm that this was an acceptable and accessible choice. R is a command-driven language, and the various scripts and procedures used in the analysis are documented in Annex B. <u>R Studio</u> was used as the graphic interface, and <u>R Shiny</u> has been used to provide dynamic presentations of results via a web browser. The <u>Tidyverse</u> library set has been used within R to provide the majority of the analytical and presentation tools used (Wickham & Grolemund, 2017).

2. National Forest Inventory 2006

2.1. Sample plot design and tree measurements

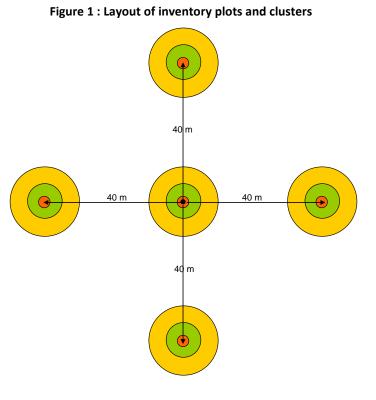
The main features of the forest inventory design were set out in Schade (2005) and are also contained in the MoF SOP documentation for the inventory. The main points are set out here only for reference. Circular plots were used, laid out in clusters of 5 as shown in Figure 1. Each plot is 40 m from a central plot in the cardinal directions, identified in the data set by the letters N,S, E, W, and C (centre). The plots have an area of 400 m² (11.28 m radius) on which all trees over 20 cm dbh¹ are measured. There is an inner plot of 100 m2 (5.64 m radius) on which trees over 5 cm dbh are measured. The protocol also describes a regeneration plot of 1.78 m radius at the centre (red in the figure), but this data was included in the analysis.

On the plots, trees were measured for diameter, and those over 40 cm dbh were measured for bole height, to the first major branch.

2.2. Location of sampling clusters

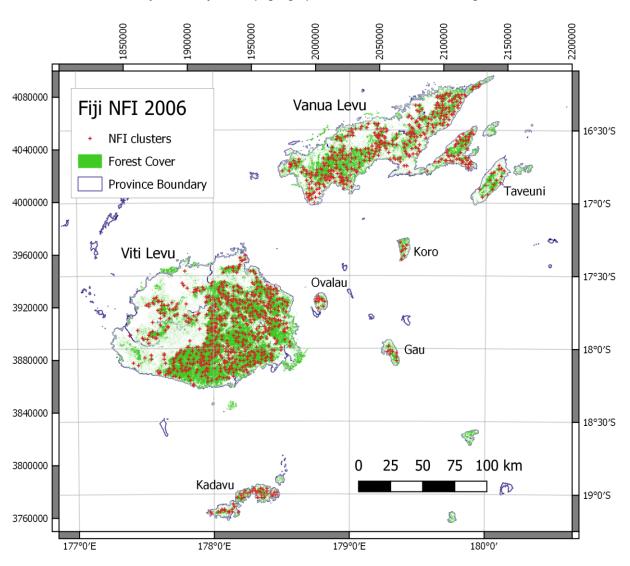
Figure 2 overleaf shows the location of the sampling clusters as red crosses. The green areas are forest cover (using 2017 land cover mapping). Only the main islands where sampling took place are shown.

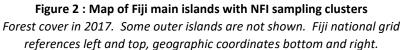
Locations were determined randomly using satellite imagery to determine forested zones. There were 1023 clusters. Table 1 shows cluster counts by island and province. Not all clusters had the intended 5 plots. There were 950 complete clusters and 73 incomplete ones with 1-4 plots. In total, there were 5010 plots.



| Table 1 : Sampling clusters by island and province | | | | | | | |
|--|----------------|----------|-------|--|--|--|--|
| Island | Province | Clusters | Total | | | | |
| Viti Levu | Ва | 68 | | | | | |
| | Nadroga/Navosa | 84 | | | | | |
| | Naitasiri | 144 | | | | | |
| | Namosi | 58 | | | | | |
| | Ra | 78 | | | | | |
| | Rewa | 14 | | | | | |
| | Serua | 56 | | | | | |
| | Tailevu | 62 | 564 | | | | |
| Vanua Levu | Bua | 99 | | | | | |
| | Cakaudrove | 157 | | | | | |
| | Macuata | 125 | 381 | | | | |
| Kadavu | Kadavu | 42 | 42 | | | | |
| Taveuni | Cakaudrove | 15 | 15 | | | | |
| Gau | Lomaiviti | 7 | | | | | |
| Koro | Lomaiviti | 4 | | | | | |
| Ovalau | Lomaiviti | 10 | 21 | | | | |
| Total | | | 1023 | | | | |

¹ Dbh : Diameter at breast height, measured at 1.3 m above ground. However, for buttressed trees it may be measured higher. The <u>SOP</u> describes measurement standards.





2.3. Statistical and error calculation

2.3.1. Methods

The inventory design involves a top-level stratification by forest types with random location of clusters. In a cluster sample, the variance of the stratum mean for a plot-level per hectare variable such as volume, biomass, basal area, is given by the following equation (Kangas & Maltamo, 2009, page 29):

$$S^{2} = (1 - f) \frac{s^{2}}{nm} [1 + (m - 1)\rho]$$
 {eqn. 1}

where:

 S^2 is the variance of the sample mean for the stratum.

- f is the ratio of area sampled to total stratum area. (1 f) is known as the finite population correction (FPC). It is often treated as 1 when the sampling fraction is small (less than 1%).
- s^2 is the variance for the plots, without regard to the clusters.
- *n* is the number of clusters.
- *m* is the number of plots per cluster.
- ρ is the intra-cluster correlation coefficient (ICC).

Equation 1 assumes all clusters have the same number of plots, whereas in this data set, some of the clusters (73 out of 1023 or 7%) have less than the full 5 plots. The ICC is a key parameter for any cluster sampling, and is usually estimated by ANOVA as:

$$\rho = \frac{s_b^2 - \frac{s_w^2}{m-1}}{s^2}$$
 {eqn.2}

with the symbols ρ , s^2 , m as previously defined, and s_b^2 , s_w^2 being between-cluster and within-cluster variances.

R has a package, <u>Survey</u>¹, which will perform all the calculations of means, sampling errors and confidence limits for one stage or multi-stage cluster sampling (Lumley, 2010), including with variable sized clusters. This has been used here to derive all the outputs presented, via the FFIDE app presented in section 2.7.

2.3.2. <u>Results</u>

Table 2 shows mean values, standard error, 95% confidence intervals and cluster sampling parameters (design effect, intra-cluster correlation) for the overall data set. These are taken directly from FFIDE (see §2.7.3, page 15).

| Variable | Mean | StdErr | Lower.CL | Upper.CL | ConfInt | Deff | ICC |
|-----------------------------|---------|--------|----------|----------|---------|------|------|
| Number per ha | 1052.07 | 11.65 | 1029.23 | 1074.9 | ± 2.2 % | 2.88 | 0.47 |
| Above Ground Biomass (t/ha) | 144.12 | 2.33 | 139.55 | 148.69 | ± 3.2 % | 2.79 | 0.45 |
| Total volume (m3/ha) | 258.13 | 4.19 | 249.92 | 266.35 | ± 3.2 % | 2.83 | 0.46 |
| Basal Area (m2/ha) | 27.82 | 0.38 | 27.07 | 28.57 | ± 2.7 % | 2.97 | 0.49 |

Table 2 : Overall inventory results based on single-stage cluster sampling analysis

In §2.8 and 2.9, some contrasts are explored between close and open forest, upland and lowland types, and the main sampling zones.

2.4. Data validation and quality

There are many quality checks which should be carried out on inventory data as it is collected. In the present case, no detailed report on the inventory was written at the time, and it is not known what checks were carried out. The data is in an Access database with an entry form corresponding, presumably, to the field forms, but much information about the data collection process and error

¹ For documentation, see <u>https://cran.r-project.org/web/packages/survey/survey.pdf</u>. Lumley (2010) illustrates the use of this package with practical case studies in his book *Complex Surveys*.

checking was not available. Error checking should be done whilst data is being collected and routinely include the following:

- Identification of diameter outliers and their verification.
- Checking of height outliers, both directly and in combination with diameters (outliers form the diameter-height regression.
- Digit preference checks. This will pick up fabricated data, malfunctioning instruments, or their incorrect use.
- At the plot level, stocking and basal area outliers.
- A sub-sample of plots (around 5%) should be remeasured periodically by a different team to the original measurements to verify quality of species identification and instrument measurements.

Where bad data is suspected, plots must be re-measured. To be effective therefore, these quality controls need to be planned before the inventory starts, all teams need to be briefed that they are in place and that they will have to re-measure plots if abnormalities are detected, and the checks need to be done in real time during data collection. The process is aided if data collection is done with tablet devices rather than paper forms, as there is no delay in data processing, and some checks can be built-in to the form coding on the tablet, such as diameter and height outliers.

For the 2006 inventory, it seems probable as discussed in §2.5 below that many height measurements are too low, and that there may be some excess of large diameter measurements over 100 cm. However, without field verification of these outliers at the time of data collection, it is impossible to be certain, and for the present analysis the data has been accepted as is.

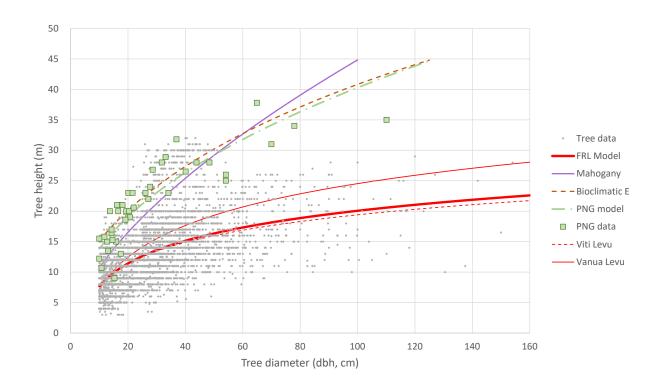
2.5. Height-diameter functions

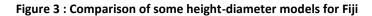
Height estimation is important for measurement of volume and biomass. The NFI 2006 data includes bole heights, but not tree total height, which is required for allometric functions of biomass, as discussed in section 2.6. In preparing the Fiji Forest Reference Level scenario, (Mundhenk et al, 2019) describe the equations used for calculating above-ground biomass (AGB) from tree height and diameter. The procedure and related discussion is in the FRL report section A.2.4.1, pages 67-68. They make the following point with respect to tree heights:

Initially, Equation 7 in Chave et al. [2014] was selected as the most promising candidate model, because total tree height was not measured during the NFI 2006 field campaigns and Eq. 7 provides a substitute for tree height (i.e., a so-called environmental stress factor enters the equation). However, when Eq. 7 from Chave et al. [2014] was tested on data collected during Fiji's Permanent Sample Plot (PSP) program, predicted tree AGB was much higher when using the environmental stress factor (as a substitute for trees height) compared to using the measured heights in Eq. 4 in Chave et al. [2014]. During the PSP heights of trees > 10 cm DBH were recorded. It was found that the environmental stress factor assumes much taller trees compared to the heights measured during the PSP. The same holds true for Eq. II.5 Wet in Chave et al. [2005]. In the latter, tree height is not used as an input (only DBH and the wood density are used as inputs) but an inherent relationship between DBH, total tree height and AGB is assumed. It was, therefore, decided to use the PSP data to derive a height model, predict the heights of NFI 2006 trees using the fitted model and then use Eq. 4 in Chave et al. [2014] to predict the AGB of NFI 2006 trees.

The highlighted sentence indicates the low biomass values obtained using measured tree heights compared to a height-independent equation. The consultant reviewed the tree height data from the PSPs, and found that the heights appear relatively low, with large trees in the 40 -100 cm diameter range frequently having recorded heights below 15 m. Figure 3 shows the individual trees from the PSP measurements of round 1 (2010-2012 measurements), filtered to only include those with both

bole and total height measured, and exclude any noted as with broken tops. A number of different height models are shown for comparison.





The heavy red line is the FRL function:

$$H_{tot} = -4.681 + 5.3715 \ln(D)$$
 {eqn.3}

Here, H_{tot} is tree total height in m, and D is tree diameter (dbh) in cm. This equation is given in Mundhenk et al (2019) on page 68, Annex A, section A.2.4.1. It is also noted in Vesa (2018). This was fitted by regression to PSP data, but the exact data set is not known. However, it lies close to the regression line of the same form through the data points shown.

