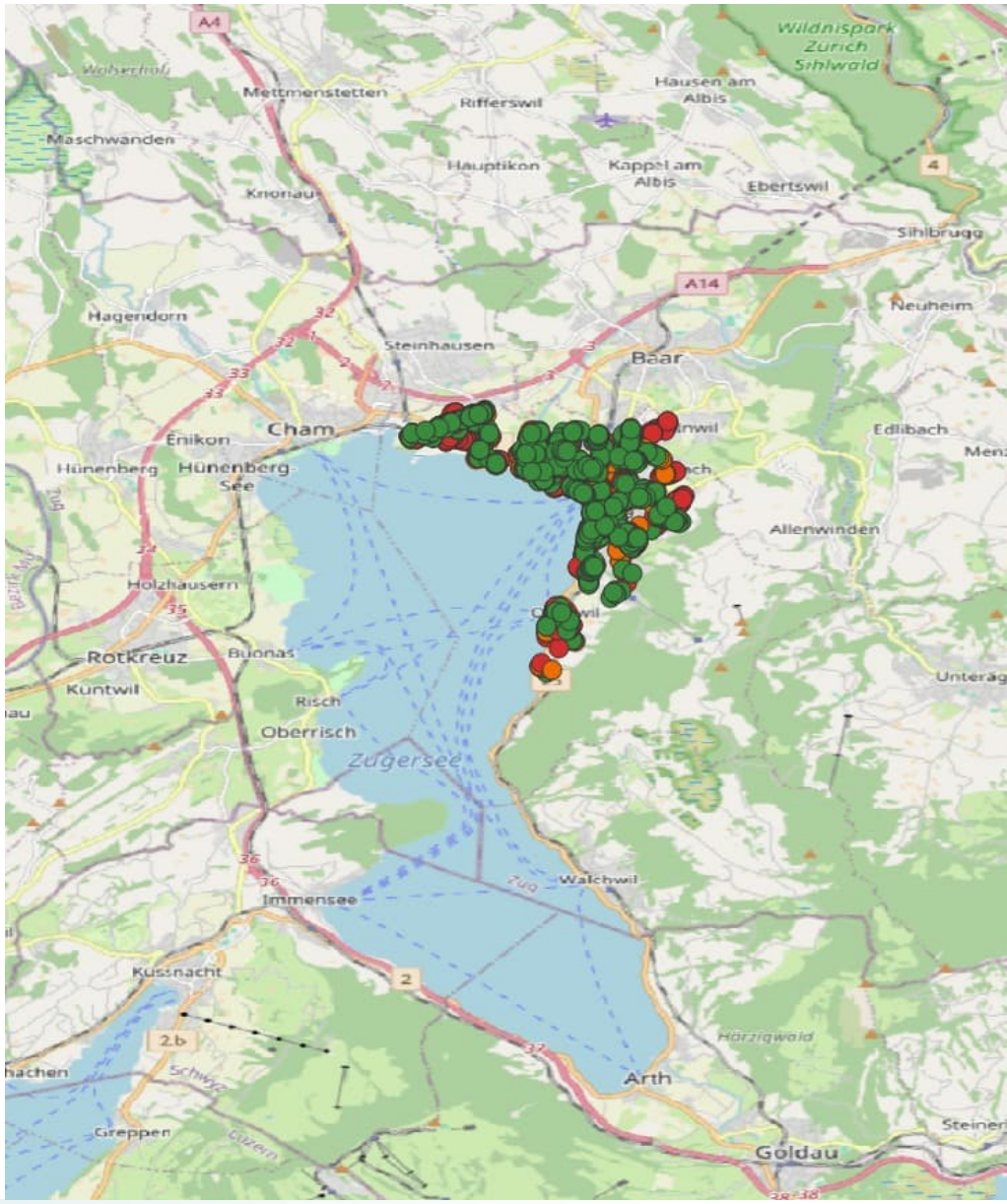
FREE3 tool

A step-by-step user guide

Decision-support tool for assessing urban tree inventories by harmonising species names, screening for potential pest–host associations, and analysing tree diversity and population structure

Part 2 of 3 Shiny app: analysis and report (Steps 8–10)

Also Part 1: Table and QGIS plugin · Part 3: Troubleshooting



Version 2.0 / October 2026

FREE3 user guide

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Click any line to jump to that slide. G1-G3: see Part 1 (QGIS), 2 (Shiny app) or 3 (Troubleshooting).

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Start here

The 10 steps

1 Table

Check your table

Find the species column; note names

Guide 1 ›

2 Table

Prepare the table

5 yes/no questions; fix the NOs

Guide 1 ›

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Install QGIS + plugin

Once: QGIS 3.44 LTR + plugin ZIP

Guide 1 ›

4 QGIS

Harmonise names

Tree icon › Run harmonization

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Run screening; explore the map

Guide 1 ›

7 QGIS

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Save Features As… › CSV

Guide 1 ›

8 Shiny app

Install R, run the app

Once: R + RStudio; then Run App

slide 9 ›

9 Shiny app

Upload, map columns

Browse… › choose the columns

slide 13 ›

10 Shiny app

Results and report

Read, download, check

slide 15 ›

Where are you now?

First time on this computer	New inventory, tools installed	I have the harmonised CSV	I have done this before	Something doesn't work
Before you start · slide 5 ›	**Step 1 Guide 1›**	**Step 8 · Slide 9 ›**	**Quick reference · Guide 3 ›**	**Troubleshooting · Guide 3 ›**

From tree inventory to pest–host screening

Prepare › Harmonise › Screen › Inspect › Export › Analyse

Prepare your tree inventory in a supported format with a species column.

Match species names against the reference taxonomy.

Cross-reference each tree against the FREE3 pest–host database.

Explore the screening map in QGIS and inspect individual trees.

Export the harmonised inventory as a CSV file.

Upload the CSV to the Shiny app, map the columns, review the analyses and export the report.

Input | **QGIS plugin** | **Shiny app**

your_inventory.xlsx | harmonized_inventory.gpkg | …_pest_risk.gpkg | pest_risk_summary.csv | harmonized_inventory.csv | FREE3_report.docx

Why harmonise first?

