FREE3 tool

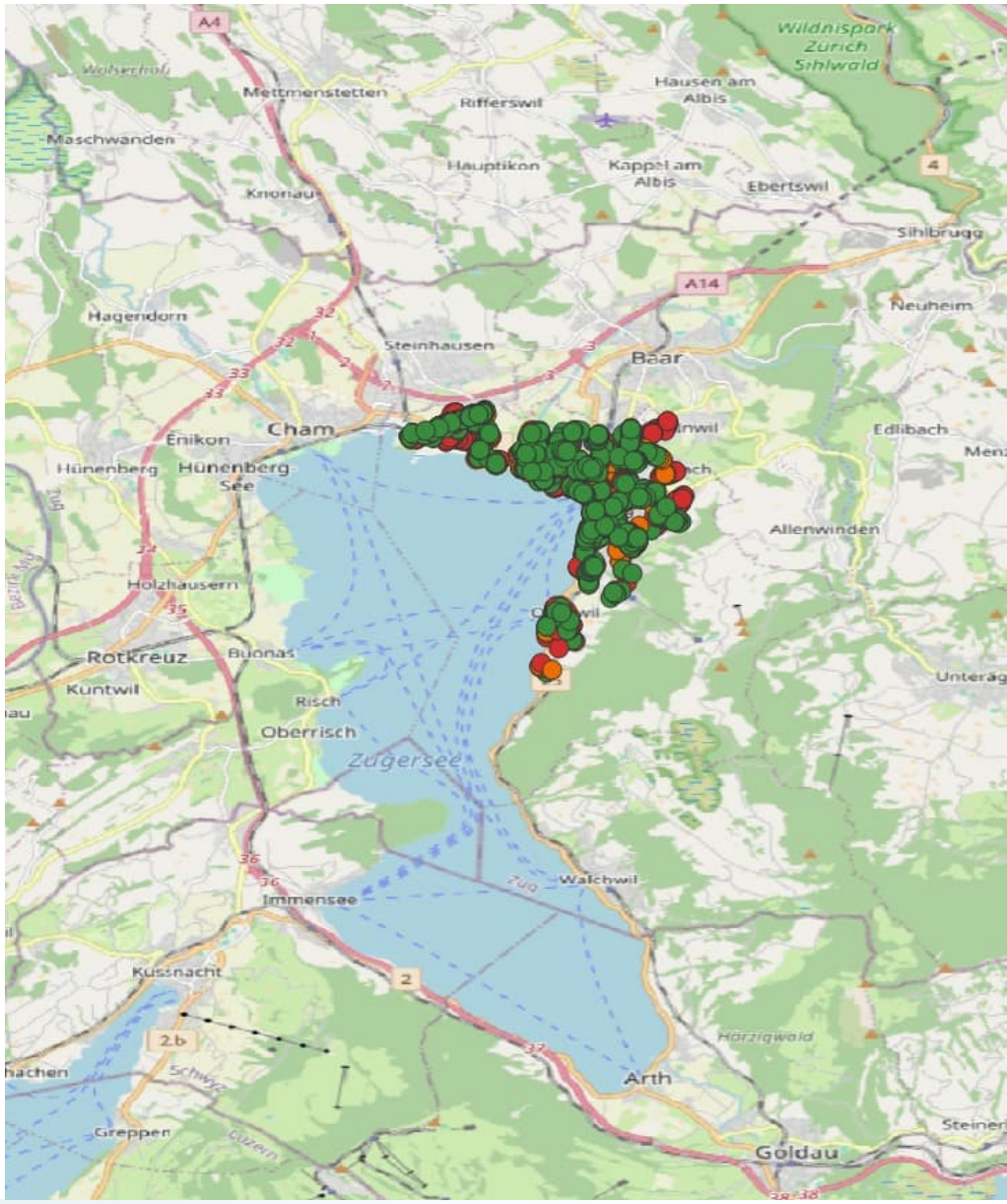
A step-by-step user guide

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

Tool 1 QGIS plugin — species-name harmonisation + pest–host screening

Tool 2 Shiny app — diversity, structure and reporting

Version 2.0 / October 2026



FREE3 user guide

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Click any line to jump to that slide. The bar at the bottom of every page brings you back here.

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Start here

The 10 steps

1 Table

Check your table

Find the species column; note names

slide 8 ›

2 Table

Prepare the table

5 yes/no questions; fix the NOs

slide 10 ›

3 QGIS

Install QGIS + plugin

Once: QGIS 3.44 LTR + plugin ZIP

slide 16 ›

4 QGIS

Harmonise names

Leaf icon › Run harmonization

slide 21 ›

5 QGIS

Check the matches

Review unmatched records

slide 22 ›

6 QGIS

Screen for pest hosts

Run screening; explore the map

slide 24 ›

7 QGIS

Export the CSV

Save Features As… › CSV

slide 30 ›

8 Shiny app

Install R, run the app

Once: R + RStudio; then Run App

slide 35 ›

9 Shiny app

Upload, map columns

Browse… › choose the columns

slide 39 ›

10 Shiny app

Results and report

Read, download, check

slide 41 ›

Where are you now?

First time on this computer

Before you start · slide 5 ›

New inventory, tools installed

Step 1 · slide 8 ›

I have the harmonised CSV

Step 8 · slide 35 ›

I have done this before

Quick reference · slide 50 ›

Something doesn’t work

Troubleshooting · slide 54 ›

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

i **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

Steps 1–2
Your inventory table
Check your own table and fix only what is needed (P1–P5).