This can be compared with tree height diameter from Papua New Guinea, extracted from Chave et al. (2014)'s published data set¹, which is shown as green squares on Figure 3, with the regression line as dot-dash green. This height-diameter function is quite similar to the Fiji plantation Mahogany height-diameter function given in Payton & Weaver (2011). Also very similar is the orange broken line, labelled Bioclimatic E. This is Chave et al. (2014)'s equation 6a:

$$ln(H_{tot}) = 0.893 - E + 0.760 ln(D) - 0.0340 [ln(D)]^2$$
 {eqn.4}

with the bioclimatic E value set to -0.0153. Chave et al. (2014) provide a world-wide raster data set for calculated E values, also available to download². E itself is a composite index based on temperature and rainfall seasonality and drought stress. From the raster data set, an average value was calculated for Fiji. There is considerable variation across the island, as indicated in Figure 4, which shows the Fiji raster data and some comparable rainfall data. The brown areas indicate more

¹ <u>http://chave.ups-tlse.fr/pantropical_allometry/Chave_GCB_Direct_Harvest_Data.csv</u>

² http://chave.ups-tlse.fr/pantropical allometry/E.nc.zip

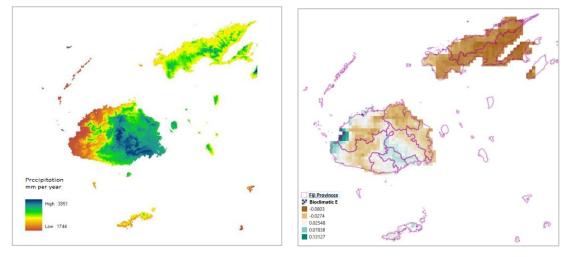
negative values of E (less bioclimatic stress), and the more blue-green areas, more positive values. The range is from -0.08 to +0.13, with a mean of -0.015.

It is apparent on Figure 4 that the Bioclimatic E suggests more favourable forest growing conditions on Vanua Levu and Taveuni than Viti Levu. To check this with the PSP data, average regressions were calculated for the height diameter function for these two zones. These are shown on Figure 3 as the thin red solid and dotted lines respectively.

Figure 4 : Variation in rainfall and the bioclimatic stress index (E) on the main islands of Fiji

(a) Rainfall patterns¹

(b) Bioclimatic stress index [data from Chave et al, 2014]



¹ https://www.pinterest.com.au/pin/510877151477223740/

As Mundhenk et al (2019) note, the use of bioclimatic E gives considerably higher height estimates (and hence biomass) than the direct height-diameter function from the PSP data. The latter was used for the FRL report, and has been retained as the primary measure of AGB.

In the consultant's opinion, without being able to make on-site verification, the PSP total height measurements appear to be for the most part to be either ocular estimates, or bole height estimates or measurements, and are therefore biased low, consequently leading to underestimation of overall biomass values.

Whilst calculated AGB values based on equation {3} have been used for the Fiji REDD+ Forest Reference Level, and are therefore used here as the primary measurement of above ground biomass, it is the author's view that these are very likely too low, and the true biomass function is likely to be closer to equation {4}. Future inventories should pay particular attention to the derivation of an accurate height-diameter functions, as noted in the recommendations of this report (§0).

2.6. Allometric equations for volume and biomass

2.6.1. Forest Reference Level methodology for biomass

The FRL report (Mundhenk et al, 2019) uses the following equation to estimate AGB, after Chave et al (2014):

AGB =
$$0.0673 (\rho.H.D^2)^{0.976}$$
 {eqn.5}

Here AGB is tree biomass in kg, ρ is mean wood density (g/ml), H is tree total height (m), and D is tree dbh (cm). To apply this equation, H is estimated from D using equation {3} above, as given by Vesa (2018) and equation A.7 in Mundhenk et al (2019). Wood density is taken from the wood density database of Zanne et al (2009).

2.6.2. <u>Tree total volume</u>

There are no natural forest volume equations that have been developed for Fiji. Past inventories (1992 and earlier) have used lower and upper stem diameter measurements and log length measurements to estimate volumes. However, equation {5} can be used as a total volume equation if wood density ρ is omitted and the result scaled by 1000 to give m³, giving:

$$V_{tot} = 0.0000673 (H.D^2)^{0.976}$$
 {eqn.5}

Here, H is estimated height in m, D is diameter at dbh in cm, and V_{tot} is volume overbark down to the practical limit of measurement. This function is taken from Chave et al's (2014) database, which as they note, includes volumes measured to a variety of standards and limits, but in the most part the upper diameter limit is between 5 and 10 cm.

The height term H, for consistency with other regional volume equations (see figure 5), should be calculated from equation {4}.

2.7. Fiji inventory data explorer (FFIDE) Shiny app

2.7.1. Purpose of FFIDE

There are many ways in which a set of forest inventory data such as the Fiji NFI 2006 study can be viewed and interpreted, including various sub-set views by region, district, island, forest type, altitude, etc. Various statistics can be of relevance for different purposes, trees numbers per hectare, basal area, biomass, volume. Of interest may be diameter distributions or values above given diameter limits, broken down by species or in totals. It may be of interest to highlight particular species or groups of species, etc. Traditionally this would be accomplished by printing out voluminous tables giving as many possible views as possible, resulting in massive and unwieldy documents that are difficult to print or use. The FFIDE app is designed to give access to the NFI 2006 data in processed form, with a dynamic interface via a computer browser, that allows all this possible information to be accessed in a compact and easy to use form.

At the same time, the app has a didactic or training objective: To provide an example of R procedures for various purposes, such as the construction of stand tables by diameter classes and species, using the R statistical language, and to show by example how such functions can be wrapped up as a web-enabled Shiny app.

2.7.2. <u>Code listing and access</u>

A working copy of FFIDE is available directly via the link below:

https://ffide.shinyapps.io/ffide/

A listing of the code is given in Annex B.3. This also explains how it may be set up in <u>R Studio</u> for local use and development. Line numbers in the following sections are given as (#220-230) and refer to this listing, in this example lines 220 to 230. Symbolic names used in code are underlined. The

technical descriptions of the R code are indented in italics, and can be ignored by the more general reader.

2.7.3. Initial screen

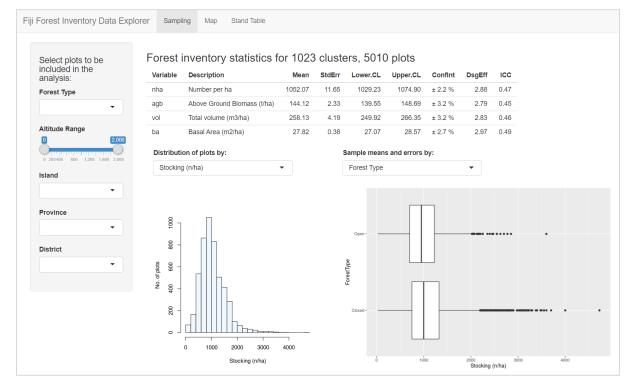


Figure 5 : FFIDE initial screen

When FFIDE starts, it shows the view above. This includes all the inventory data, for 1023 clusters and including 5010 plots (nominally 5 plots per cluster, but with a few incomplete clusters). A table of statistics are shown at the top, a data filter tool in the left side panel, a histogram of diameter distributions at the lower left main panel, and a box plot in the lower right main panel.

The layout is controlled by code in lines #493-529, creating a side bar and main panel. Note that these are assigned to the <u>ui</u> object, in accordance with R Shiny specifications. Subsidiary objects are the various <u>selectInput()</u> functions that create drop-down menus for forest types and islands, the <u>sliderInput()</u> function for altitude range, and <u>uiOutput</u> specifications for provinces and districts. These are created dynamically as the island selection is changed, at lines #573-577 of the <u>server()</u> function.

The filter tool allows selection by forest type (closed or open forest), altitude range, island, province or district. Note that as the island or province are selected, the lists in the district drop-down menu will update. When a filter selection is changed, all the information changed will update automatically. This can take several seconds, during which time the screen may blank or go grey.

Filtering is done in code by the routines <u>includeClusters()</u>, <u>includeTrees()</u>, <u>includePoints()</u>, and <u>filterTable()</u> at lines #17-72. These are called as needed by the <u>server()</u> interface at lines #579-594. The current cluster and tree subsets are defined as reactive functions which change whenever the applicable controls are modified (#579-586). The inventory design object <u>invdo</u> (for the <u>survey</u> package) is also updated reactively (#588-590). The table output function depends on these and is also reactive (#592-594).

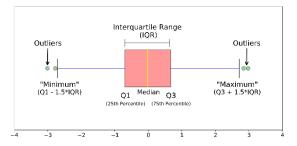
The table at the top shows sampling statistics for each of the variables analysed. These variables are stocking, or trees per hectare; above ground biomass, in tonnes per hectare; total volume, in cubic metres per hectare; and basal area in square metres per ha. The table gives the mean value, standard error, lower 95% confidence limits, upper 95% confidence limits, the confidence interval as a percentage of the mean, and for the cluster sample, the design effect and inter-cluster correlation coefficient, as discussed in section 2.3.

The inventory statistics are calculated using the R <u>survey</u> package. At lines #399-404, function <u>doInventory()</u> returns a survey design object, based on a single stage cluster sample (#402). Function <u>invStatsTable()</u> calculates the various statistics from the design object and returns it as a data table. At line #600, this table is output via the <u>renderTable()</u> Shiny function. This is a reactive function that is called whenever <u>invdo()</u> changes. This also reactive, as declared at line #588, and will be triggered whenever the set of selected clusters is modified, at #579.

The lower left histogram shows the distribution of sample plots by a selected metric (stocking, biomass, volume or basal area), according to the choice made from the drop-down menu above the diagram.

This histogram is produced by the function <u>invStatsPlot()</u> at lines 434-446. This depends on the inventory design object <u>invdo</u>, derived from function <u>doInventory()</u> (#399-404). These functions are called by <u>server()</u> at line #601 whenever the filtering changes, affecting <u>invdo</u> (#588), or the variable <u>input\$selHistVar</u> is changed (#509-514). <u>invStatsPlot()</u> returns a ggplot2 object, which is rendered on the screen by the Shiny function <u>renderPlot()</u> at line #601.

The lower right box plot shows the data mean and distribution by a selected characteristic from the drop-down menu above, which may be Forest Type, Altitude Class, Island, Province or District. The altitude class divides plots below and above 600 m (lowland and upland). The factors included will be influenced by the filtering characteristics set, so districts, for example, will be limited to any filters



set by island or province. The diagram at the right¹ shows the standard layout and definitions of a box plot. The bottom axis is the number of standard deviations for normally distributed data.

The box plot is produced via line #602, which will call <u>invBoxplot()</u> at lines #449-462.

2.7.4. The leaflet map

The **Map** tab of FFIDE brings up a leaflet map. Leaflet is an open source library in Javascript, also available in R, for rendering GIS files with full pan and zoom capabilities. There is a substantial library of free background layers, of which two are used for this map, both from OpenStreetmap², the street map and the topographic layer, which shows contour intervals at larger scales. The map will show these features together with the NFI 2006 sample plots for the selected data set, according to the filter tool settings on the Sample panel. The example shown in Figure 7 overleaf includes all data.

In code, the user interface object <u>ui</u> (#492) has a placeholder for the map set up at line #530. In the <u>server()</u> function, at #613, a set of points for plot locations is created by the <u>includePoints()</u> function, filtered according to current settings of the **Sample** filter panel, indicated by the reactive function <u>clset()</u>.

¹ from <u>https://towardsdatascience.com/understanding-boxplots-5e2df7bcbd51</u>

² see https://www.openstreetmap.org/#map=7/-18.494/178.383

Then at lines #615-622, the map is created using leaflet. Documentation for leaflet can be found at <u>https://rstudio.github.io/leaflet/shiny.html</u>. In order to make the map fully reactive to updates, lines #624-628 watch for sample changes and modify the map accordingly.