Tree inventories often contain spelling variants, synonyms, cultivar names, abbreviations and hybrids. Harmonisation standardises these names against the reference taxonomy, allowing records to be matched more reliably with the FREE3 pest–host database.

Before you start

QGIS

Use QGIS 3.44 LTR. Do not use QGIS 4.x unless the FREE3 team confirms plugin compatibility.

qgis.org

The plugin ZIP

The Tree Inventory Harmonizer archive. Keep it zipped — do not extract it.

Supplied by the FREE3 team

R

The statistical environment required to run the Shiny app. Install R before RStudio.

cran.r-project.org

RStudio

Used to open and launch the Shiny application. Install after R.

posit.co

The app script

app3.1.R — the Shiny application file.

Supplied by the FREE3 team

! **Install R before RStudio.**
RStudio needs an existing R installation in order to run the app.

i **Note**
On managed computers, software installation may require approval from your IT department.

How to read this guide

How to follow the steps

1 **Step number.** Follow the numbered steps in order.

1 **Screenshot marker.** The same number appears on the screenshot to show where to click.

File names. File and folder names are shown in this typeface (file_name.gpkg).

Buttons and menus. Buttons, menus and fields are shown in quotation marks (‘Run harmonization’).

Boxes you will see

Note background on what the tool is doing.

Tip A shortcut or a useful way to simplify a step.

Important something that is easy to miss or get wrong.

How the guide is organised

Guide 1
Your inventory table

Check your own table and fix only what is needed (P1–P5).

Guide 1
The QGIS plugin

Install, harmonise names, screen for pest hosts, export the CSV (A1–A14).

Guide 2
The Shiny app

Run the app, map columns, read the results, get and check the report (B1–B7).

Guide 3
At the back

Quick reference, troubleshooting and glossary.

Part B

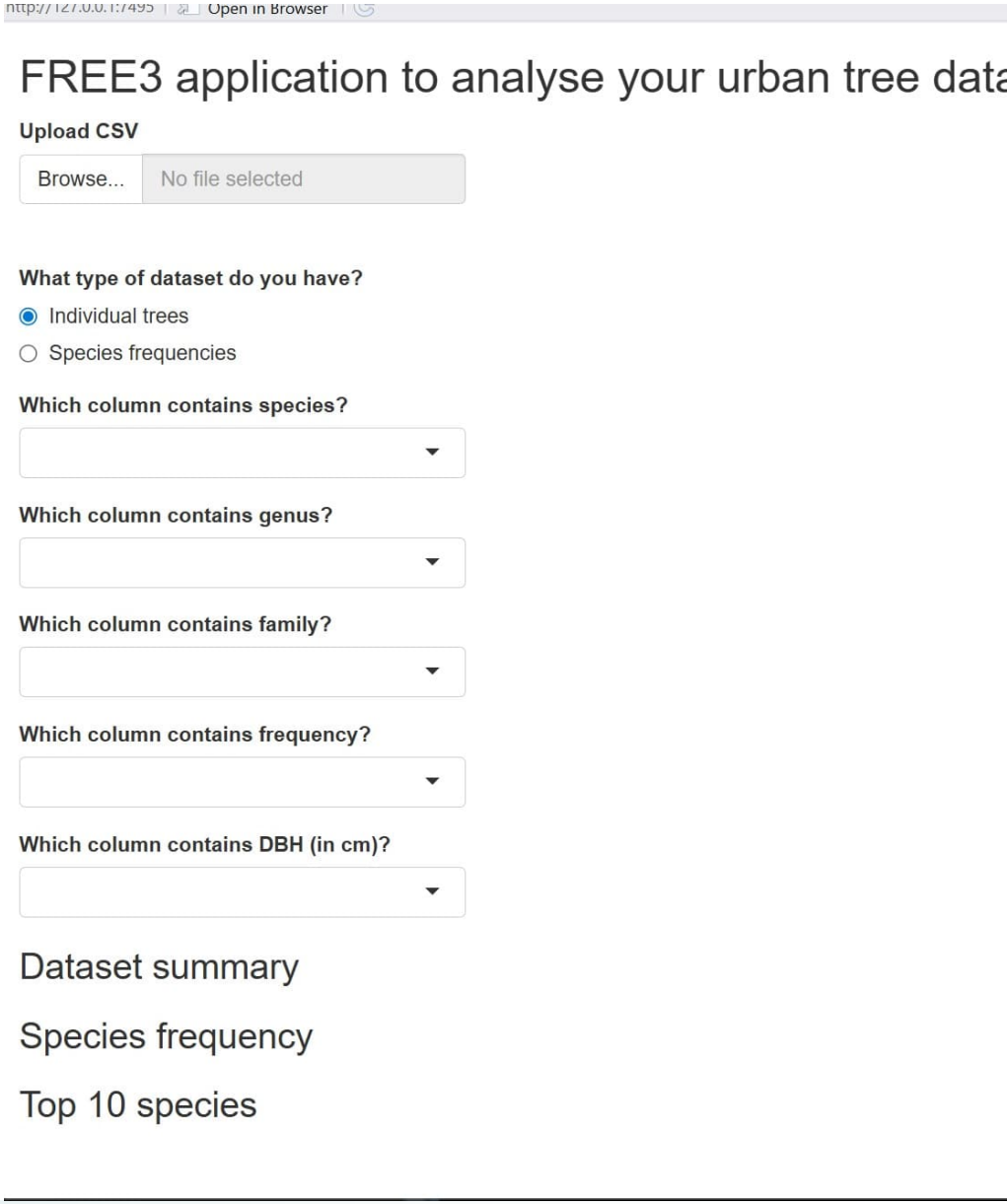
The Shiny app

Steps 8–10 · B1–B7

8 Install R and run the app

9 Upload the CSV and map columns

10 Read the results, get and check the report



What the Shiny app analyses

Five analyses are generated once the relevant columns have been mapped.

Species frequency and abundance

Number of trees per species and each species' share of the inventory. Includes a top-10 summary.