Steps 3–7
The QGIS plugin
Install, harmonise names, screen for pest hosts, export the CSV (A1–A14).

Steps 8–10
The Shiny app
Run the app, map columns, read the results, get and check the report (B1–B7).

Reference
At the back
Quick reference, troubleshooting and glossary.

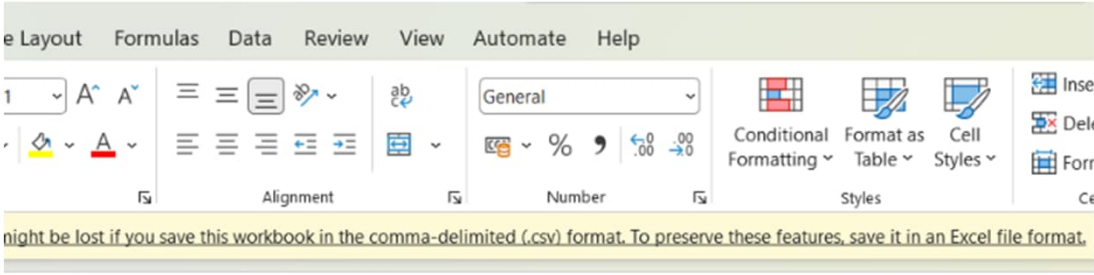
Preparation

Inventory table

Steps 1–2 · P1–P5

1 Check your own table

2 Prepare it — only where needed



	E	F	G	H	I	J	K	L	M	N	O
S84	y_WGS84	coord.poin	x_WGS84_	y_WGS84_	species_fu	lang	DBH	plant_year			
5429	41.9816	yes	12.06591	41.98326	Acer negur	Italian	30	NA			
5879	41.97918	yes	12.06591	41.98326	Acer negur	Italian	31	NA			
5375	41.97931	yes	12.06591	41.98326	Acer negur	Italian	45	NA			
5895	41.97453	yes	12.06591	41.98326	Acer negur	Italian	35	NA			
5494	41.97549	yes	12.06591	41.98326	Acer sp.	Italian	33	NA			
9976	41.99662	yes	12.06591	41.98326	Ailanthus a	Italian	58	NA			
9903	41.99686	yes	12.06591	41.98326	Ailanthus a	Italian	62	NA			
5881	41.97783	yes	12.06591	41.98326	Albizia julit	Italian	35	NA			
5827	41.97615	yes	12.06591	41.98326	Albizia julit	Italian	40	NA			
5894	41.97633	yes	12.06591	41.98326	Albizia julit	Italian	30	NA			
5254	41.98248	yes	12.06591	41.98326	Albizia julit	Italian	30	NA			
0531	41.98245	yes	12.06591	41.98326	Albizia julit	Italian	20	NA			
6177	41.97937	yes	12.06591	41.98326	Albizia julit	Italian	21	NA			
5691	41.97628	yes	12.06591	41.98326	Betula pen	Italian	30	NA			
9938	41.99817	yes	12.06591	41.98326	Cedrus atl	Italian	34	NA			
9931	41.99811	yes	12.06591	41.98326	Cedrus atl	Italian	44	NA			
9941	41.99803	yes	12.06591	41.98326	Cedrus atl	Italian	47	NA			
9945	41.99814	yes	12.06591	41.98326	Cedrus atl	Italian	39	NA			
7774	41.98851	yes	12.06591	41.98326	Cedrus atl	Italian	21	NA			
8989	41.99163	yes	12.06591	41.98326	Cedrus atl	Italian	60	NA			
8992	41.99161	yes	12.06591	41.98326	Cedrus atl	Italian	50	NA			
8952	41.99124	yes	12.06591	41.98326	Cedrus atl	Italian	55	NA			
8621	41.98692	yes	12.06591	41.98326	Cedrus atl	Italian	29	NA			
5475	41.98251	yes	12.06591	41.98326	Cedrus atl	Italian	40	NA			
5497	41.9808	yes	12.06591	41.98326	Cedrus atl	Italian	55	NA			

Step P1

Check your own table

Open your inventory as it is. Find each column below and note its name — you pick the same names in QGIS (A6) and in the app (B5).

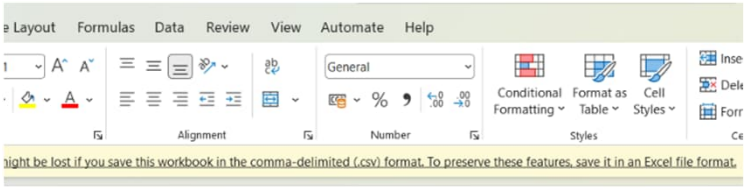
What	What it looks like	Name in your file	Needed for
Species	Latin names, e.g. *Tilia cordata*, *Acer* sp. Often called species, species_full, specie, Art.	_____	Required — every analysis
Genus	Tilia	_____	10–20–30 and Melbourne at genus level
Family	Malvaceae	_____	10–20–30 and Melbourne at family level
DBH	Trunk diameter. Which unit: cm, mm or circumference?	_____ unit: ____	Size classes and basal area
Frequency	Number of trees per row — only in species-count tables.	_____	Species-count datasets
x / y	Coordinates — or a spatial file (SHP, GPKG, GeoJSON).	_____	The map in QGIS

File formats
SHP · GPKG · GeoJSON · CSV · XLSX all open in the QGIS plugin. In an XLSX, keep the data on the first sheet.

Nothing to rename or copy
Only species is required. Missing columns simply leave out those analyses. The next slide shows a real example.