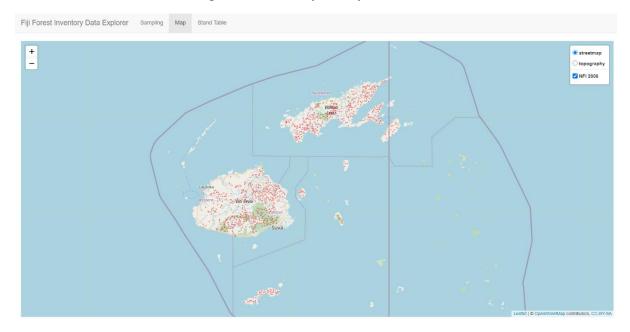


Figure 6 : Leaflet map of NFI plots in FFIDE

2.7.5. The main stand table

The stand table tab of FFIDE shows a table as below by default. The main table has one row for each species, with various diameter classes. The default diameter classes are as shown but these can be varied as required.

| Figure 7: FFIDE main | stand | table |
|----------------------|-------|-------|
|----------------------|-------|-------|

| Stand Table of | By S | Species | Totals | | | | | | | | | | |
|--------------------------------|------|---------|-------------------|--------|----------------------|-------|-------|-------|---------|----------|---------|-------|------|
| Species by Diameter Classes | Сору | y Excel | Show 10 v entries | | | | | | | | Search: | | |
| Options: | | spp | spname | 5-10 | 10-20 | 20-30 | 30-50 | 50-70 | 70-90 ≬ | 90-110 🔅 | 110-150 | 150+ | tota |
| Diameter classes (cm) | 1 | 137 | MYRIS CAST | 28.982 | 37.026 | 6.986 | 9.187 | 1.277 | 0.165 | 0.005 | 0.000 | 0.000 | 83.6 |
| 5,10,20,30,50,70,90,110, | 2 | 270 | GIRON CELT | 36.567 | 36.826 | 1.332 | 0.180 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 | 74.9 |
| Species names | 3 | 402 | CLEIS EUGE | 19.960 | 25.090 | 3.837 | 3.872 | 0.589 | 0.220 | 0.010 | 0.015 | 0.000 | 53.5 |
| Short - | 4 | 65 | CALOP VITI | 10.798 | 15.828 | 2.715 | 4.731 | 1.038 | 0.205 | 0.035 | 0.020 | 0.000 | 35.3 |
| Variable | 5 | 109 | MACAR HARV | 15.449 | 15.010 | 1.502 | 0.639 | 0.040 | 0.005 | 0.000 | 0.000 | 0.000 | 32.6 |
| Stocking (n/ha) 🔹 | 6 | 162 | DILLE BIFL | 9.940 | 14.691 | 2.480 | 1.153 | 0.050 | 0.015 | 0.010 | 0.000 | 0.000 | 28.3 |
| Sample scope: | 7 | 213 | BACCA SEEM | 16.128 | <mark>11.4</mark> 17 | 0.364 | 0.035 | 0.005 | 0.000 | 0.000 | 0.000 | 0.000 | 27.9 |
| Clusters 1023 | 8 | 163 | GARCI MYRT | 9.441 | 11.497 | 2.061 | 1.382 | 0.095 | 0.025 | 0.000 | 0.000 | 0.000 | 24.5 |
| Plots 5010 | 9 | 146 | HAPLO FLOR | 7.804 | 9.641 | 1.622 | 1.482 | 0.120 | 0.065 | 0.005 | 0.000 | 0.000 | 20.7 |
| | 10 | 247 | PARIN INSU | 4.790 | 7,166 | 2.081 | 4.247 | 1.178 | 0.210 | 0.035 | 0.010 | 0.000 | 19.7 |

The controls for the table allow various numbers of rows to be shown at a time, via the **Show...entries** box. This always has an option to show all the species in the dataset if required. The species are sorted in descending order on the **total** column by default, with the most abundant being shown first. However, all the columns have sort buttons (up-down arrows) beside them, which will re-sort the table up or down when clicked.

The **search box** will search for any text in the table and limit the display to lines that match the search box. For example, entering 'myris' will limit the display to all species short names including this string (genus Myristica). This is particularly useful for species names, but could be used equally for numeric strings if required.

The **Copy** and **Excel** buttons will allow the data to be transferred to other software. **Excel** creates an Excel worksheet well-formatted with the table data and headings. **Copy** copies the data to the clipboard using tab separated columns, which works well for pasting to other software.

The table options in the left-hand panel allow **diameter classes** to be changed. These are given as the class lower bounds in cm. The last class listed will always include all data above that class. The smallest trees measured in the dataset were 5 cm dbh, so giving a class below this will not include any additional data and may be misleading. For example, the string 10,20,30,40 would create the classes 10 to 19.99 cm, 20 to 29.99 cm, 30 to 29.99 cm, and 40 cm or larger. If incorrect data is given, such as 40,30,20, the table will not update, and the specification will be ignored.

The **species names** options allows short names, full botanical names, or local Fijian names to be shown.

The **variable selector** allows the choice of stocking, above ground biomass, volume or basal area in the table, using the indicated units.

The table is always restricted to the sample selection, as defined on the **Sample** tab. The current sample selection is shown under the **sample scope** heading, and will show applicable island, region or district constraints, as well as forest type and altitude range. The total number of clusters and plots in the sample will be shown.

In code, the stand table is implemented by the function <u>standTable()</u> at lines #89-143, which outputs a <u>DT</u> (data table) object¹. The various controls for filtering, sorting, table size, and copy/excel buttons are built-in to DT, with the options at lines #134-141 controlling their appearance and position on the table. The position of the table in the user interface is specified at #545. The <u>standTable()</u> function is called in the <u>server()</u> at lines #637-638. The parameter <u>trset()</u> is a reactive function defined at line #586 which gives the current dataset, limited by the sampling filters.

2.7.6. Stand table totals and supplementary information

The **totals** tab of the stand table tool is shown in Figure 9 with default settings. At the top are two lines of totals, labelled *Table* and *Sample*. The *Table* row is for the visible table, with whatever filters may be applied. The *Sample* row is for the entire sample, as shown by the sample scope information. As with the main stand table, this has buttons to allow the table to be copied to the clipboard or to an Excel worksheet.

The **cumulative % table** at the lower left shows the totals above a given diameter limit for both the visible table and for the entire sample. The central **histogram** gives the same information as the totals table above, but in a visual form that may be more useful for demonstrating some points in publication. The **species abundance** chart shows the species in the visible stand table (ie subject to any filtering conditions) in order of their total abundance as measured by the current variable (stocking, biomass, volume, basal area), as a percentage of the sample total.

In code (Annex B.3), the total table is produced by function <u>totStandTable()</u>, lines #145-182, whilst the corresponding histogram is <u>plotTotStandTable()</u>, lines #184-220. This draws on the function

¹ see <u>https://rstudio.github.io/DT/</u> for documentation.

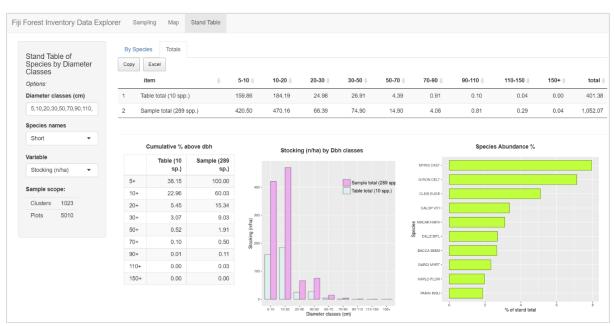


Figure 8 : Stand table totals, cumulative values, bar chart and species abundance

<u>draw.Legend()</u>, lines #222-250. The cumulative table is produced by <u>cumTotalTable()</u>, lines #253-304, and the species abundance chart by <u>abundancePlot()</u>, lines #306-323. In the user interface, the positioning of the elements for this page is at lines #546-561. The reactive elements in <u>server()</u> are at lines #639-652.

2.8. Species distribution and composition

The NFI 2006 data contains 289 recorded species, of which the top 25 in terms of canopy dominance are listed in Table 3 below. The table shows ranking by basal area (canopy dominance), tree numbers (which tends to be strongly influenced by regeneration in gaps and disturbed areas), and ranking in low-altitude (up to 600 m) and high-altitude (above 600 m) forest.

| | | Abundance | metric | Cumulative | Ab | undance (B | A) Ranking | g by forest cl | ass |
|---------------------------|-------------|-----------|--------|------------|---------|------------|------------|----------------|--------|
| Botanical Name | Local Name | % N/ha | % BA | % BA | Overall | Closed | Open | Lowland | Upland |
| Myristica castaneifolia | Kaudamu | 7.9% | 9.0% | 9.0% | 1 | 1 | 1 | 1 | 5 |
| Endospermum macrophyllum | Sisisi | 1.5% | 5.5% | 14.5% | 2 | 2 | 4 | 2 | 4 |
| Calophyllum vitiense | Yasiyasi A | 3.4% | 5.0% | 19.6% | 3 | 3 | 9 | 4 | 1 |
| Cleistocalyx eugenioides | Damanu | 5.1% | 5.0% | 24.6% | 4 | 4 | 5 | 3 | 3 |
| Parinari insularum | Gadoa | 1.9% | 4.3% | 28.8% | 5 | 5 | 2 | 5 | 10 |
| Dysoxylum richii | Kuluva | 1.5% | 2.9% | 31.7% | 6 | 8 | 3 | 7 | 6 |
| Agathis vitiensis | Midra | 0.6% | 2.8% | 34.5% | 7 | 6 | 20 | 9 | 2 |
| Gironniera celtidifolia | Laubu | 7.1% | 2.8% | 37.3% | 8 | 7 | 10 | 6 | 11 |
| Bischofia javanica | Kaunigai | 0.6% | 2.3% | 39.6% | 9 | 9 | 7 | 8 | 7 |
| Syzygium fijiense | Sa | 1.7% | 2.0% | 41.6% | 10 | 11 | 16 | 12 | 8 |
| Dillenia biflora | Yasidravu | 2.7% | 2.0% | 43.6% | 11 | 12 | 13 | 10 | 43 |
| Haplolobus floribundus | Tadalo | 2.0% | 1.8% | 45.4% | 12 | 13 | 21 | 13 | 12 |
| Garcinia myrtiflora | Kautoa | 2.3% | 1.8% | 47.2% | 13 | 10 | 28 | 14 | 9 |
| Gymnostoma vitiense | Sasawira | 1.1% | 1.8% | 49.0% | 14 | 19 | 8 | 11 | 87 |
| Canarium harveyi | Kauvula | 1.3% | 1.6% | 50.7% | 15 | 14 | 18 | 16 | 19 |
| Macaranga harveyana | Diriniu | 3.1% | 1.6% | 52.3% | 16 | 15 | 17 | 17 | 18 |
| Palaquium porphyreum | Во | 0.8% | 1.5% | 53.8% | 17 | 16 | 19 | 18 | 22 |
| Pommetia pinnata | Kaunicina A | 0.9% | 1.5% | 55.4% | 18 | 20 | 12 | 15 | 68 |
| Intsia bijuga | Moivi | 0.3% | 1.4% | 56.8% | 19 | 32 | 6 | 19 | 49 |
| Kingiodendron platycarpum | Sole | 1.3% | 1.4% | 58.1% | 20 | 24 | 15 | 20 | 38 |
| Other species (269 spp) | | 52.8% | 41.9% | 100.0% | | | | | |
| Total | | 100.0% | 100.0% | | | | | | |

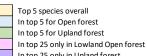
Table 3 : Overall most common species with abundance rankings by forest types

Table 4 shows the most abundant species in rank order, for lowland closed, lowland open and upland forest types. The distribution of clusters in these forest types are shown in the maps in Figure 9.