The 10–20–30 rule

Checks whether any species, genus or family exceeds the 10%, 20% or 30% threshold.

Melbourne recommendations

Applies a stricter 5–10–20 diversity benchmark for species, genus and family representation.

DBH and basal area

Summarises size-class distribution and basal area by species. Requires a DBH column.

Pest–host screening by species and pest

Shows which tree species are associated with regulated pests and which pests are linked to the largest share of the inventory.

The app adapts to your data

Each analysis depends on the availability of the relevant columns. A species column enables species frequency and pest–host screening. Adding genus and family allows the diversity benchmarks to be assessed, while DBH enables the structural analyses. If a required column is missing, that section is simply omitted from the report.

Step B1

Install R, then RStudio

Two separate programs are required, and the installation order matters.

R

The statistical engine

R performs the calculations used by the Shiny app. Download the version for your operating system and follow the default installation settings.

cran.r-project.org

Install R first

Install R before RStudio. RStudio needs an existing R installation in order to run the Shiny app correctly.

RStudio

The interface used to run the app

RStudio provides the working environment used to open and launch the Shiny application. Install RStudio Desktop after R.

posit.co/download/rstudio-desktop

Required r packages

On the first run, the app may download the R packages it requires, including shiny, dplyr and ggplot2. This requires an internet connection and may take a few minutes.

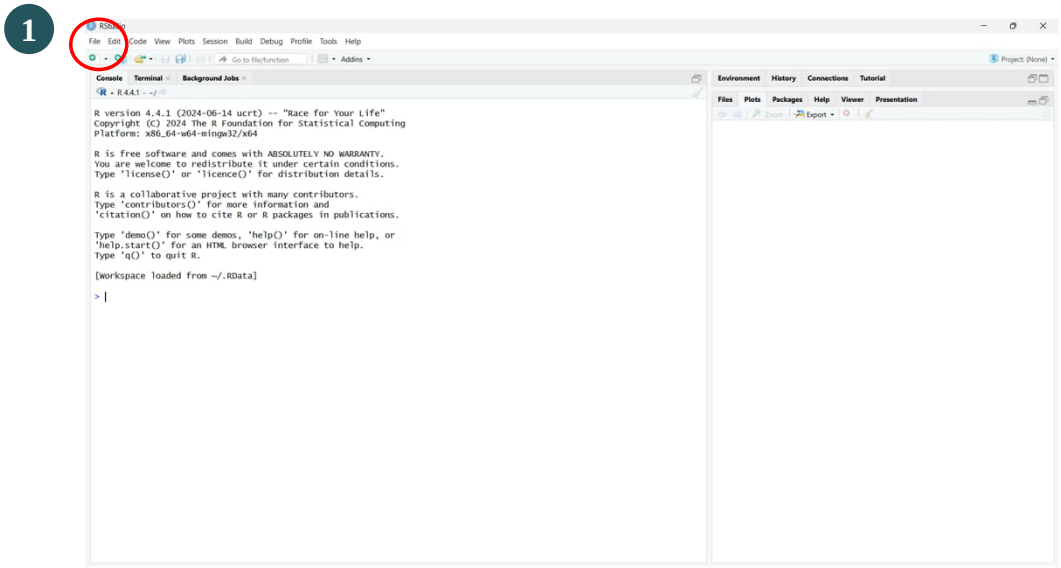
Step B2

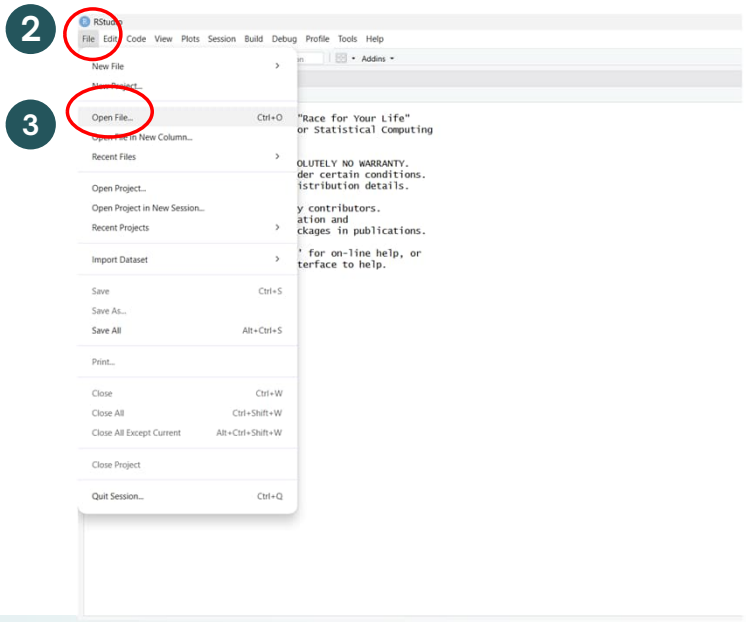
Open the app file in RStudio

1. **Open RStudio.** The console will display start-up text; this is normal.

2. **Click 'File' in the menu bar.**

3. **Click 'Open File…'** A file browser will open. Continue to Step B3.





> **i** **'Open file', not 'open project'**
>
> The Shiny app is provided as a single R script rather than an RStudio project. 'Open Project…' will not find it.