Example inventory and the information required for a complete report

An example municipal tree inventory. The table on the right shows the variables used by the Shiny app and indicates which are already available in this dataset.



S84	y_WGS84	coord.poin	x_WGS84_	y_WGS84_	species_fu	lang	DBH	plant_year
5429	41.9816	yes	12.06591	41.98326	Acer negur	Italian	30	NA
5879	41.97918	yes	12.06591	41.98326	Acer negur	Italian	31	NA
5375	41.97931	yes	12.06591	41.98326	Acer negur	Italian	45	NA
5895	41.97453	yes	12.06591	41.98326	Acer negur	Italian	35	NA
5494	41.97549	yes	12.06591	41.98326	Acer sp.	Italian	33	NA
9976	41.99662	yes	12.06591	41.98326	Ailanthus a	Italian	58	NA
9903	41.99686	yes	12.06591	41.98326	Ailanthus a	Italian	62	NA
5881	41.97783	yes	12.06591	41.98326	Albizia julit	Italian	35	NA
5827	41.97615	yes	12.06591	41.98326	Albizia julit	Italian	40	NA
5894	41.97633	yes	12.06591	41.98326	Albizia julit	Italian	30	NA
5254	41.98248	yes	12.06591	41.98326	Albizia julit	Italian	30	NA
0531	41.98245	yes	12.06591	41.98326	Albizia julit	Italian	20	NA
5177	41.97937	yes	12.06591	41.98326	Albizia julit	Italian	21	NA
5691	41.97628	yes	12.06591	41.98326	Betula pen	Italian	30	NA
9938	41.99817	yes	12.06591	41.98326	Cedrus atl	Italian	34	NA
9931	41.99811	yes	12.06591	41.98326	Cedrus atl	Italian	44	NA
9941	41.99803	yes	12.06591	41.98326	Cedrus atl	Italian	47	NA
9945	41.99814	yes	12.06591	41.98326	Cedrus atl	Italian	39	NA
7774	41.98851	yes	12.06591	41.98326	Cedrus atl	Italian	21	NA
9989	41.99163	yes	12.06591	41.98326	Cedrus atl	Italian	60	NA
9992	41.99161	yes	12.06591	41.98326	Cedrus atl	Italian	50	NA
9952	41.99124	yes	12.06591	41.98326	Cedrus atl	Italian	55	NA
9621	41.98692	yes	12.06591	41.98326	Cedrus atl	Italian	29	NA
5475	41.98251	yes	12.06591	41.98326	Cedrus atl	Italian	40	NA
5497	41.9808	yes	12.06591	41.98326	Cedrus atl	Italian	55	NA

Variables required by the Shiny app

Column	Needed for	In this inventory
Species	Taxonomic harmonisation, pest–host screening	species_full
Genus	Genus limit; 10–20–30 rule	- (added by plugin)
Family	Family limit; Melbourne check	- (added by plugin)
DBH (cm)	Size classes, basal area	DBH
Frequency	Species-count datasets only	- (nor needed)
x / y	QGIS map, Tool 1 only	x_WGS84 / y_WGS84

What is missing, and why it matters

Species and DBH are sufficient for the dataset summary, species-frequency analysis, top-10 assessment, DBH distribution, basal area and pest–host screening.

Step P2

Is your table ready?

Answer five questions about your own table. Fix only what gets a NO.

	Question	If the answer is no	
1	**Is the header in row 1 of the first sheet?**	Delete title rows above it; move the data to the first sheet.	**P4 · slide 12 ›**
2	**Is every tree in its own row?**	A species-count table is fine — choose ‘Species frequencies’ in B5. Mixed rows: see P3.	**P3 · slide 11 ›**
3	**Are species names in their own column, one per cell, without notes?**	Move notes to another column; split cells with two species.	**P3 · slide 11 ›**
4	**Is DBH a number in centimetres — or is there no DBH?**	Convert mm or circumference; remove ‘cm’ text from the cells.	**P4 · slide 12 ›**
5	**Are there no merged cells, totals or empty rows in the list?**	Unmerge, then delete totals and empty rows.	**P4 · slide 12 ›**

✓ **All yes**

Your table is ready. Save it if you changed anything (P5) and continue with Step 3 — install QGIS and the plugin.

Step 3 · slide 16 ›

★ **Very messy, or not in a table yet?**

Start from the FREE3 template or try fixing the old file.

Template · slide 13 ›

Step P3 · if needed

Standardise the values

Write every cell of a column the same way. Column names here are examples, keep your own.

Column	Write it like this	Avoid
species	Tilia cordata · Platanus × hispanica · Acer platanoides 'Crimson King' · Acer sp.	common names only (lime), two species in one cell, notes such as ‘dead?’
genus / family	Tilia · Malvaceae — one word, capital first letter	abbreviations (Mal.), mixed languages, empty for some rows only
dbh_cm	34.5 — a number, in centimetres, one value per tree	‘34 cm’, ranges (30–40), mm or circumference values, 0 for unknown
frequency	12 — whole number, species-count datasets only	text, decimals, a value on individual-tree rows
x / y	12.1012 / 41.9935 — decimal degrees, WGS84 (x = longitude)	degrees-minutes-seconds, swapped x and y, mixed coordinate systems
empty values	leave the cell empty	n/a, –, 0, ‘unknown’, ‘?’
non-tree rows	move to a separate sheet	stumps, empty planting pits and totals inside the tree list

Standardise the structure, not the spelling

Small spelling variants and synonyms are corrected by the plugin in Step A6. Your job is clean, consistent cells.