| Lowla | nd, Clo | sed (632 clusters) | Cum % | Lowla | nd, Open (271 clusters) | Cum % | Uplan | d (120 clusters) | Cum % |
|-------|---------|----------------------------|-------|-------|---------------------------|-------|-------|--------------------------|-------|
| Rank | Code | Species | BA | Code | Species | BA | Code | Species | BA |
| 1 | 137 | Myristica castaneifolia | 9% | 137 | Myristica castaneifolia | 10% | 65 | Calophyllum vitiense | 8% |
| 2 | 150 | Endospermum macrophyllum | 16% | 247 | Parinari insularum | 14% | 402 | Cleistocalyx eugenioides | 16% |
| 3 | 65 | Calophyllum vitiense | 21% | 150 | Endospermum macrophyllum | 18% | 59 | Agathis vitiensis | 23% |
| 4 | 402 | Cleistocalyx eugenioides | 26% | 257 | Dysoxylum richii | 21% | 150 | Endospermum macrophyllum | 28% |
| 5 | 247 | Parinari insularum | 31% | 402 | Cleistocalyx eugenioides | 25% | 137 | Myristica castaneifolia | 34% |
| 6 | 270 | Gironniera celtidifolia | 34% | 346 | Intsia bijuga | 28% | 257 | Dysoxylum richii | 37% |
| 7 | 59 | Agathis vitiensis | 37% | 345 | Gymnostoma vitiense | 31% | 394 | Syzygium fijiense | 40% |
| 8 | 257 | Dysoxylum richii | 39% | 158 | Bischofia javanica | 34% | 158 | Bischofia javanica | 43% |
| 9 | 162 | Dillenia biflora | 41% | 442 | Spathodea campanulata | 37% | 163 | Garcinia myrtiflora | 45% |
| 10 | 163 | Garcinia myrtiflora | 43% | 65 | Calophyllum vitiense | 39% | 247 | Parinari insularum | 47% |
| 11 | 158 | Bischofia javanica | 45% | 270 | Gironniera celtidifolia | 41% | 270 | Gironniera celtidifolia | 50% |
| 12 | 394 | Syzygium fijiense | 47% | 76 | Pommetia pinnata | 43% | 146 | Haplolobus floribundus | 52% |
| 13 | 146 | Haplolobus floribundus | 49% | 162 | Dillenia biflora | 45% | 61 | Hernandia olivacea | 53% |
| 14 | 143 | Canarium harveyi | 51% | 331 | Mimosaceae spp. | 47% | 159 | Podocarpus neriifolius | 55% |
| 15 | 209 | Gonystylus punctatus | 53% | 109 | Macaranga harveyana | 49% | 188 | Dysoxylum quercifolium | 57% |
| 16 | 20 | Palaquium porphyreum | 54% | 218 | Kingiodendron platycarpum | 51% | 274 | Schefflera seemanniana | 59% |
| 17 | 345 | Gymnostoma vitiense | 56% | 394 | Syzygium fijiense | 53% | 134 | Turrillia vitiensis | 60% |
| 18 | 109 | Macaranga harveyana | 57% | 143 | Canarium harveyi | 54% | 109 | Macaranga harveyana | 61% |
| 19 | 76 | Pommetia pinnata | 59% | 20 | Palaquium porphyreum | 56% | 143 | Canarium harveyi | 62% |
| 20 | 11 | Palaquium vitilevuense | 60% | 146 | Haplolobus floribundus | 58% | 148 | Dysoxylum hornei | 64% |
| 21 | 291 | Pagiantha thurstonii | 62% | 291 | Pagiantha thurstonii | 59% | 213 | Baccaurea seemannii | 65% |
| 22 | 248 | Palaquium hornei | 63% | 141 | Semecarpus vitiensis | 60% | 20 | Palaquium porphyreum | 66% |
| 23 | 244 | Heritiera ornithocephala | 65% | 59 | Agathis vitiensis | 61% | 209 | Gonystylus punctatus | 67% |
| 24 | 218 | Kingiodendron platycarpum | 66% | 103 | Xylopia pacifica | 63% | 201 | Storckiella vitiensis | 68% |
| 25 | 25 | Viticipremna vitilevuensis | 67% | 392 | Premna serratifolia | 64% | 80 | Cryptocarya constricta | 69% |
| | | Others (232 spp) | 100% | | Others (200 spp) | 100% | | Others (200 spp) | 100% |
| | | Total (257 spp) | | | Total (225 spp) | | | Total (177 spp) | |

Table 4: Top 25 species in lowland closed and open forest, and upland forest

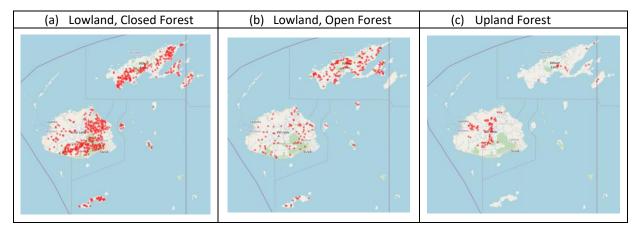
The most common species overall are *Myristica, Endospermum, Calophyllum, Cleistocalyx* and *Parinari*. These account for about 30% of basal area. In the Lowland Open forest and Upland forests, a number of characteristic species occur in the top 25 that are



In top 25 only in Upland forest Common to top 25 in all forest types

distinctive of these types. Overall, the top 25 species account for just over two-thirds (67%) of basal area, with the remaining 264 species contributing one-third. Although there are distinctive differences in speciation between the forest types, they are not large. Neither are there large structural differences, with all having basal areas around 27 m2/ha.





2.9. Forest areas

The FAO (2015) country report for Fiji includes tabulated figures from MoF internal reports¹. These are summarised in Table 5 below, together with the 2006 baseline areas from the FRL report (Mundhenk et al, 2019). MoF has used a classification based on open and closed forest for many years, with some adjustments. The FRL, on page 6 notes that these categories could not be reliably distinguished on the available satellite imagery and instead adopts the upland and lowland classes, based on the 600 m contour as a dividing line. The area total for the FRL is slightly different from the 2007 MoF/FAO figure, but the difference is small (<0.1%). For this study, the FRL figure is adopted as the 2006 total for reasons of consistency.

| FAO | 1991 | 2007 | 2010 | FRL | 2006 |
|--------|---------|---------|---------|---------|---------|
| Closed | 704,856 | 556,385 | 526,453 | Lowland | 670,300 |
| Open | 152,665 | 342,845 | 388,415 | Upland | 229,098 |
| Total | 857,521 | 899,230 | 914,868 | | 899,398 |

Table 6 shows the areas partitioned between open and closed forest types for each altitude class, using proportional adjustment to give totals consistent with the MoF 2007 figures, slightly adjusted so that the grand total adds to the FRL figure.

Table 6 : Estimated forest class areas in 2006

(hectares)

| | Closed | Open | Total |
|---------|---------|---------|---------|
| Lowland | 414,738 | 255,562 | 670,300 |
| Upland | 141,751 | 87,347 | 229,098 |
| Total | 556,489 | 342,909 | 899,398 |

These area estimates are used to give total figures in §2.10.

2.10. Total stocking and biomass by forest type

Table 7 shows the overall stocking (trees per hectare), above-ground biomass, and estimated wood volume, together with the 95% confidence intervals for the main forest types. These statistics do not show great variation between the forest types, and the biomass differences are not statistically

| Table 7 : Stand parameters by forest types, with area t | otals |
|---|-------|
|---|-------|

| | | | Sto | king (N/ł | na) | | Basal Area | Volume | AG Biomass | | Total AG |
|-----------------|-----------|------|-------|-----------|-----|-------|------------|--------|------------|-------|--------------|
| Forest Type | Area (ha) | 5-20 | 20-30 | 30-50 | 50+ | Total | m2/ha | m3/ha | t/ha | ±CI% | Biomass (Mt) |
| Closed, Lowland | 414,738 | 922 | 69 | 80 | 21 | 1092 | 28.86 | 267.50 | 149.30 | 4.00% | 61.92 |
| Open, Lowland | 255,562 | 837 | 62 | 65 | 20 | 985 | 26.15 | 244.49 | 138.28 | 6.20% | 35.34 |
| Upland | 229,098 | 842 | 63 | 70 | 17 | 992 | 26.02 | 238.90 | 129.63 | 8.70% | 29.70 |
| Total | 899,398 | 891 | 66 | 75 | 20 | 1052 | 27.82 | 258.13 | 144.12 | 2.70% | 129.62 |

¹ The FAO (2015) assessment includes both reported MoF figures and calibrated figures based on FAOSTAT land area. The calibrated figures have not been used, being some 7% higher and not consistent with the FRL or MoF data.

significant. As has been noted by Vesa (2018), the stratification between open and closed woodland does not show statistically significant differences, though the closed type is somewhat heaver stocked, and with a higher basal area and biomass, than the other two types. However, the types are distinct in terms of species composition, as has been noted in §2.9 (see Table 4).

The <u>Total</u> row of Table 7 is not the direct sum or average of the rows above, but are weighted¹ by the number of clusters for each sample type, also shown in the top row of Table 4. All the figures shown are taken directly from the FFIDE app, using the <u>Sample</u> bar to select closed/open forest and altitude range.

Basal area of natural forest is a useful indicator of forest condition. Values above 30 m^2 /ha are typical of undisturbed, mature moist tropical forest. Values below 30 show increasing levels of disturbance, but still with a mainly unbroken canopy down to about 25 m^2 /ha. Below this, down to about $17-18 \text{ m}^2$ /ha, the forest is still recognisably intact, but with numerous gaps. These are values which may typify well managed selection forest immediately after logging. Below 15-17 m²/ha, the forest is clearly degraded and damaged and in need of long-term protection if it is to recover. The indications from these figures are that the forests show some signs of disturbance, no doubt related to cyclones as well as the history of exploitation, and will show an accretion of biomass if strictly protected. It will be borne in mind that these data are from 2006, and do not reflect subsequent changes due to growth, cyclone damage or human impacts.

¹ To a close approximation. Weighting by cluster numbers for closed lowland, open lowland, and upland forest gives 632, 271 and 120 clusters (see Table 4), or weights of 0.618, 0.265, 0.117. Empirically, the weights are 0.615, 0.268, 0.118. The difference is due to the R Survey package used in the calculation, which also considers variations in the intra-cluster correlation coefficient and plot numbers. See also §2.3.1.

3. Conclusions

3.1. Headline findings

The 2006 national forest inventory established 1023 clusters, each nominally of 5 plots, randomly located in forests on the main islands of Fiji, being Viti Levu, Vanua Levu, Kadavu, Taveuni, Gau, Koro and Ovalau (Table 4, p 8). The plots comprised an outer circular plot of 400 m² on which trees of 20 cm and above dbh were measured, and an inner plot of 100 m² recording trees over 5 cm dbh. The plots were arranged in a cross-shaped cluster at the end of 40 m 'arms' (Figure 1, p 8). In all 5010 plots were assessed. The forest was stratified into 'open' and 'closed' classes, but in the end there was relatively little difference in stocking density between these classes (§2.10, p 21). A total of 899,398 ha of forest were surveyed.

The data was recorded in an Access database, but at the time of the inventory was not comprehensively written up, though the data has been processed and used for various reports subsequently, and was available internally for the MoF for planning and management purposes. Several published and unpublished reports have been based on the data, including DoE (2010), Leslie & Tuinivanua (2010), Weaver & Payton (2011), FAO (2015), Vesa (2018) and Mundhenk et al (2019). The latter comprises the Forest Reference Level (FRL) scenario for Fiji's REDD+ programme.

The data has been reviewed and to the extent possible, cross-checked for validity. Stand structure and diameter class distributions appear as expected for moist tropical forest, although there appears to be some excess in the number of the largest trees, which may reflect uncorrected coding errors. There are however no obvious gross outliers, and the diameter data used in this report has not been filtered in any way.

However, the situation with respect to height measurements is more doubtful, and is reviewed in detail in §2.5 and summarised in Figure 3. Recorded tree heights are in many cases evidently too low, there is clear evidence of digit heaping around 15,20, 25, 30 m, and in general all indications are of a mixture of measurements that may be crown break heights or ocular estimates. Mundhenk et al (2019) were to some extent aware that these height measurements were abnormally low, but nonetheless elected to use them in calculating the FRL biomass values for REDD+. Because this is now an accepted official document, the consultant has likewise used the same biomass estimation method for this report. Nonetheless, an alternative is presented in equation {4}, using Chave et al (2014) bioclimatic, height-independent equation. §2.5 discusses this, and the FFIDE app can be quickly adapted to recalculate all biomass values using this equation.