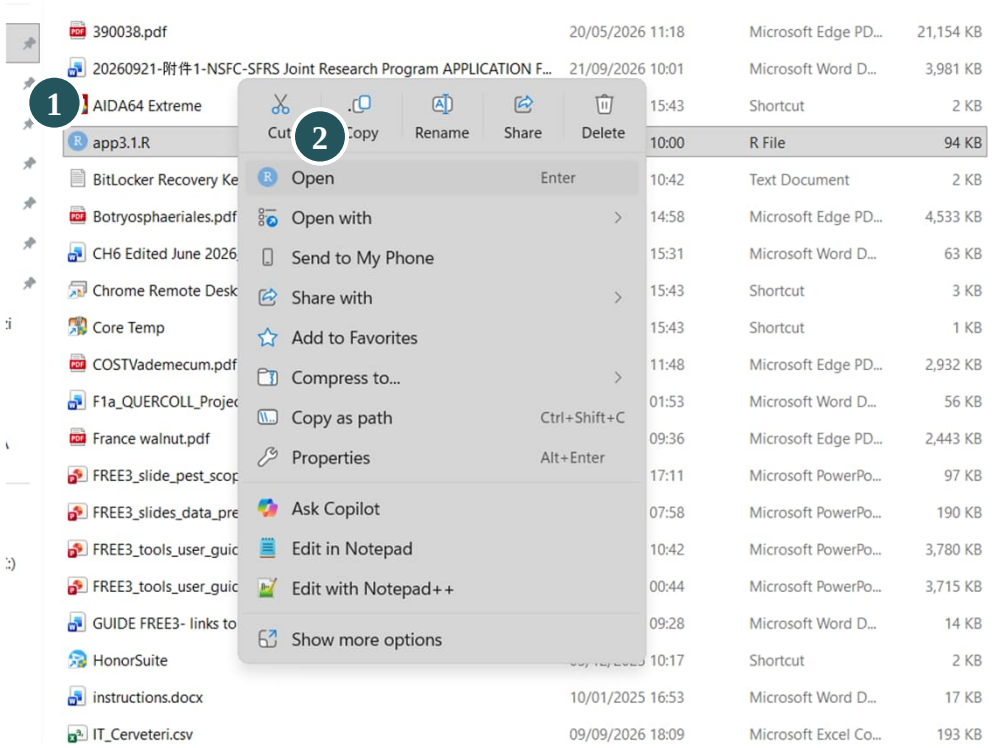
> **★** **Next time**
>
> After the file has been opened once, you can access it from 'File' › 'Recent Files'.

Step B3

Select the app script

Browse to the folder where you saved the file provided by the FREE3 team.

1. Locate the app file— app3.1.R, or the most recent version provided to you.
2. Select the file and click **'Open'.** The script will open in the RStudio editor.



Check the version number

The folder may contain several versions of the app. Open the most recent version supplied by the FREE3 team, as older scripts may not match the current pest–host database.

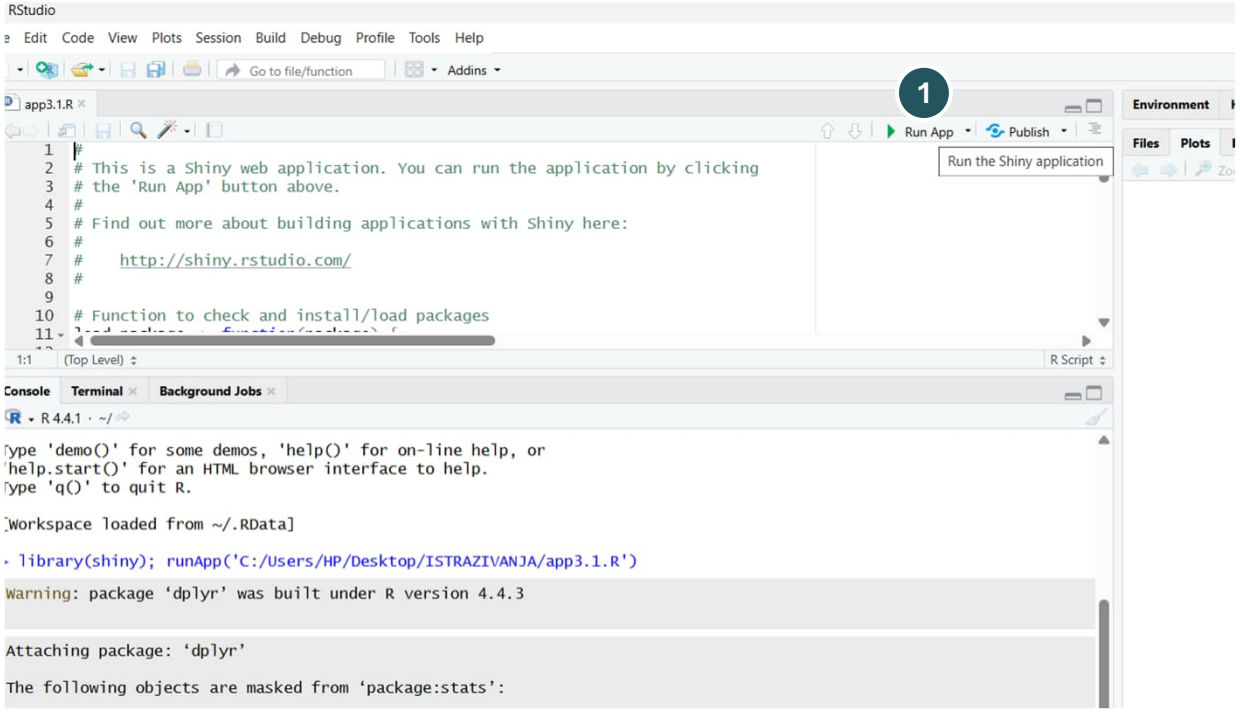
The app has not started yet

Opening the script only loads it into RStudio. The app itself starts in Step B4.

Step B4

Run the app

1. **Click 'Run App'** in the upper-right corner of the editor pane.
   RStudio recognises Shiny scripts and displays this button automatically.
2. **Wait while packages load.** The first run may take a few minutes, especially if packages need to be downloaded. Subsequent runs are usually faster.
3. **The app opens in its own window** titled 'FREE3 application to analyse your urban tree dataset'.



★ **Open in a web browser**

Click 'Open in Browser' at the top of the app window if you prefer to view the interface at full screen width.