Step P4 · if needed

Clean the table in Excel

Work on a copy of the original file. Each line is a menu path in Excel for Windows or Mac.

1	**Unmerge cells**	**Select all** (Ctrl + A) › **Home** › **Merge & Center** › **Unmerge Cells**
2	**Remove stray spaces**	**Empty column: =TRIM(B2)** › **fill down** › **Copy** › **Paste Values over species**
3	**Fill or delete rows without species**	**Data** › **Filter** › **species header arrow** › **(Blanks)** › **fill in or delete**
4	**Turn text into numbers**	**Select the DBH cells** (green corner = text) › **warning icon** › **Convert to Number**
5	**Convert DBH to cm**	**Empty column: =E2/10** (from mm) › **or =E2/PI()** (from circumference) › **fill down** › **Paste Values over dbh_cm**
6	**Spot typos in genus and family**	**Data** › **Filter** › **genus header arrow** — look for near-duplicates (Tilia / tilia)
7	**Delete everything that is not a tree**	Totals, notes, extra header rows, empty rows at the bottom.

! **Don’t use ‘go to special › blanks › delete row’**
It also deletes real trees that only have an empty DBH cell. Filter on the species column instead (line 3).

★ **Stop Excel turning numbers into dates**
Before pasting, select the DBH, x and y columns › Home › Number Format › ‘Number’.

Optional

Start from the template

Only if your table is very messy or not digital yet. Otherwise skip this page, your own table works as it is.

	A	B	C	D	E	F	G	H
1	**tree_id**	**species**	**genus**	**family**	**dbh_cm**	**frequency**	**x**	**y**
2	T0001	Tilia cordata	Tilia	Malvaceae	34.5		12.1012	41.9935
3	T0002	Platanus × hispanica	Platanus	Platanaceae	61		12.1018	41.9941
4	T0003	Acer platanoides 'Crimson King'	Acer	Sapindaceae	18		12.1025	41.9930
5	T0004	Quercus ilex	Quercus	Fagaceae	47.2		12.1031	41.9927

Row 1 = headers only

One header row with short, unique names. No title, logo or empty row above it.

One row = One tree

Each tree gets its own row and a unique tree_id. Leave frequency empty.

Then continue with P5

Paste your data as values from cell A2 (Home › Paste › Paste Values), then save.

Species counts instead of individual trees?

Use one row per species, put the number of trees in frequency, and leave dbh_cm, x and y empty. Choose ‘Species frequencies’ as dataset type in Step B5.

Step P5

Check and save the table

If you changed anything, run through this list once more and save. Then go to Step 3.

Checklist

- [ ] Data is on the first sheet; the header is in row 1
- [ ] Column names are short and unique
- [ ] One tree per row (or one species per row with a frequency)
- [ ] Every row has a species name
- [ ] No merged cells, totals, notes or empty rows in the list
- [ ] DBH is a number in centimetres
- [ ] Unknown values are empty cells
- [ ] Coordinates, if present, are decimal degrees in WGS84

Save it

File › Save As › Excel Workbook (*.xlsx)

Name it with place and date:
city_inventory_2026-10_clean.xlsx

Keep the original file untouched in the same folder, so the cleaning can be checked later.

You don’t need to make the CSV yourself
The plugin reads .xlsx directly. The CSV for the Shiny app is written by QGIS in Step A14, with the harmonised names already in it.