The data was analysed using the R statistical system. The key data sets, comprising the tree measurements, plot and cluster details, and maps of plot locations, have been bundled into a single directory called FFIDE, available as a zip file from https://bio-met.co.uk/proj/fiji/FFIDE.zip. The R survey package was used to analyse the data as a single-stage cluster design. An application (app) was written using R shiny to surface various aspects of the data, also called FFIDE, an acronym for Fiji Forest Inventory Data Explorer. This app is listed in an Annex to the report and explained in §2.7. It allows subsets of the data to be selected by combinations of forest class (open, closed), altitude range, island, province or district. The sample statistics for the subset (mean, standard error, confidence interval, intra-cluster correlation coefficient [ICC]">survey distribution of plot values is shown as a histogram, and a box plot allows the data distribution to be partitioned by forest type, altitude class, island, province or district. Full stand tables of species by size class are shown for any selected

variable (stocking, biomass, volume, basal area), with cumulative size class distribution. The stand table can also be searched, sorted or sub-setted by species.

FFIDE is accessible online without requiring any installation, use or knowledge of R, at the address <u>ffide.shinyapps.io/ffide</u>. The online version does not allow any access to the raw data or program code.

Using FFIDE, the species distributions by forest types are reviewed. It is noted that there are several major species common to and dominant in all forest types, but also some distinctive species characteristic of the open and upland (over 600 m) forests. These are discussed in §2.8, which in Table 4 lists the top 25 most common species in each of the forest types. The most common species overall are *Myristica, Endospermum, Calophyllum, Cleistocalyx* and *Parinari*. These account for about 30% of basal area, or equivalently, volume or biomass. Overall, 289 species are recognised, but species abundance follows a typical Pareto-type distribution, with a few species accounting for a greater part of the stock, and many being rare. FFIDE shows a species abundance curve as one of its outputs, and by using selection and filtering criteria, this can be used to focus on particular aspects of the dataset, as may be required for example to support particular conservation policies or programmes.

Forest areas are derived from published official sources, reviewed and summarised in §2.9. It is noted that official and, by derivation, FAO reports have used the Open-Closed forest classification, whilst the FRL uses Upland and Lowland classes. Table 6 estimates the cross-classification of these types. Overall in 2006 there were 899,398 ha of natural forest, of which 670,300 ha were lowland (below 600 m altitude) and 229,098 ha upland forest. The lowland forest is subdivided into 414,738 ha of closed forest type, and 255,562 ha of open forest. It is emphasised that these are all 2006 figures, and not current ones.

In section §2.10 and Table 7, overall mean and total parameters, with confidence interval are given for these forest classes (lowland closed and open forest, upland forest). It is found that the structural differences in terms of diameter distribution, volume, basal area and biomass are not large enough to be statistically significant, although the lowland closed forest has the highest stocking by a small margin. Biomass per ha in 2006 was 144.12 t/ha ±2.7% overall, with a total stock for natural forest of 129.62 million tonnes (Mt). The basal area of 27.82 m2/ha is indicative of closed, well stocked but somewhat disturbed forest, as may be expected from Fiji's cyclone-prone climate as well as the history of forest use.

3.2. Recommendations

Recommendations arising from this analysis which are of relevance to current and future work are the following:

- <u>Height measurement</u>: Total height measurements need to be made rigorously on a sub-sample of about 300 trees to validate the height-diameter curve for Fiji's natural forest. This should be undertaken by a specialist allometric research crew using modern laser instruments (see right), and carefully differentiate buttress, crown point and total height.
- <u>Data analysis</u> should be properly costed, allowed for and be conducted in parallel with field operations, to allow for data checking and re-measurement whilst

Figure 10 : A laser hypsometer



field teams are still active and corrections to data outliers can be made. Typically, a forest biometrician should be assigned for the duration of the forest inventory and for at least 6-months thereafter.

- <u>Imagery analysis</u> and interpretation should likewise be conducted at the same time as field work and closely integrated with it, to effectively ground truth the analysis and efficiently stratify field work in order to minimize effort. High resolution (10 m) Sentinel C-band SAR, optical and NIR imagery is these days freely available via the <u>Copernicus portal</u>.
- <u>Data checking</u> should be ongoing during the field work, looking for outlying or atypical observations, and also abnormal diameter distributions or digit heaping (abnormal high or low frequencies for some figures), the latter being indicative of poor training, damaged instruments, or fabrication of data. Where errors are found, they should be corrected by remeasurement of plots.
- <u>Use of coded notes</u>: All trees should have coded 2-letter notes recorded for trees form, quality of diameter measurement, and health status. Coded notes can be more reliably processed than free text, which often embody variable spelling and language that makes computer analysis very difficult. Examples of suitable coded notes are given on page 87 of <u>Alder & Synnott (1992)</u>.
- <u>Tablet data collection</u>: The use of tablets instead of paper forms, combined with a welldesigned form using the <u>XLSForm</u> design software or a similar system, speeds up data collection, improves accuracy of field work, and can provide pre-selected lists for species and coded notes and is highly recommended.

None of the above recommendations are 'high-budget' items, and should be considered routine in any modern inventory. More exotic ideas, such as the use of LIDAR surveys, would certainly add accuracy, but are high cost items which may not be feasible. Satellite L-Band SAR imagery analysis would likewise add accuracy to biomass estimation, but generally requires specialist contractors for its analysis. High resolution hyperspectral satellite imagery likewise can give very detailed information but is costly to purchase and involves very large datasets that require specialist software and skills that may not be easily available.

3.3. General conclusions

This report is the first part of a 2-part series covering the analysis of Fiji's 2006 National Forest Inventory. The second part will cover the analysis and results from permanent sample plots in Fiji's natural forest measured between 2010 and 2018.

Denis Alder (Dr.) Oxford, 21 October 2020 post@denisalder.com

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Annex A : Consultant's Terms of Reference

The following paragraphs are extracted verbatim from the Consultant's contract for this assignment.

Objectives

The objective of this assignment is to analyse the NFI 2006 and PSP measurement data (2010, 2012, 2014, 2016, and 2018); and to prepare reports with the analysis of NFI and PSP data reflecting the status of Fiji forest resources.

Methodology

Standard Operating Procedures exist for both NFI and PSP measurements. The Consultant is expected to review the documents related to NFI and PSP prior to conducting analysis of NFI and PSP measurement data. The Consultant is expected to use open source software for conducting statistical analysis of the data.

Scope of work and main responsibilities

The Consultant will analyse the NFI and PSP data, and prepare reports. The Consultant work program will include the following tasks.

Task 1. Analysis of data

The Consultant will liaise with the REDD+ Unit and the Ministry of Forestry (MoF) to get access to the data. The Consultant should share the data analysis to REDD+ Unit and the Ministry of Forestry to validate the analysis before writing the reports. Checks on data quality needs to performed to detect and correct errors in data. The statistical analysis of data should cover plot and stratum level descriptive statistics of the inventory, diameter- height relationships, basal area, growing stock, increment, site index and other relevant inventory metrics

Task 2. Result report

The consultant is expected to prepare - Report on the NFI and PSP measurements.

(i) NFI 2006 Data Analysis Report

The reports should contain annexes which explain the software used, scripts used to analyze the data, and equations used to estimate volume and biomass. A detailed description of the methods and estimation procedures should be presented to ensure replication of the results of analysis. The consultant is expected to use open source statistical software as far as possible for the data analysis. The report or analysis should include maps, graphs, tables, and other illustrations to communicate the results of analysis in an effective way and to support the analysis.

The NFI report should include the following analysis;

- Historical background of Fiji's forest
- Description of the previous National Forest Inventories or assessments
- Description of sampling approach, sample frame and sample plot designs of NFI2006
- Description of method used for NFI data collection and sampling design of the NF
- Tree count by diameter classes, merchantable height classes, and tree species
- Forest attributes such as forest cover, basal area, volume, tree counts by strata District, Province, and Division

- Volume and biomass of upland and lowland forests differentiated with data from using Digital Elevation Model (DEM) as well as distinguishing the closed and open forests based on basal area/canopy cover measures.
- The growing stock in terms of volume and biomass should be presented with uncertainty estimates.
- Volume by diameter class, by merchantable height class, and by major tree species
- Gaps in the design and implementation of 2006 NFI recommendations for improving the design of future National Forest Inventory and data collection.

The Consultant can consult the NFI 2006 team which is still working under the Ministry of Forestry for greater details if documented information related to NFI is not sufficiently available.

(ii) PSP Data Analysis Report

The PSP report should cover at least the following aspects;

- Background to the PSP Program
- Features of PSP measurements campaigns (2010, 2012, 2014, 2016, 2018) common and consistent features of PSP measurement campaigns
- Description of sampling approach, sample frame and sample plot designs of PSP
- Data collected and methods used for data collection on PSP at measurement campaigns
- Descriptive statistics of sample plot measurement attributes
- Diameter-height relationships by tree species
- Volume and biomass increments measured at each measurement campaigns
- Gaps in the PSP sample plots framework and gaps in the data of measurement campaigns
- Recommendation to improve the design of PSPs
- Scope for integrating PSP sample frame with the REDD+ requirement

(iii) Capacity building of government Staff and other Stakeholders

The Consultant will visit Suva and conduct a training to the Client's staff and other REDD+ relevant stakeholder on NFI and PSP data analysis and result. This will enable the Client's staff to produce similar kind of report in the future. The period of training will be a maximum of 5 days. The Ministry of Forestry will bear the cost of the training.

Deliverables

- Analysis and report on the National Forestry Inventory 2006. The report should be well referenced.
- Analysis and report on the Permanent Sample Plot Measurement. The report should be well referenced.
- Dataset of 2006 NFI used for statistical analysis.
- Datasets of PSP measurement 2010, 22012, 2014, 2016, and 2018 used for statistical analysis.

Reporting arrangements

The Consultant will report to Fiji REDD+ Unit and address it to Ilai Tulele (tulele.ilai@live.com) REDD+ Program Leader, Dr. Narendra Chand (narendrachand@gmail.com), and Mr. Viliame Tupua (vtupua@gmail.com).

Annex B : R code and data table definitions

1. Inventory cluster, plot and tree data formats

The tree, cluster and plot data tables were imported from the Excel file supplied to the consultant as three tables. The structure for <u>trees</u> is as shown below. The listing shows only the first 10 lines of data.

| τre | es | | | | | | | | | | | |
|-----|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|--|
| # A | tibbl | e: 76, | ,968 x | 11 | | | | | | | | |
| | | clid | | | ppos | spp | wd | dbh | pht | agb | nha | |
| | <int></int> | <int></int> | <chr></chr> | <chr></chr> | <chr></chr> | <int></int> | <db1></db1> | <db1></db1> | <db1></db1> | <db1></db1> | <int></int> | |
| 1 | 68 | 11 | 4 | r3 | W | 218 | 0.49 | 54.2 | 16.8 | 1.27 | 25 | |
| 2 | 95 | 11 | 4 | r3 | N | 244 | 0.68 | 48.3 | 16.2 | 1.35 | 25 | |
| 3 | 120 | 11 | 4 | r3 | N | 146 | 0.71 | 42.1 | 15.4 | 1.03 | 25 | |
| 4 | 57 | 11 | 4 | r3 | W | 150 | 0.4 | 40.5 | 15.2 | 0.538 | 25 | |
| 5 | 26 | 11 | 4 | r3 | S | 162 | 0.616 | 34.3 | 14.3 | 0.559 | 25 | |
| 6 | 125 | 11 | 4 | r3 | E | 247 | 0.713 | 32.2 | 14.0 | 0.556 | 25 | |
| 7 | 54 | 11 | 4 | r3 | W | 146 | 0.71 | 32 | 13.9 | 0.546 | 25 | |
| 8 | 86 | 11 | 4 | r3 | С | 183 | 0.324 | 31.5 | 13.8 | 0.245 | 25 25 | |
| 9 | 136 | 11 | 4 | r3 | Ň | 247 | 0.713 | 30.8 | 13.7 | 0.502 | 25 | |
| 10 | 90 | 11 | 4 | r3 | С | 183 | 0.324 | 30.5 | 13.7 | 0.227 | 25 | |
| # . | wit | h 76.9 | | re row: | S | | | | | | | |

The column names are as follows:

+ = = = = =

clusters

| id A unique tree identification number | |
|---|---|
| d Unique cluster identification number | |
| no An alternative cluster number in the original data, retained for checkin | g |
| er r3 is the main plot, r2 the subplot. See section 2.1. | |
| pos Plot position in the cluster, E, S, N, W or C. See section 2.1. | |
| p Species code of the tree. See <u>species</u> table (section B.2). | |
| d Wood density (t/m³) | |
| ph Tree dbh in cm. | |
| nt Calculated tree height. See section 2.x for discussion. | |
| b Estimated above ground biomass, tonnes, using pht as tree height. | |
| na Equivalent number of trees per ha to one tree sampled on the plot. | |

The cluster information is stored in the table <u>clusters</u>:

| # A tibble: 1,023 x 10 | | | | | | | | | | | | | |
|------------------------|-------------|-------------|--|--------|-------------|-------------|-------------|------|---------|-------------|---------|--|--|
| | clid | c1no | islaı | nd | province | district | ftype | altm | altcl | xcoord | ycoord | | |
| | <int></int> | <int></int> | <chr.< th=""><th>></th><th><chr></chr></th><th><chr></chr></th><th><fct></fct></th><th></th><th></th><th><int></int></th><th></th><th></th></chr.<> | > | <chr></chr> | <chr></chr> | <fct></fct> | | | <int></int> | | | |
| 1 | 11 | | | | | Veivatuloa | | | | 1943000 | | | |
| 2 | 16 | 2 | Viti | Levu | Namosi | Veivatuloa | Hardwood | 110 | Lowland | 1936000 | 3871000 | | |
| 3 | 21 | 77 | Viti | Levu | Serua | Nuku | Open | 237 | Lowland | 1922995 | 3865999 | | |
| 4 | 28 | | | | Namosi | Veivatuloa | Closed | | | 1946000 | | | |
| 5 | 59 | 78 | Viti | Levu | Serua | Nuku | Open | 150 | Lowland | 1925000 | 3868004 | | |
| 6 | 65 | 76 | Viti | Levu | Serua | Nuku | Open | 170 | Lowland | 1919004 | 3865010 | | |
| 7 | 74 | | | | Namosi | Veivatuloa | Hardwood | 137 | Lowland | 1938000 | 3873000 | | |
| 5 6 7 8 9 | 77 | 3 | Viti | Levu | Namosi | Veivatuloa | Closed | 21 | Lowland | 1941000 | 3873000 | | |
| 9 | 84 | | | | Serua | Nuku | Pine | 231 | Lowland | 1916000 | 3864000 | | |
| 10 | 95 | | | | Namosi | Veivatuloa | Open | 29 | Lowland | 1947000 | 3870999 | | |
| # . | wit | h 1,01 | 13 moi | re rov | vs | | | | | | | | |

Here clid and clno are as above, island, province and district are self-explanatory, ftype and altcl are forest type and altitude classes, altm is altitude in m, and xcoord and ycoord are coordinates in metres on the Fiji map grid¹.

Plot level data was not imported, but can be inferred from the <u>trees</u> table to give plot count per cluster, which is the only important information required at the plot level. The following R code creates <u>plotlist</u>, <u>clus_pno</u>, and tabulates the count of clusters according to the number of plots they contain. <u>plotlist</u> is a list of plots identified by cluster number and plot position (<u>ppos</u>) letter, <u>clus_pno</u> gives the number of plots in each cluster.

¹ EPSG:3460 - Fiji 1986 / Fiji Map Grid - Projected

```
# make list of cluster and plot ids
plotlist <- unique(trees %>% transmute(clid, plotid=paste(clid,ppos,sep='')))
# plot counts for each cluster
clus_pno <- unique(plotlist %>% group_by(clid) %>% summarise(clid, pno=n()))
# plot numbers tabulated by cluster size (1-5), sent to clipboard
table(as.factor(clus_pno$pno)) %>% write.table(., 'clipboard', sep='\t')
```

2. The species list

chaciac

The species list was imported from the PSP data files, and is stored in table <u>species</u>, with the following appearance:

The column <u>spp</u> is the unique species code, matching the same column in the trees table. <u>botname</u> is the scientific name, <u>locname</u> the local name, <u>family</u> is the botanical family, habit is either palm or tree, <u>spcode</u> is another inherited coding system in use in some data files, but not generally used here, and <u>rgrp</u> is the royalty group, with higher numbers being generally more valuable timber trees.

3. FFIDE Shiny app

The following is the code listing of the Shiny app. See main text for a discussion of the various functions and processes. The app code can be downloaded from:

https://bio-met.co.uk/proj/fiji/FFIDE.zip

The Zip folder should be extracted to a sub-directory of an R-Studio working folder. Then, with that working folder as the current directory, the command <u>runApp('FFIDE')</u> will open the Shiny app. The Shiny app can also be used without any installation or download via:

https://ffide.shinyapps.io/ffide/

Code listing

```
# FFIDE - Fiji Forest Inventory Data Explorer
# Provides various analyses and views of Fiji NFI 2006 data
require(shiny) # basic for Shiny app
require(magrittr) # for reverse pipe operator %<>%
require(tidyverse) # for data manipulation with dplyr, ggplot etc
require(leaflet) # for GIS outputs
require(sf) # various GIS functions
require(DT) # data table output functions
require(survey) # complex survey design and calculation
# load as global variables inventory data sets: trees, clusters, species, plots
load('NFI.RData')
# ------ processing functions -------
includeClusters <- function(clusters, island, forestType, altitude, province, district){</pre>
```

17

```
# gets a list of selected cluster IDs that satisfy the various filters
     # Note names with initial capital are column names in Clusters, lower case parameter
# equivalents contain text values to be matched. Blank test values ('') are ignored.
     # set values that could be NULL to blank to avoid errors later
     if(is.null(province)){province <- ''}
if(is.null(district)){district <- ''}</pre>
     # start logic chain with all clusters
selclus <- clusters</pre>
     # filter for altitude
selclus %<>% filter(Altitude >= altitude[1] & Altitude <= altitude[2])</pre>
     # filter for island if applicable
     if(!island==''){selclus %<>% filter(Island == island)}
     # filter for forest type if applicable
     if(!forestType==''){selclus %<>% filter(ForestType == forestType)}
     # filter for province if applicable
     if(!province==''){selclus %<>% filter(Province == province)}
       filter for district if applicable
     if(!district==''){selclus %<>% filter(District == district)}
     return(selclus)
}
includeTrees <- function(trees, clset){</pre>
     # returns 'trees' filtered by current clusters
clset %>% transmute(clid) %>% inner_join(trees, by='clid') -> trset
     return(trset)
}
includePoints <- function(cluster_points, selected_clusters){</pre>
     # returns a sub-set of cluster_points where the cluster ID matches the 'clno'
     # field in selected_clusters
     v <- cluster_points$Id %in% selected_clusters$clno</pre>
     return(cluster_points[v,])
}
filterTable<- function(clusin, island, forestType, altitude, province, district){</pre>
     # returns a table describing filters in use and total clusters and plots
if(is.null(province)){province <- ''}
if(is.null(district)){district <- ''}</pre>
     # get number of plots and clusters
     ns <- as.character(sampleCount(clusin))</pre>
     # create table with cluster and plot counts
     tb <- data.frame(item=c('Clusters', 'Plots'), value=c(ns[1], ns[2]), stringsAsFactors=F)</pre>
     # add text for other filters in use to bottom of table
     #browser()
     if(!forestType==''){tb %<>% add_row(item="Forest Type", value=forestType)}
     # filter for altitude
    if(altitude[1]>0 || altitude[2]<2000){tb %<>% add_row(item="Altitude Range",
            value=paste0(altitude[1],"-",altitude[2]))}
if(!island==''){tb %<>% add_row(item="Island", value=island)}
if(!province==''){tb %<>% add_row(item="Province", value=province)}
     if(!province==''){tb %<>% add_row(item="Province", value=province)}
if(!district==''){tb %<>% add_row(item="District", value=district)}
     #print(paste(forestType, forestType==''))
     #print(tbl)
     return(tb)
}
correct_points <- function(sfc_obj){</pre>
     # corrects for anitimeridian artefacts by adding 360 deg to points with longitude < -150 deg
     # for SFC objects with POINT topology only. Returns adjusted SFC object.
     # loop through points
     for (i in 1:length(sfc_obj$geom)){
    # test if i'th point longitude (coord[1]) is less than -150
          if(sfc_obj$geom[[(i)]][1]<(-150)){
# if so, add 360 to it
               sfc_obj$geom[[(i)]][1] <- sfc_obj$geom[[(i)]][1]+360</pre>
         }
     # return adjusted object
     return(sfc_obj)
}
standTable <- function(treesf, varnum=1, namefmt=1, dctxt="5,10,20,30,50,70,90,110,150"){</pre>
     # forms a stand table of species by diameter classes for a variable.
                                                                                             Parameters are:
         trees - table of tree data, filtered as necessary - all data will be included in the table
     #
         varnum - variable to be calculated (1=N/ha, 2=AGB, 3=Vol/ha, 4=BA/ha)
     #
         namefint - species name format (1=short, 2 = full, 3=local name)
dctxt - diameter class lower bounds as a comma separated list
    #
     # convert diameter class list to a vector
     dc = as.double(strsplit(dctxt, ',')[[1]])
     # join trees table with appropriate species name data as treesn
nameField <- c('genspp','botname','locname')</pre>
     # count unique plots
     np <- with(treesf, length(unique(paste(clid,ppos))))</pre>
     # create subset table tt with required columns. Slightly different if colsum is 1 or a variable name.
```