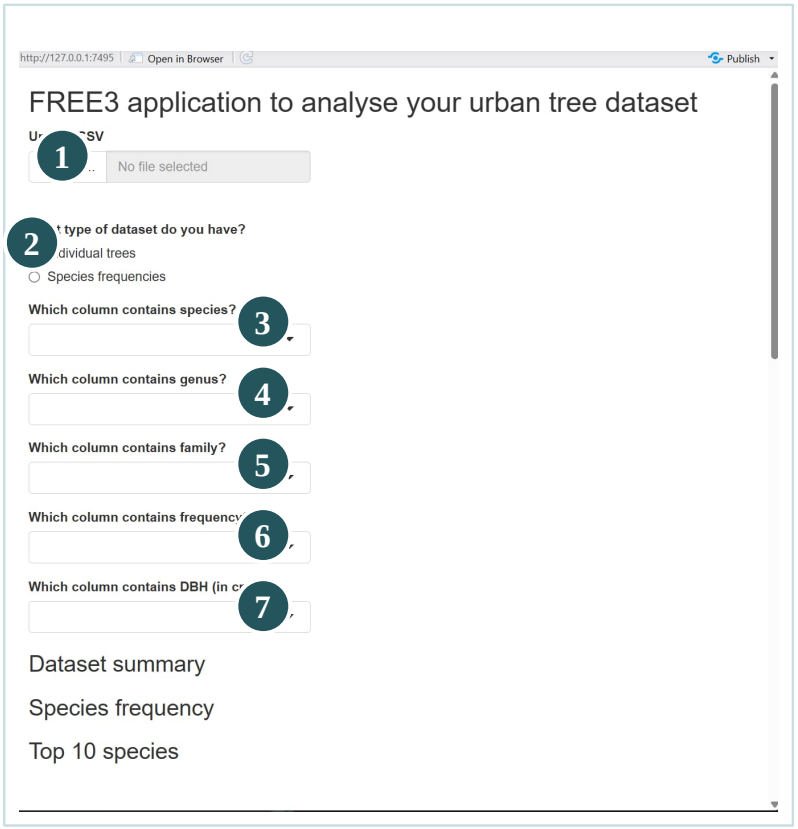
! **Keep RStudio open**

RStudio needs to remain open while the Shiny app is running. Closing RStudio will stop the app.

Step B5

Upload your data and map the columns

Use the drop-down menus to tell the app which columns contain each type of information.



1. **Upload CSV — 'Browse…'** and select the file you exported in Step A14.
2. **What type of dataset do you have? "Individual trees" if each row represents one tree, or "Species frequencies" if each row represents a species with a count.**
3. **Select the species column.**
   Choose the column containing the harmonised species names.
4. **Select the genus column.**
   Required for the genus-level 10–20–30 assessment.
5. **Select the family column.**
   Required for the family-level diversity assessments, including the Melbourne recommendations.
6. **Select the frequency column**, if you chose Species frequencies.
   Leave this field empty for individual-tree datasets.
7. **Select the DBH column (cm).**
   This enables the size-class and basal-area analyses.

★ **Results update automatically**

The analyses appear as soon as the required columns are mapped. Scroll down to view the results as they are generated.

Which columns are required for each analysis

If a section is missing from the report, use this table to check which input column is required.

Analysis	Requires	What you learn	If missing
Dataset summary	Species	Total number of trees, species richness and families represented	Analysis unavailable
Species frequency & top 10	Species	Relative abundance and the most common species	Section omitted
10–20–30 rule	Species + genus + family	Whether any taxon exceeds the recommended threshold	Partial assessment
Melbourne recommendations	Species + genus + family	Diversity against the stricter 5–10–20 benchmark	Partial assessment
DBH distribution	DBH (cm)	Distribution of trees across size classes	Section omitted
Basal area per species	Species + DBH	Relative structural contribution of each species	Section omitted
Pest-host screening	Species	Pest–host associations by tree species and regulated pest	Section omitted

Tree numbers and basal area provide different information

Species abundance describes how many trees are present, whereas basal area reflects their relative structural contribution. A species represented by relatively few large trees may therefore account for a substantial proportion of the total basal area.

Step B6

Read the results

Scroll through the app to review each analysis and its interpretation.

1	**Dataset summary** Does the uploaded dataset look correct?	Shows the total number of trees, species and families. Check this first to confirm that the correct file and dataset type were selected.
2	**Species frequency & top 10** Which species are most common in the inventory?	Ranked table of species with counts and shares. The top 10 usually accounts for most of the population.
3	**10–20–30 rule and Melbourne check** Is the inventory overly dependent on a small number of taxa?	Flags species, genera or families that exceed the recommended diversity thresholds.
4	**DBH distribution & basal area** What does the size structure of the population look like?	Summarises tree size classes and basal area by species. Requires a DBH column.
5	**Pest–host screening by species and pest** Which pest–host associations are most relevant to the inventory?	Matches tree species against regulated pests and summarises which pests are associated with the largest share of the inventory.

! **Watch out** “No pest–host matches found” can be a valid result, but first check that the species column has been mapped correctly.

Dataset summary and species frequency

The first two panels confirm that the right file was loaded and show which species dominate the inventory.

1. **Dataset summary**

   Shows the total number of trees, species, genera and families. Check the tree count first to confirm that the correct dataset was loaded.

2. **Taxonomic diversity**

   Species, genus and family counts reflect harmonised names. Synonyms and spelling variants are consolidated, which may reduce the original counts.

3. **Mean basal area (m²)**

   Average trunk cross-sectional area at breast height, calculated from DBH. It indicates average tree size and requires valid DBH measurements.

4. **Species frequency**

   Species ranked by tree count using harmonised scientific names. Entries identified only to genus remain at genus level.

In this example

The inventory contains 1,643 trees, representing 49 species, 30 genera and 21 families. Mean basal area is 0.2147 m² per tree. *Pinus pinea* (429) and *Eucalyptus* (313) together account for approximately 45% of all trees.