Part A

The QGIS plugin

Steps 3–7 · A1–A14

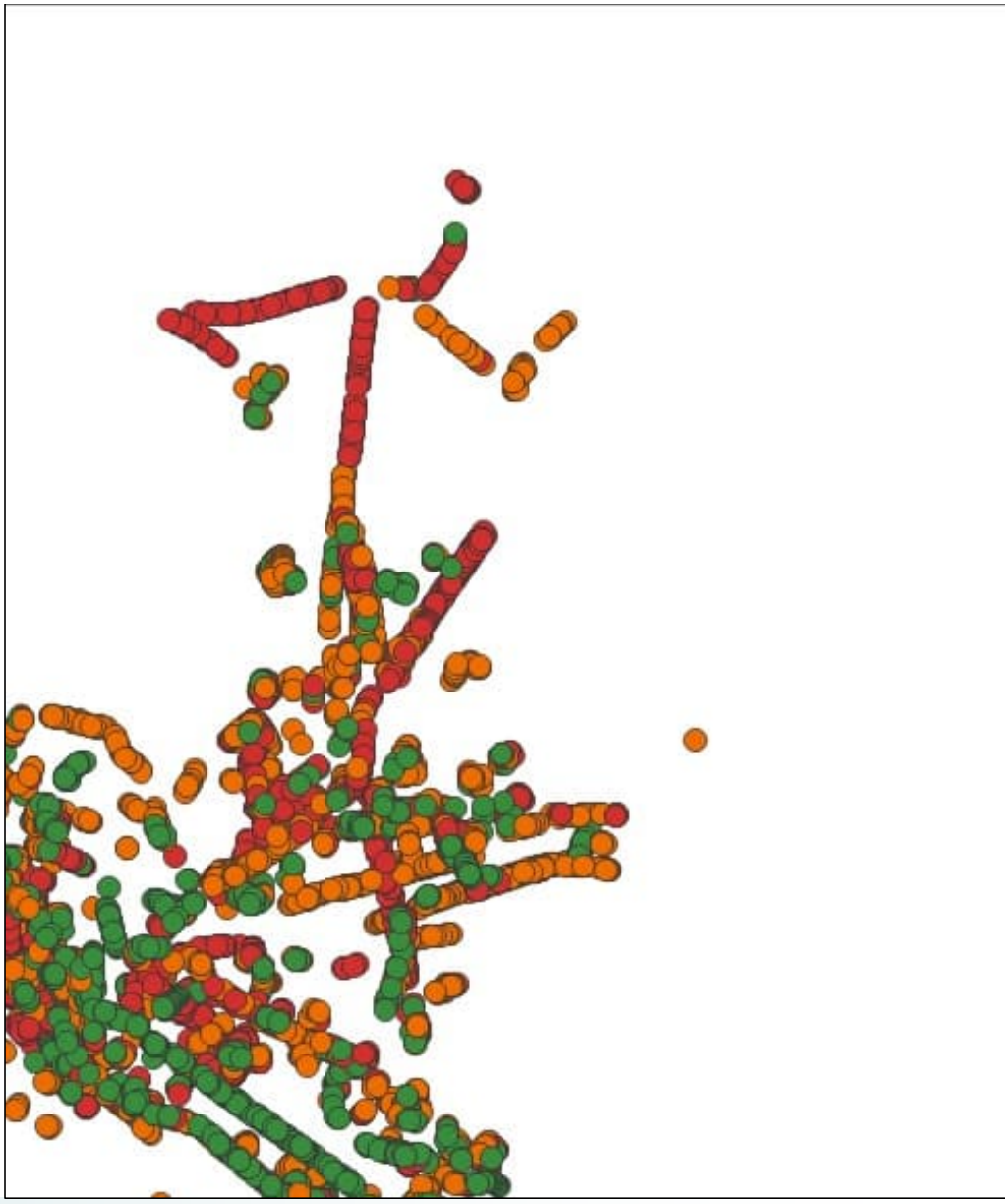
3 Install QGIS and the plugin

4 Harmonise names

5 Check the matches

6 Screen for pest hosts

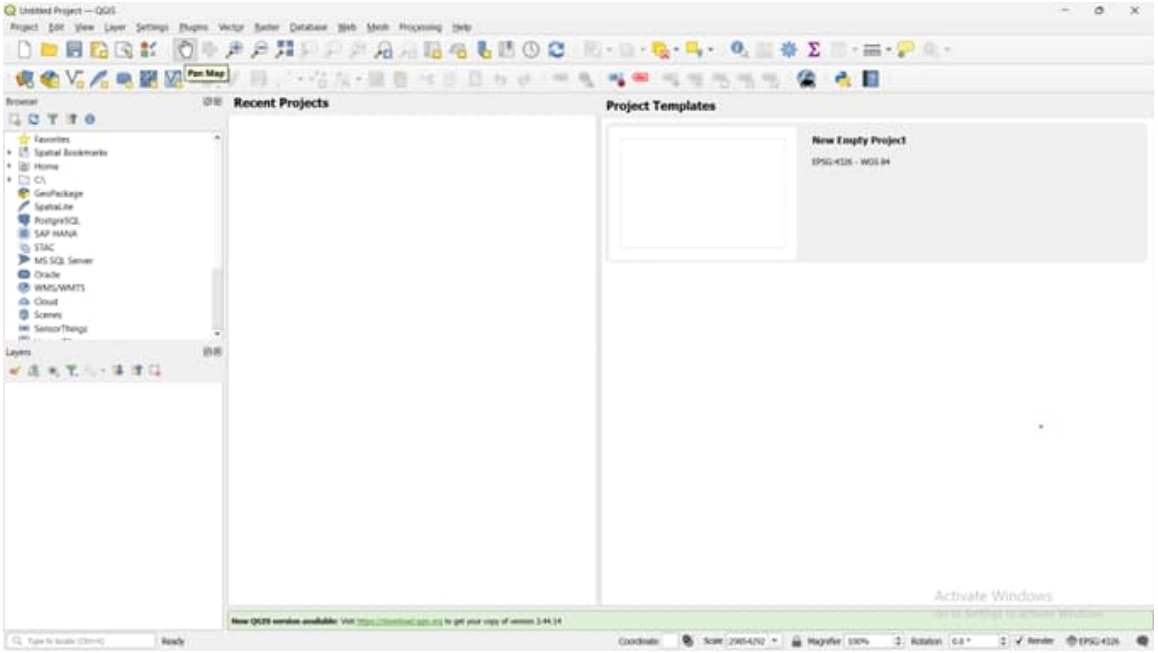
7 Export the CSV



Step A1

Install QGIS

1. **Open qgis.org in a browser.**
2. **Download the long-term release (LTR) for your operating system. The LTR is more stable than the latest release and is what the plugin is tested against.**
3. **Run the installer** and accept the default options.
   The download is relatively large, so installation may take a few minutes.
4. **Open QGIS.** The start screen will display “Recent Projects”.
   You do not need to create a project before using the plugin.



What is QGIS?
A free, open-source geographic information system used to view and work with spatial data. The FREE3 plugin runs within QGIS, and no previous GIS experience is required.