19 20 21

22 23

24 25

26 27 28

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31 32

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34 35

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80 81 82

83

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86 87

88

89 90

91

92

93

94 95 96

97

98 99 100

101

```
103
                 tt <- treesf %>% transmute(spp=as.factor(spp),
104
                                             dbh, nha, dc=map_chr(dbh, get_dclass, dc), v=treevar(., varnum))
                 # convert into basic stand table with sums by species and diameter classes
105
106
                 st <- tt %>% group_by(spp, dc) %>% summarise(tot=sum(v)/np) %>% spread(dc, tot, fill=0)
                 # get sums for each row
107
108
                 L <- length(st[1,])
                 st$total <- apply(st[,2:L], 1, sum)
# returns a vector of diameter class labels in same order as entries in dclasses</pre>
109
110
111
                 cl <- unlist(map(dc, get_dclass, dc))</pre>
                 # add species name, choice of 3 possibilities according to namefmt param
112
                 a <- nameField[as.numeric(namefmt)]</pre>
113
                 splist <- species[,c('spp', a)]</pre>
114
115
                 # rename species column to a standard name (also used as column heading)
                 names(splist)[2] <- 'spname'</pre>
116
117
                 # convert spp code to a factor for compatibility with st table
118
                 splist %<>% mutate(spp=as.factor(spp))
119
                 # merge the species names into the st table
                 st %<>% inner_join(splist, by='spp')
120
121
                 # add any empty columns to st
122
                 missing_cols <- setdiff(cl, names(st))</pre>
123
                 empty_cols <- as_tibble(matrix(0,length(st[,1]), length(missing_cols)))</pre>
124
                 names(empty_cols) <- missing_cols</pre>
125
                 st %<>% add_column(empty_cols)
                 # get columns in correct order: code, species, ascending diameter classes, total
126
                st <- st[,c('spp', 'spname', cl, 'total')]
# sort into order</pre>
127
128
129
                 st %<>% arrange(desc(total))
130
                 # last column number for decimal formatting, total rows in table
131
                 m <- length(dc)+3</pre>
132
                 n <- as.numeric(count(ungroup(st)))</pre>
                 # convert st to a DT datatable and set some options and formats
133
134
                 st <- DT::datatable({st}, extensions='Buttons', options=list(</pre>
135
                              searching=T,
136
                              paging=T,
137
                              ordering = T,
                              pageLength = 10,
lengthMenu = c(10,25,50,100,n),
138
139
140
                              dom='Blfrtip',
141
                              buttons=c('copy', 'excel'))) %>% formatRound(3:m, 3)
142
                 return(st)
143
            }
144
            totStandTable <- function(stMain=NULL, stRows=NULL){</pre>
145
                 # forms a bottom row totals of stand table by diameter classes for a variable. Parameters are:
146
147
                 # stMain - dataTable object from main stand tables
148
                     stRows - visible rows in the main table
                 #
149
150
                # species count in visible table
                 nv <- length(stRows)</pre>
151
152
                 # column count
153
                m <- length(stMain$x$data[1,])</pre>
                 # save full table (dft) and visible rows (dfv) as dataframes, convert characters to numbers
154
                 dft <- stMain$x$data %>% summarise(across(4:m, as.numeric, names='{.cols}'))
155
                 dfv <- stMain$x$data[stRows,] %>% summarise(across(4:m, as.numeric, names='{.cols}'))
156
                 # adjust column count for lost columns
157
158
                 m <- m-3
159
                 # column sums for whole table (trt) and visible rows (trv)
160
                 trt <- colSums(dft)</pre>
161
                 trv <- colSums(dfv)</pre>
162
                 # convert them to tibbles
163
                trt <- as_tibble_row(trt)
trv <- as tibble row(trv)</pre>
164
165
                 # row count, whole table
                 nt <- length(dft[,1])</pre>
166
167
                 # labels for each table row
                 txtt <- paste0('Sample total (',nt,' spp.)')
txtv <- paste0('Table total (',nv,' spp.)')</pre>
168
169
                 # add the labels to the table
170
                 trt %<>% mutate(item=txtt)
171
172
                 trv %<>% mutate(item=txtv)
173
                 # bind the two rows into one table
174
                 tt <- rbind(trv, trt)</pre>
175
                 # reorder columns so label is first column
                 tt <- tt[,c(names(tt)[m+1], names(tt)[1:m])]</pre>
176
177
                 # convert to a DT datatable and set some options and formats
                 dt <- DT::datatable({tt}, extensions='Buttons', options=list(</pre>
178
179
                     dom='Bt'.
180
                     buttons=c('copy', 'excel'))) %>% formatRound(columns=c(names(tt)[2:m], 'total'), digits=2)
181
                 return(dt)
182
            }
183
184
            plotTotStandTable <- function(nvar, dt){</pre>
185
                 # creates a histogram of the totals table, and returns it as plot object
186
                 # v-axis label
187
                 ylbl <- var.name(nvar)</pre>
```

```
188
                # vectors for Table (Visible) and sample (Total) data extracted from DT object
189
                df <- dt$x$data
                                            # DT object data extracted as dataframe
                                            # number of columns
190
                m <- length(df[1,])</pre>
191
                mc <- 3:(m-1)
                                            # subset of columns omitting first and last
                xlbl <- names(df)[mc]</pre>
                                            # diameter class labels for x-axis
192
193
                xs <- as.numeric(df[2,mc]) # sample data (all selected data)
xv <- as.numeric(df[1,mc]) # table data (visible stand table)
ymax <- max(xs) # largest value for y axis, to position legend</pre>
194
195
                196
197
                lbls <- as.character(df$item[2]) # label for 'sample' data</pre>
198
                # create a dataframe oganised for a simple ggplot histogram
199
                # d<-< data.frame(dbh.class=xlbl, table.data=xv, sample.data=xs) # histogram data, in columns
# make sure dbh.class labels are assigned factor levels in their natural order</pre>
200
201
                hd$dbh.class <- factor(hd$dbh.class, levels=hd$dbh.class)
203
                # base plot
204
                fig <- ggplot(data=hd)</pre>
                # bars for visible table, in light blue
205
206
                fig <- fig + geom_col(mapping=aes(x=dbh.class, y=table.data),</pre>
207
                                  colour='azure4', fill='azure2'
208
                                  width=0.4, position=position_nudge(x=-0.2))
                # bars for whole sample, in plum color
209
                210
211
212
213
                # axis labels
214
                fig <- fig + ylab(ylbl)+ xlab('Diameter classes (cm)')</pre>
215
                # legend
                216
217
218
                                     box.size=c(0.05, 0.05), pad=c(0.01, 0.01), text.size=2)
219
                return(fig)
220
            }
221
222
            draw.legend <- function(fig, colors, lines, labels, limits, legend.pos, box.size, pad, text.size){</pre>
                # draws a legend on a histogram/bar plot. Parameters as follows:
                # fig

    a ggplot object on which legend is to be drawn
    vector of color names. No. elements is no of legend items.

224
225
                # colors
226
                # lines
                             - outline colour of boxes (colour names)

    label for each legend entry, should have same dimension as colors.
    vector (x,y) of maximum x and y axes. Categoric x axis max is no. categories + 1

227
                # labels
228
                # limits
                # legend.pos- legend lower left position as (x,y) vector in relative coordinates (0-1)
229
                # box.size - size of color box, as (x,y) vector, in relative coordinates
# pad - padding as (x,y) vector, x is between box and text, y is between lines
230
231
                # text.size - text size, in annotate units
232
233
                #---
                                          _ _ _ _ _ _ _ _ _
234
                nc <- length(colors)</pre>
                                                  # no categories, = no legend entries
                                                 # legend low left position in plot coordinates
                Lpos <- limits * legend.pos
Lbox <- limits * box.size
235
236
                                                 # box size in plot coordinates
                Lpad <- limits * pad
237
                                                  # x and y padding in plot coordinates
238
                for(i in 1:nc){
239
                     # add legend symbol (a coloured rectangle)
                     240
241
242
                     # add legend text
243
                     fig <- fig + annotate("text", x=Lpos[1]+Lbox[1]+Lpad[1], y=Lpos[2]+Lbox[2]/2,</pre>
244
                                            label=labels[i], hjust='left')
245
                     # adjust y coordinate for start of next item
246
                     Lpos[2] <- Lpos[2] + Lbox[2] + Lpad[2]</pre>
247
248
                # return annotated ggplot object
249
                return(fig)
250
            }
251
252
253
            cumTotalTable <- function(dctxt, stMain, stRows){</pre>
                # forms a table with rows as diamter class lower bounds, and two columns for (a)
254
                # displayed stand table, and (b) sample total showing values above those limits,
                # both converted to % of sample total
256
257
                    dctxt - diameter classes as comma separated list
                #
                    stMain - dataTable object from main stand tables
258
                #
259
                    stRows - visible rows in the main table
                #
260
                #_.
261
                # species count in visible table
262
                nv <- length(stRows)</pre>
263
                # column count
264
                m <- length(stMain$x$data[1,])</pre>
265
                # save full table (dft) and visible rows (dfv) as dataframes, convert characters to numbers
266
                dft <- stMain$x$data %>% summarise(across(4:m, as.numeric, names='{.cols}'))
                dfv <- stMain$x$data[stRows,] %>% summarise(across(4:m, as.numeric, names='{.cols}'))
                # adjust column count for lost columns
268
269
                m <- m-3
270
                # column sums for whole table (trt) and visible rows (trv)
271
                trt <- colSums(dft)</pre>
272
                trv <- colSums(dfv)</pre>
```

255

```
273
                  # convert them to tibbles
274
                  trt <- as_tibble_row(trt)</pre>
275
                  trv <- as_tibble_row(trv)</pre>
276
                  # bind the two rows into one table
277
                  tt <- rbind(trv, trt)</pre>
278
                  # transpose result
                  tt <- t(tt)
279
280
                  # get grand total from last cell
281
                  gt <- tt[length(tt[,1]), 2]</pre>
282
                  # convert values to percentages
283
                  tt <- tt/gt*100
                  # drop last row of table (totals)
284
                  tt <- tt[-m,]</pre>
285
286
                  # convert percentages to cumulative sums rounded to 1 dp
287
                  tt[,1] <- accumulate_right(tt[,1], sum)</pre>
                  tt[,2] <- accumulate_right(tt[,2], sum)</pre>
288
                  # change the row labels to 5+, 10+ etc
289
                  lbl = as.character(strsplit(dctxt, ',')[[1]])
lbl <- paste0(lbl,'+')</pre>
290
291
292
                  #browser()
293
                  rownames(tt) <- lbl</pre>
                  # convert result to a dataframe
294
295
                  df <- data.frame(tt)</pre>
                 # rename columns as printable hadings
# - row count, whole stand table (equivalent to number of species)
296
297
                  nt <- length(dft[,1])</pre>
298
                  # - labels for each table column
299
                  txtt <- paste0('Sample (',nt,' sp.)')
txtv <- paste0('Table (',nv,' sp.)')</pre>
300
301
302
                  names(df) <- c(txtv, txtt)</pre>
303
                  return(df)
304
             }
305
306
             abundancePlot <- function(stMain, stRows){</pre>
307
                  # returns plot of species abundance - bar chart of species qty as % of total
308
                  # parameters are:
309
                 # nvar - variable number 1-4: stocking, biomass etc.
# stMain - main stand table, as DT object
310
311
                  # stRows - rows in main table appearing in visible table : used in chart
312
313
                  # extract visible rows species names and totals
                  df <- stMain$x$data[stRows,c('spname', 'total')]</pre>
314
                  # get total from main table
315
                  gt <- sum(stMain$x$data[,'total'])</pre>
316
317
                  dfp <- df %>% mutate(percent=round(total/gt*100,2))
                 318
319
320
321
                  return(fig)
322
323
             }
324
325
             var.name = function(nvar){
                  # given a variable number, returns name
326
                  # nvar - variable no. for caption (1=N/ha, 2=AGB, 3=Vol/ha, 4=BA/ha)
327
328
                  nm <- switch(as.numeric(nvar),</pre>
                                                      "Stocking (n/ha)",
329
                                    "Above-ground Biomass (t/ha)",
                                    "Total volume (m3/ha)",
330
                                   "Basal Area (m2/ha)")
331
332
             }
333
             get_dclass <- function (diam, dclasses){
    # finds diameter class of 'diam' from list of lower bounds in dclasses</pre>
334
335
                  # returns class label, eg 20-30, 70+ or NA if below lower bound
336
337
338
                  # get values above and below diam
                  b <- which(dclasses>diam)[1]
339
340
                  a <- which(dclasses<=diam)</pre>
341
                  a <- a[length(a)]
342
                  # test for end conditions (too big, too small) and construct labels
                 if(is.na(b)){ # bigger than top class
    label <- paste(dclasses[a], "+", sep='')</pre>
343
344
                  }else if(length(a)==0){ #small than bottom class
345
346
                      label <- NA
                  }else{ # normal situation, d in interval a-b (d>=a, d<b)
label <- paste(dclasses[a], "-", dclasses[b], sep='')</pre>
347
348
349
                  }
350
                  return(label)
351
             }
352
353
             dc_check <- function(dctxt, no_msg=FALSE){</pre>
354
                  # check diameter classes are in ascending order and returns true or false
                 # convert diameter class list to a vector
dc = as.double(strsplit(dctxt, ',')[[1]])
ok <- FALSE  # error flag, flipped to TRUE on normal completion</pre>
355
356
357
```

```
trv({
         inseq = TRUE
         for(i in 1:(length(dc)-1)){
             if(dc[i]>=dc[i+1]){
                  inseq <- FALSE
                  break
             }
         }
         ok <- TRUE
    }, silent=no_msg)
     return(ok && inseq)
}
treevar <- function(trees, varnum){</pre>
    # returns tree variable depending on varnum.
     # (1) n/ha (2) agb (3) volume (4) basal area
     v <- switch(as.numeric(varnum),</pre>
                  trees$nha,
                                                             # stocking
                  trees$agb*trees$nha,
                                                             # biomass
                  trees$agb*trees$nha/trees$wd,
                                                             # volume
                  trees$dbh^2*trees$nha*0.00007854
                                                             # basal area
    )
     return (v)
}
uniqueNames <- function(dt, a='', v='', b){
# extracts a set z of unique names from data table dt where column a equals v.
    # names are returned from column b
if(is.null(v)){v <- ''} # to avoid warning message on IF
if(a=='' || v==''){</pre>
         # select all unique values in column b if a or v is undefined
         z <- dt %>% transmute(!!sym(b)) %>% distinct() %>% arrange(!!sym(b)) %>% pull()
     }else{
        # select unique values in b where column a matches v
         z <- dt %>% filter(!!sym(a)==v) %>% transmute(!!sym(b)) %>% distinct() %>% arrange(!!sym(b)) %>% pull()
    # add a blank at start of vector
z <- append(z, '', after=0)</pre>
    return(z)
}
doInventory <- function(clusin){</pre>
     # returns inventory design object for clusters included in the sample (clin)
     plots.in <- plots %>% inner_join(select(clusin, clid), by='clid')
     doinv <- svydesign(id=~clid, data=plots.in, weights=~1)</pre>
     return(doinv)
}
invStatsTable <- function(invdo){</pre>
 ..... # returns inventory statistics for current design object as a table layout # table of mean, SE, Deff
    tm <- svymean(~nha+agb+vol+ba, invdo, deff='replace')</pre>
     # confidence intervals
     cl <- confint(tm)</pre>
     tm <- data.frame(tm)</pre>
     cl <- data.frame(cl)</pre>
     desc <- data.frame(desc=c(nha='Number per ha',</pre>
                                  agb='Above Ground Biomass (t/ha)',
                                  vol='Total volume (m3/ha)',
                                  ba='Basal Area (m2/ha)'))
    tbl <- cbind(desc, tm, cl)
names(tbl)[5:6]=c('LCL', 'UCL')</pre>
    # inter-cluster correlation, (Deff - 1)/(plots per cluster -1)
tbl %<>% rownames_to_column(var='variable')
    tbl %<>% transmute(Variable=variable,
                  Description=desc,
                  Mean=mean,
                  StdErr=SE,
                  Lower.CL=LCL,
                  Upper.CL=UCL,
                  ConfInt=fmtPct((UCL-LCL)/2/mean, 1),
                  DsgEff=deff
                  ICC=(deff-1)/4)
    return(tbl)
}
invStatsPlot <- function(invdo, var='nha'){</pre>
             ...... # returns a histogram for of plots x variable, for stand variable stvar,
    # and current inventory design object
     # set Y axis label from variable
     xlbl <- switch(var, nha="Stocking (n/ha)";</pre>
                      agb="Above-ground Biomass (t/ha)",
                      vol="Total volume (m3/ha)",
                      ba="Basal Area (m2/ha)")
```