Dataset summary

Metric	Value
Total number of trees	1643
Number of species	49
Number of genera	30
Number of families	21
Mean basal area (m²)	0.2147

Species frequency

species	frequency
Pinus pinea L.	429
Eucalyptus L'Hér.	313
Populus nigra L.	212
Quercus ilex L.	153
Olea europaea L.	124
Cupressus arizonica Greene	83
Ligustrum L.	38
Cupressus sempervirens L.	28
Populus nigra var. italica (Moench) Koehne	27
Cedrus atlantica (Endl.) Manetti ex Carriere	23
Pinus halepensis Mill.	22
Robinia pseudoacacia L.	20
Cedrus deodara (Lamb.) G.Don	13
Laurus nobilis L.	12
Populus alba L.	12
Magnolia grandiflora L.	11

Top 10 species by number of trees and by basal area

1 **Two different questions**

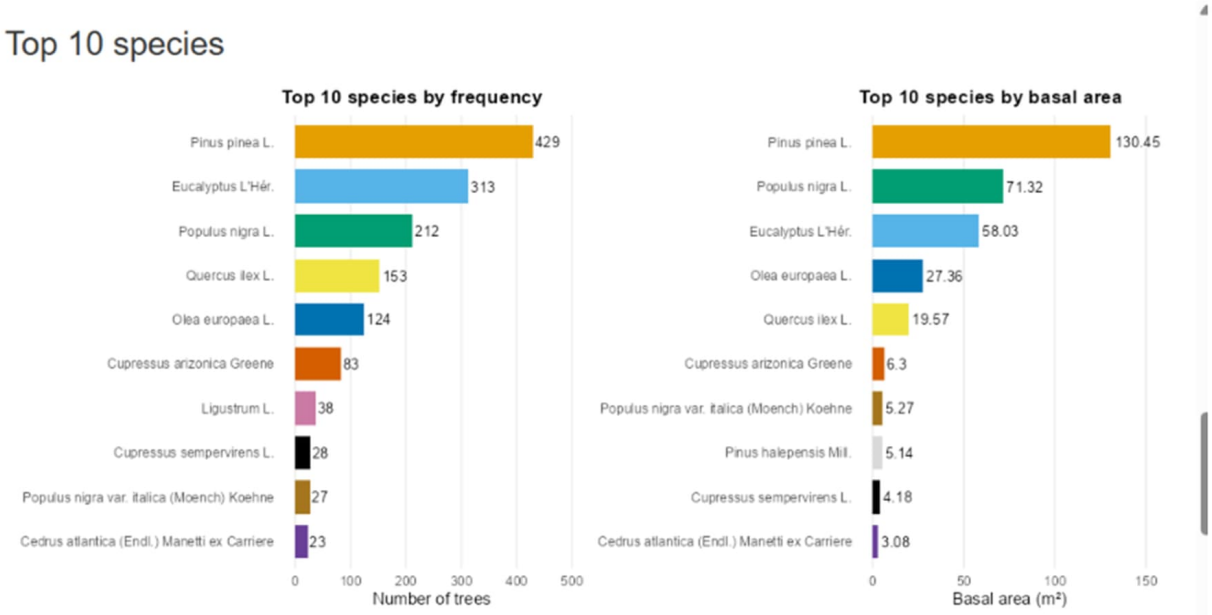
Tree count shows species abundance, while basal area indicates structural dominance. Common species do not necessarily contribute the most basal area.

2 **The ranking changes**

Populus nigra rises from third by count to second by basal area, while *Eucalyptus* drops to third. Quercus ilex has 153 trees but only 19.57 m² of basal area.

3 **Why both are needed**

Together, these measures provide a clearer picture of species composition and stand structure.



i **In this example**

Pinus pinea leads both measures (429 trees; 130.45 m²), contributing 36.7% of total basal area. *Pinus halepensis* ranks higher by basal area than by tree count, suggesting fewer but larger trees.

DBH distribution by diameter classes

The number of trees in each 5 cm diameter class, from 10–15 cm up to an open 75+ class.

1 **How to read it**

5 cm DBH classes. Interpret the open-ended 75+ cm class separately.

2 **What the distribution reveals**

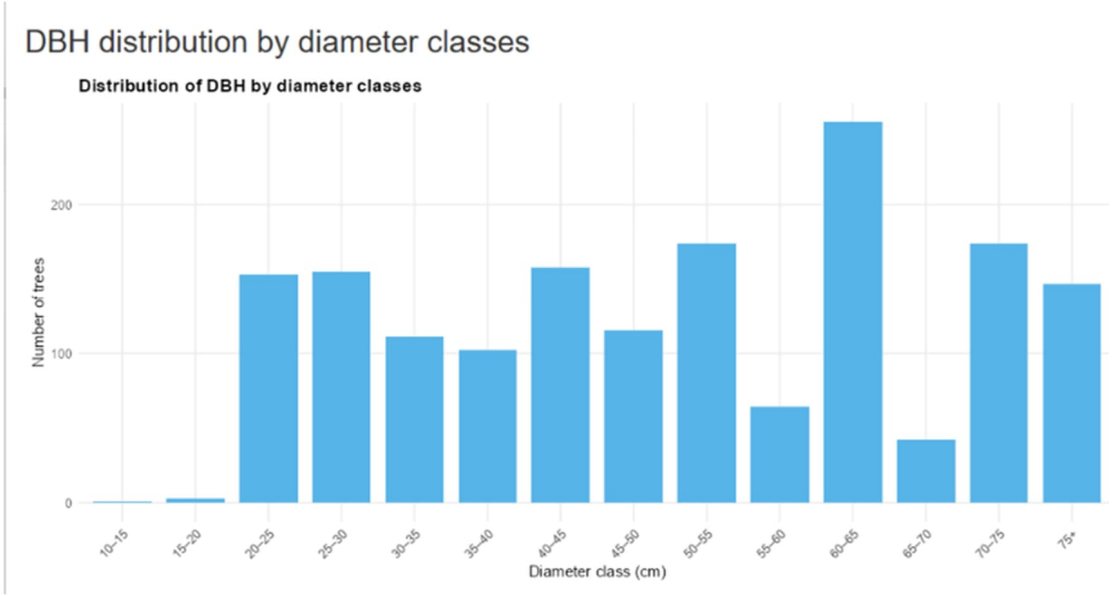
Tree size structure, possible recruitment gaps and historical planting patterns.

3 **In this inventory**

Few trees below 20 cm DBH; the highest frequency occurs at 60–65 cm..

! **Check the units before you read the chart**

DBH must be in centimetres. Values recorded in millimetres, or trunk circumference used instead of diameter, shift every tree into the wrong class and make the whole chart misleading.