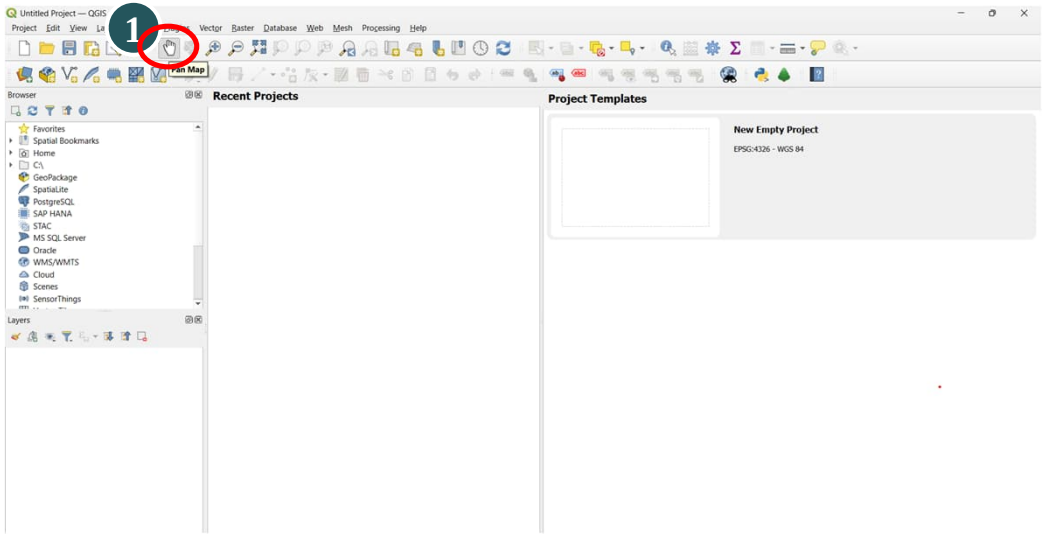
Already have QGIS?
Skip to Step A2. If the plugin does not install, check your QGIS version under Help → About.

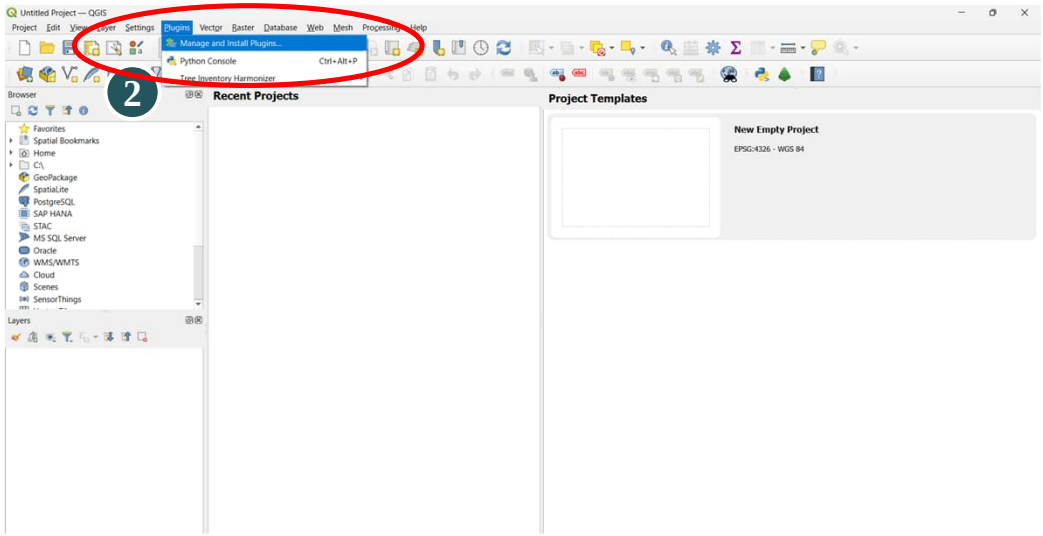
Step A2

Open the Plugin Manager

1. **In the QGIS menu bar, click 'Plugins'.**

2. **Choose 'Manage and Install Plugins…'** The Plugins dialog opens. This is where every QGIS add-on is installed and switched on.





> **Note**
> The 'Plugins' menu is always in the top menu bar, between ‘Settings' and 'Vector'. It does not depend on having a project or a map open.