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```
# generate plot
     svyhist(as.formula(paste('~',var)), invdo, probability = F, breaks=20,
              col='AliceBlue', main="", xlab=xlbl, ylab="No. of plots")
}
invBoxPlot <- function(clusin, stvar, areaf){
    # given a selected list of clusters (clusin) and variable name</pre>
     # stvar (from set nha, agb, vol, ba) and stratum, being a column in
    # clusin, generates a box plot of stvar x areaf factors.
    #
    # merge plots and clusters
    plots.in <- plots %>% inner_join(clusin, by='clid')
xlbl <- switch(stvar, nha="Stocking (n/ha)",</pre>
                      agb="Above-ground Biomass (t/ha)",
                       vol="Total volume (m3/ha)",
                       ba="Basal Area (m2/ha)")
     ggplot(plots.in, aes(x=!!sym(stvar), y=!!sym(areaf))) +
         geom_boxplot() + xlab(xlbl)
}
sampleCount <- function(clusin, invdo=NULL){</pre>
    # returns a vector with (1) number of clusters, (2) number of plots,
    # (3) degrees of freedom.
    #
    # number of clusters
    nc <- as.numeric(count(clusin))</pre>
    # number of plots
     np <- as.numeric(count(inner_join(clusin, plots, by='clid')))</pre>
     if(is.null(invdo)){
         # if design object not given, just return cluster and plot count
         return(c(nc, np))
     }else{
         # otherwise, also give degrees of freedom
         df <- degf(invdo)</pre>
         # return results as a vector
         return(c(nc, np, df))
    }
}
fmtPct <- function(p, d){</pre>
     # formats a number as +/- a percentage
     paste('±',round(p*100,d),"%")
}
#----- Shiny functions -----
# Define UI for application with menu
ui <- navbarPage("Fiji Forest Inventory Data Explorer",
    tabPanel("Sampling",
         # left hand column, dropdown menus for data filtering by Island etc.
         sidebarPanel(
               h4('Select plots to be included in the analysis:'),
              selectInput('selForestType', "Forest Type", uniqueNames(clusters, b="ForestType")),
sliderInput('sldAltitude',"Altitude Range", min=0, max=2000, step=50, value=c(0,2000)),
selectInput('selIsland',"Island", uniqueNames(clusters, b="Island")),
              uiOutput('uioProvince'),
              uiOutput('uioDistrict'),
              width=2
         ),
         # column with inventory statistics summary table and graph of Plot distribution
         mainPanel(
          ..... h3(textOutput("txtInvStats")),
          ..... tableOutput("tblInvStats"),
          ...... column(4,
              ..... selectInput('selHistVar',"Distribution of plots by:",
                                    c("Stocking (n/ha)"='nha',
               . . . . .
                                   "Aboveground Biomass (tons/ha)"='agb',
"Total Volume (m3/ha)"='vol',
               . . . . .
               . . . . .
                                   "Basal Area (m2/ha)"='ba'),
               . . . . .
                                   selected=1),
               . . . . .
               .... plotOutput("pltHistogram")
          ....),
          ...... column(6,
                              selectInput('selBoxY',"Sample means and errors by:",
c("Forest Type"='ForestType',
"Altitude Class"='AltClass',
     . . . . . . . . . . . . .
     . . . . . . . . . . . . .
     . . . . . . . . . . . . .
                                                "Island"='Island',
     . . . . . . . . . . . . .
                                                "Province"='Province'
     . . . . . . . . . . . . .
                                               "District"='District'),
     . . . . . . . . . . . . .
                                             selected=1),
     . . . . . . . . . . . . .
                              plotOutput("pltBoxPlot")
     . . . . . . . . . . . . .
     .....),
          ..... width=10
```

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```
528
                   )
530
               tabPanel("Map", leafletOutput("map1", width='100%', height='700px')
                    ),
               tabPanel("Stand Table", sidebarPanel(
532
                   h4('Stand Table of Species by Diameter Classes'),
533
                   534
535
536
537
                        "Aboveground Biomass (tons/ha)"=2, "Total Volume (m3/ha)"=3,
"Basal Area (m2/ha)"=4), selected=1 ),
538
539
                   p(strong('Sample scope')),
tags$head(tags$style(type = "text/css", "#filterTbl1 th {display:none;}")),
540
541
                   tableOutput('filterTbl1'),
543
                   width=2),
                   mainPanel(tabsetPanel(
544
545
                       tabPanel("By Species", dataTableOutput('st1')),
546
                       tabPanel("Totals", dataTableOutput('tt1') ,
                           br(),
547
548
                           hr(),
                           column(3, align="center",
549
                                   p(strong('Cumulative % above dbh')),
550
                                   #em(textOutput('ct1Title')),
551
                                   tableOutput('ct1')),
552
                           column(4, align="center")
553
554
                                  strong(p(textOutput('ctp1Title'), style='{text-align: center}')),
555
                                   plotOutput('ctp1')),
                           column(5, align="center"
556
                                  p(strong('Species Abundance %')),
558
                                   #em(textOutput('sap1SubTitle')),
559
                                   plotOutput('sap1'))
560
561
                       ), width=10)
562
                   ),
               563
564
565
566
               fluid = TRUE
567
           )
           # Define server logic
569
570
           server <- function(input, output) {</pre>
571
572
               # ------ Sampling tab ------
               # selectors for Division, Province, District (lists may vary dynamically)
output$uioProvince <- renderUI({selectInput('selProvince', 'Province',</pre>
573
574
                                                            uniqueNames(clusters, "Island",input$selIsland,"Province"))})
575
               output$uioDistrict <- renderUI({selectInput('selDistrict','District'</pre>
576
                                                            uniqueNames(clusters, "Province",input$selProvince,"District"))})
578
               # define set of clusters with current filters
579
               clset <- reactive(includeClusters(clusters)</pre>
580
                                                  input$selIsland,
                                                  input$selForestType,
                                                  input$sldAltitude,
582
583
                                                  input$selProvince
584
                                                  input$selDistrict))
585
               # set of tree data for included clusters
586
               trset <- reactive(includeTrees(trees, clset()))</pre>
587
               # inventory design object for current cluster set
               invdo <- reactive(doInventory(clset()))</pre>
588
589
               # counts of clusters, plots, df
590
               invCounts <- reactive(sampleCount(clset(), invdo()))</pre>
               # table of sample details for Stand Table side panel
591
               output$filterTbl1 <- renderTable({filterTbl()})</pre>
               # output tables and plots for inventory results
               output$txtInvStats <- renderText({</pre>
597
                   n <- invCounts()</pre>
                   paste("Forest inventory statistics for ",n[1],"clusters,",n[2],"plots")
598
599
               })
               output$tblInvStats <- renderTable(invStatsTable(invdo()))</pre>
600
               output$pltHistogram <- renderPlot(invStatsPlot(invdo(),input$selHistVar))</pre>
601
602
               output$pltBoxPlot <- renderPlot(invBoxPlot(clset(),input$selHistVar,input$selBoxY))</pre>
603
                          ----- Map tab -----
604
               # turn off some unnecessary messages from leaflet/GIS functions
               options(dplyr.summarise.inform=F)
               # read cluster data as points
               cluspts <- st_read(dsn='clustersLL.gpkg', layer='clusters', quiet=T)</pre>
608
609
               cluspts <- correct_points(cluspts)</pre>
610
               provs <- st_read(dsn='provincesLW.gpkg', quiet=T)</pre>
               # leaflet map centred on Fiji with NFI 2006 clusters and control to show/hide them
611
612
               # currently defined sample
```

531

542

557

568

577

581

592 593 594

595 596

605

606

```
613
                  clusptsf <- reactive({includePoints(cluspts, clset())})</pre>
614
                  # show the map
                  output$map1 <- renderLeaflet({leaflet() %>%
615
                       addTiles(group='streetmap') %>%
616
617
                       addProviderTiles(providers$OpenTopoMap, group='topography') %>%
618
                       addTiles('http://{s}.google.com/vt/lyrs=s&x={x}&y={y}&z={z}', group='satellite') %>%
                      setView(lat = -17.5, lng = 179.0, zoom=8) %>%
addCircles(data=clusptsf(), color='red', group = "NFI 2006") %>%
addLayersControl(overlayGroups =c("NFI 2006"), baseGroups=c('streetmap','topography'))
619
620
621
622
                  })
                  # dynamic content as sample selction varies
623
                  observe({
624
                       leafletProxy("map1", data = clusptsf()) %>%
625
                            clearShapes() %>%
626
627
                            addCircles(radius = 1, weight = 1, color = "#FF0000", fillColor = "FF7777")
628
                  })
629
630
                  # ----- Stand Tables tab -----
631
                  # stand tables check and generation
632
                  tblList <- reactiveValues()</pre>
633
                  checked_dc <- reactive({</pre>
                       validate(need(dc_check(input$dcl, no_msg=TRUE), "Diameter class list invalid!"))
634
                       input$dcl})
635
                  # show stand table by species
636
637
                  observe({tblList$st1 <- standTable(trset(), input$varnum, input$namefmt, checked_dc())})</pre>
                  output$st1 <- DT::renderDataTable({tblList$st1})</pre>
638
639
                  # show totals stand table
                  observe({tblList$tt1 <- totStandTable(tblList$st1, input$st1_rows_current)})</pre>
640
                  output$tt1 <- DT::renderDataTable({tblList$tt1})</pre>
641
642
                  # cumulative table and caption
643
                  #output$ct1Title <- renderText({var.name(input$varnum)})</pre>
644
                  output$ct1 <- renderTable({</pre>
                       tblList$ct1 <- cumTotalTable(input$dcl, tblList$st1, input$st1_rows_current)},
rownames=TRUE, colnames=TRUE, digits=2, bordered=TRUE, striped=TRUE)</pre>
645
646
647
                  # bar chart of totals by size class
648
                  output$ctp1Title <- renderText({paste(var.name(input$varnum),"by Dbh classes")})</pre>
                  output$ctp1 <- renderPlot({plotTotStandTable(input$varnum, tblList$tt1)})
# bar chart of species abundance</pre>
649
650
                  #output$sap1SubTitle <- renderText({paste("based on", var.name(input$varnum))})
output$sap1 <- renderPlot({abundancePlot(tblList$st1, input$st1_rows_current)})</pre>
651
652
653
             }
654
655
             # ----- Run the application ------
             shinyApp(ui = ui, server = server)
656
```