Basal area and compliance with the diversity rules

The overall size of the population, and how its composition scores against two diversity benchmarks.

1. **Basal area**

   Total basal area, the mean per tree and the mean DBH. These figures describe size; the tables below describe composition.

2. **The 10–20–30 rule**

   No species should exceed 10% of the population, no genus 20% and no family 30%. The tables list only the taxa that cross a threshold.

3. **Melbourne recommendations**

   A stricter 5–10–20 benchmark. A taxon can pass the 10–20–30 rule and still be flagged here, which is why both appear.

4. **Recommendation**

   Generated from the tables above. It is a prompt for planting policy, not a site-specific prescription.

i In this example

Three species exceed 10% (*Pinus pinea* 26.1%, *Eucalyptus* 19.1%, *Populus nigra* 12.9%), the genus *Pinus* exceeds 20% at 27.8%, and the family *Pinaceae* exceeds 30% at 30.4%.

Basal area

total_basal_area_m2	mean_basal_area_m2	mean_dbh_cm
355.19	0.21	48.90

Compliance with species rules

species	frequency	share	status
Pinus pinea L.	429	26.10	Exceeds 10% rule
Eucalyptus L'Hér.	313	19.10	Exceeds 10% rule
Populus nigra L.	212	12.90	Exceeds 10% rule
Quercus ilex L.	153	9.30	Exceeds limits of Melbourne's Urban Forest Strategy
Olea europaea L.	124	7.50	Exceeds limits of Melbourne's Urban Forest Strategy
Cupressus arizonica Greene	83	5.10	Exceeds limits of Melbourne's Urban Forest Strategy

Compliance with genus rules

genus	frequency	share	status
Pinus	457	27.80	Exceeds 20% rule
Eucalyptus	313	19.10	Exceeds limits of Melbourne's Urban Forest Strategy
Populus	251	15.30	Exceeds limits of Melbourne's Urban Forest Strategy
Quercus	167	10.20	Exceeds limits of Melbourne's Urban Forest Strategy

Compliance with family rules

family	frequency	share	status
Pinaceae	499	30.40	Exceeds 30% rule

Recommendation

The dataset exceeds both the classic 10-20-30 diversity rule and the stricter Melbourne Urban Forest Strategy thresholds. Future planting should prioritize underrepresented species, genera, and families, and avoid additional planting of currently dominant taxa.

Pest–host risk by tree species

Which species in the inventory are listed as hosts of the regulated pests, and how much of the population they represent.

1 One row per species

Each row lists the associated pests, number of trees and total basal area for that species.

2 Sorted by number of pests

Species associated with the highest number of screened pests appear first, regardless of their abundance.

3 Read trees and basal area together

Quercus rubra is associated with four pests but has only two trees. Populus nigra is associated with two pests but represents 212 trees and 71.32 m² of basal area.

! Absence from this table is not safety

Species absent from the table have no recorded associations with the 11 pests screened. This does not indicate freedom from other pests or actual infestation risk.

Pest-host risk by tree species

Species	Pests	Number of pests	Number of trees	Total basal area (m²)
Quercus rubra L.	Anoplophora glabripennis, Aromia bungii, Phytophthora ramorum, Xylella fastidiosa	4	2	0.18
Prunus laurocerasus L.	Anoplophora chinensis, Aromia bungii, Phytophthora ramorum, Xylella fastidiosa	4	1	0.05
Robinia pseudoacacia L.	Anoplophora chinensis, Popillia japonica, Xylella fastidiosa	3	20	1.76
Fraxinus excelsior L.	Agrilus planipennis, Phytophthora ramorum, Xylella fastidiosa	3	10	2.08
Prunus L.	Anoplophora chinensis, Aromia bungii, Xylella fastidiosa	3	10	0.58
Albizia julibrissin Durazz.	Anoplophora chinensis, Anoplophora glabripennis, Xylella fastidiosa	3	6	0.43
Platanus L.	Anoplophora chinensis, Anoplophora glabripennis, Xylella fastidiosa	3	5	0.95
Acer negundo L.	Anoplophora chinensis, Anoplophora glabripennis, Xylella fastidiosa	3	4	0.40
Acer L.	Anoplophora chinensis, Anoplophora glabripennis, Xylella fastidiosa	3	1	0.09
Betula pendula Roth	Anoplophora chinensis, Anoplophora glabripennis, Phytophthora ramorum	3	1	0.07
Populus nigra L.	Anoplophora chinensis, Anoplophora glabripennis	2	212	71.32
Quercus ilex L.	Phytophthora ramorum, Xylella fastidiosa	2	153	19.57
Olea europaea L.	Anoplophora chinensis, Xylella fastidiosa	2	124	27.36
Laurus nobilis L.	Phytophthora ramorum, Xylella fastidiosa	2	12	0.55

Pest–host risk by pest

The same screening from the other side: for each pest, which species are at risk and how much of the inventory that represents.

1. **One row per pest**
   Each row lists the associated host species, their total number of trees and combined basal area.

2. **Trees and basal area at risk**
   Values represent potential host exposure, not confirmed infestation. A tree may be counted for multiple pests, so totals cannot be added together.

3. **Use it to prioritise**
   Pests associated with more trees or greater basal area may warrant closer monitoring, alongside local occurrence and pest-specific risk factors.

In this example

Xylella fastidiosa has by far the widest host range: 707 trees and 115.80 m², about four in ten trees in the inventory. Anoplophora chinensis follows with 399 trees and 104.90 m². These figures indicate potential exposure, not actual infection.