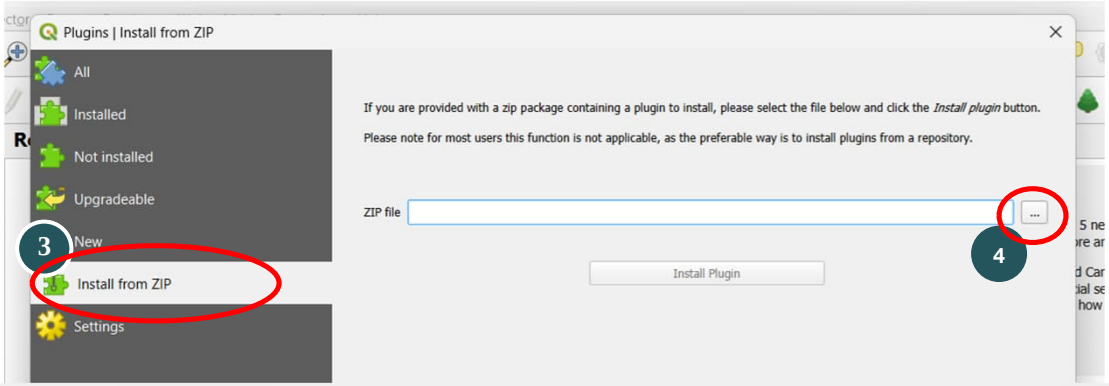
Step A3

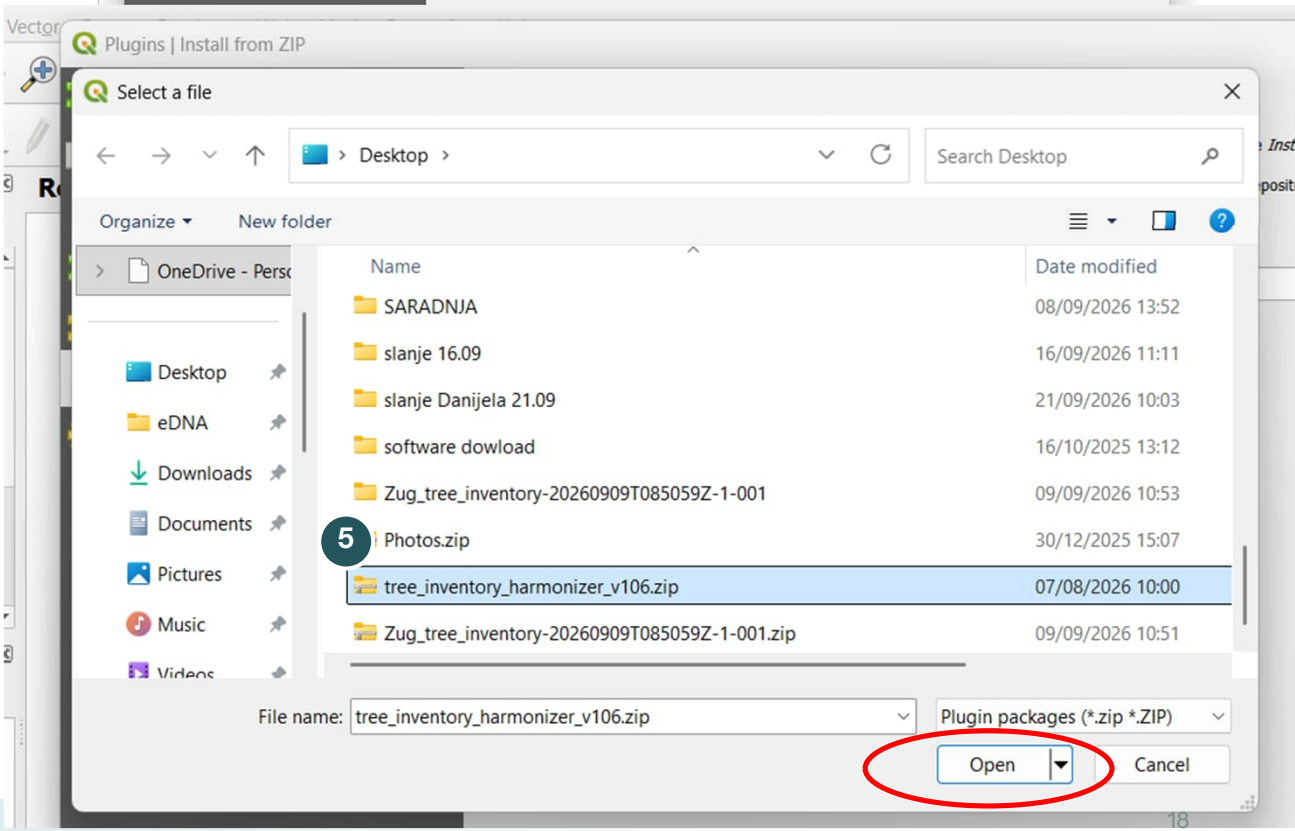
Install the plugin from the ZIP file

3 **In the left-hand list of the Plugins dialog, click 'Install from ZIP'.**

4 **Click the '…' button** at the end of the 'ZIP file' field to browse your computer.

5 **Select tree_inventory_harmonizer_….zip** and click 'Open'. The file type shown should be 'Compressed (zipped) Folder'.





! Do not unzip the file

QGIS installs the plugin from the ZIP archive itself. If you extract it first there will be no .zip to select and pointing at the extracted folder will not work.