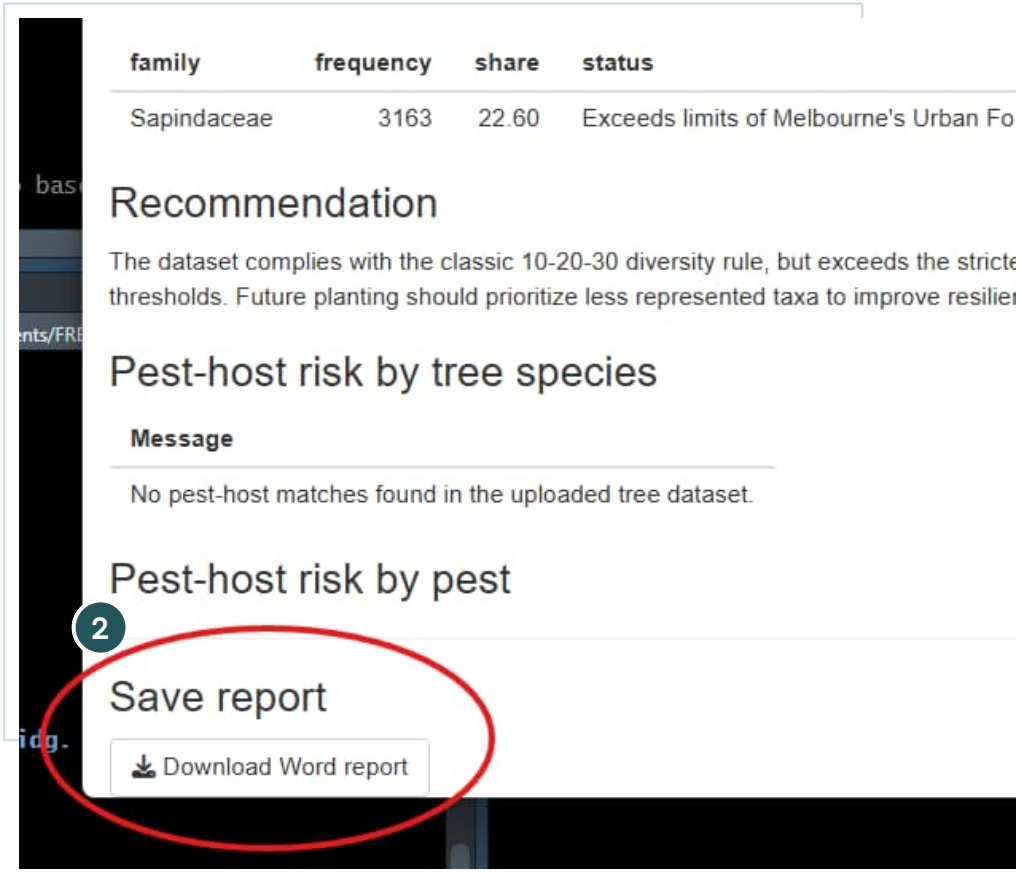
Pest-host risk by pest

Pest	Species at risk	Trees at risk	Basal area at risk (m²)
Xylella fastidiosa	Acer L., Acer negundo L., Ailanthus altissima (Mill.) Swingle, Albizia julibrissin Durazz., Cercis siliquastrum L., Eucalyptus L'Hér., Ficus carica L., Fraxinus excelsior L., Laurus nobilis L., Magnolia grandiflora L., Olea europaea L., Platanus L., Prunus cerasifera Ehrh., Prunus L., Prunus laurocerasus L., Quercus cerris L., Quercus ilex L., Quercus pubescens Willd., Quercus rubra L., Quercus suber L., Robinia pseudoacacia L.	707	115.80
Anoplophora chinensis	Acer L., Acer negundo L., Albizia julibrissin Durazz., Betula pendula Roth, Ficus carica L., Olea europaea L., Platanus L., Populus alba L., Populus nigra L., Prunus L., Prunus laurocerasus L., Robinia pseudoacacia L.	399	104.90
Anoplophora glabripennis	Acer L., Acer negundo L., Albizia julibrissin Durazz., Betula pendula Roth, Platanus L., Populus nigra L., Quercus rubra L.	231	73.44
Phytophthora ramorum	Betula pendula Roth, Fraxinus excelsior L., Laurus nobilis L., Magnolia grandiflora L., Prunus laurocerasus L., Quercus cerris L., Quercus ilex L., Quercus rubra L.	192	23.50
Popillia japonica	Populus nigra var. italica (Moench) Koehne, Robinia pseudoacacia L., Tilia cordata Mill.	50	7.48
Bursaphelenchus xylophilus	Cedrus atlantica (Endl.) Manetti ex Carriere, Cedrus deodara (Lamb.) G.Don, Picea abies (L.) H.Karst., Pinus pinaster Aiton	48	7.13
Aromia bungii	Prunus cerasifera Ehrh., Prunus L., Prunus laurocerasus L., Quercus rubra L.	20	1.06
Agrilus planipennis	Fraxinus excelsior L.	10	2.08
Rhynchophorus ferrugineus	Chamaerops humilis L.	4	0.43

Step B7

Download the Word report

1. **Scroll to the bottom of the app** to the 'Save report' section.
2. **Click 'Download Word report'.** A .docx file containing the tables, figures and recommendations currently shown in the app will be saved to your Downloads folder.
3. **Open the report in Word** and edit it as needed. You can add your own comments, logo and inventory date.



The report reflects the current results

The report contains the analyses shown at the time of download. If you change the column mapping, download the report again to generate an updated version.

Useful details to add manually

Consider adding the inventory date, the number of unmatched records from Step A7, and a contact name or organisation.

Before you share

Check the results before you send the report

- ☐ **Unmatched records reviewed** — A7
  Their number is written in the report.
- ☐ **Screening totals add up** — A9
  Major host + Host + No known risk = trees analysed.
- ☐ **Dataset type is correct** — B5
  Individual trees vs species frequencies.
- ☐ **Tree total matches your inventory** — B6
  Dataset summary vs number of rows.
- ☐ **DBH values are plausible** — P4
  No zeros, no 500 cm trees, no mm values.
- ☐ **The harmonised species column was mapped** — B5
  Not the original names.
- ☐ **Report names date, app version and the 11 pests** — B7
  So the analysis can be reproduced.
- ☐ **‘No known risk’ is described correctly** — A9
  Not listed in the database — not ‘safe’.

! **Screening is not a risk assessment**
The tool shows potential pest–host associations for 11 regulated pests. It does not show where pests are present.