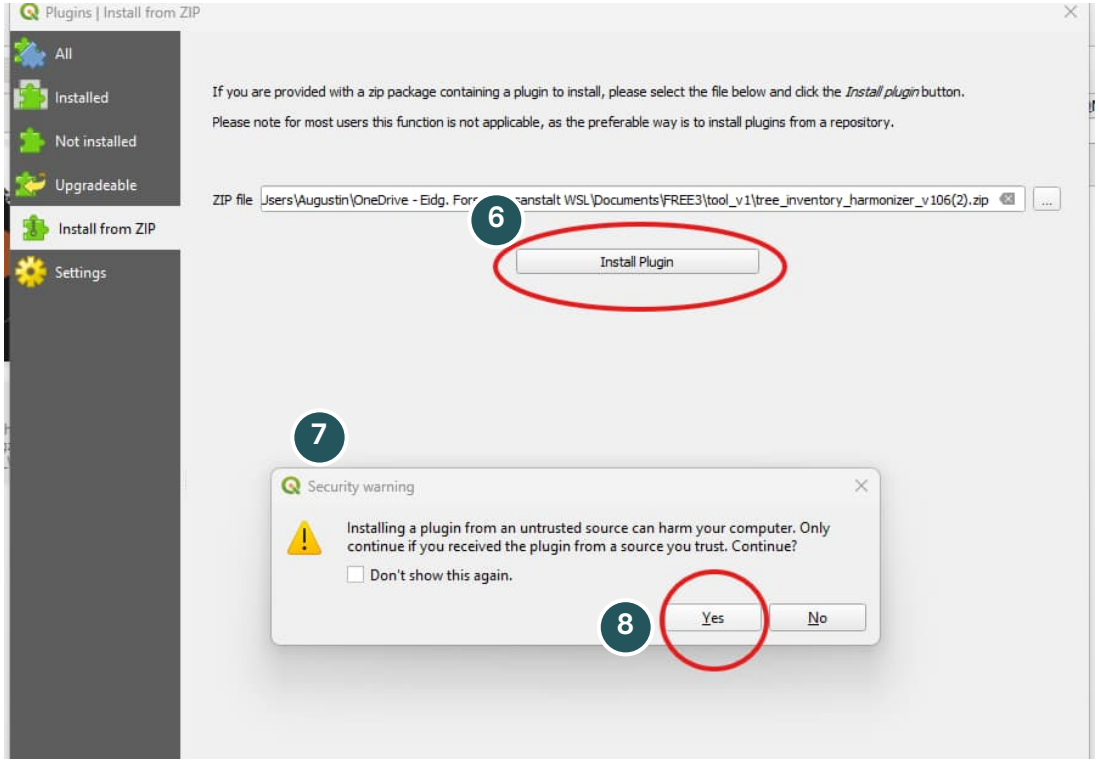
Step A4

Confirm the installation

6 **Click 'Install Plugin'.**

7 **A 'Security warning' appears.** QGIS shows this for every plugin installed from a ZIP file rather than from the official repository. It is not a sign that anything is wrong.

8 **Click 'Yes' to continue.** Installation takes a few seconds. You can then close the Plugins dialog.



Why the warning appears

Plugins from the QGIS repository are reviewed centrally; a ZIP could come from anywhere, so QGIS asks you to confirm you trust the source. Only continue if you received the ZIP from the FREE3 team.

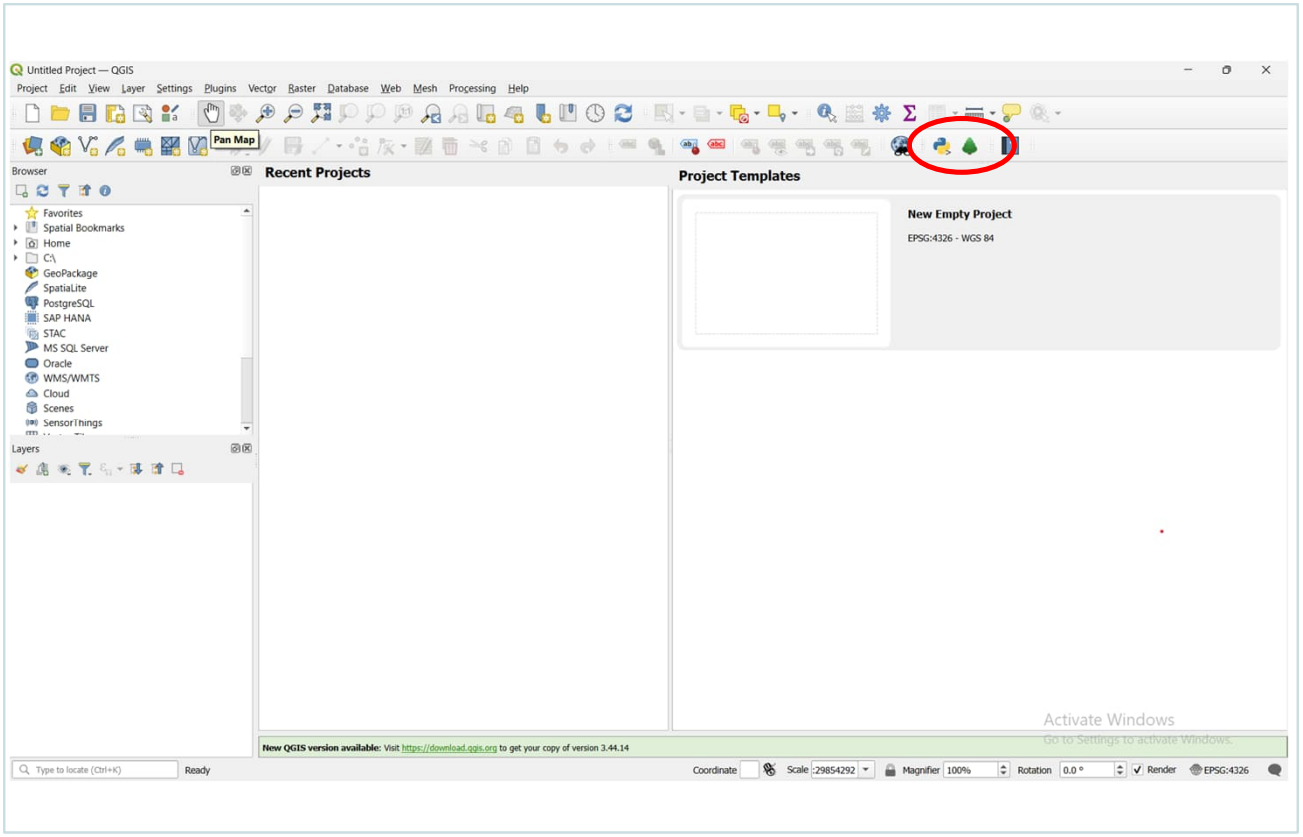
Tip

Leave 'Don't show this again' unticked so the check still runs for other plugins.

Step A5

Check that the plugin is installed

A new button should appear in the QGIS toolbar. Use this button to open the Tree Inventory Harmonizer.





Look for this button

A small green tree icon should appear in the QGIS toolbar.

Button not there?

If the button does not appear
Try the following:
Restart QGIS.
Open **Plugins → Manage and Install Plugins → Installed** and make sure **Tree Inventory Harmonizer** is enabled.
Check **View → Toolbars** and make sure the plugin toolbar is visible.
If installation failed, return to the Plugins window and check the error message.

Step A6

Harmonise your species names

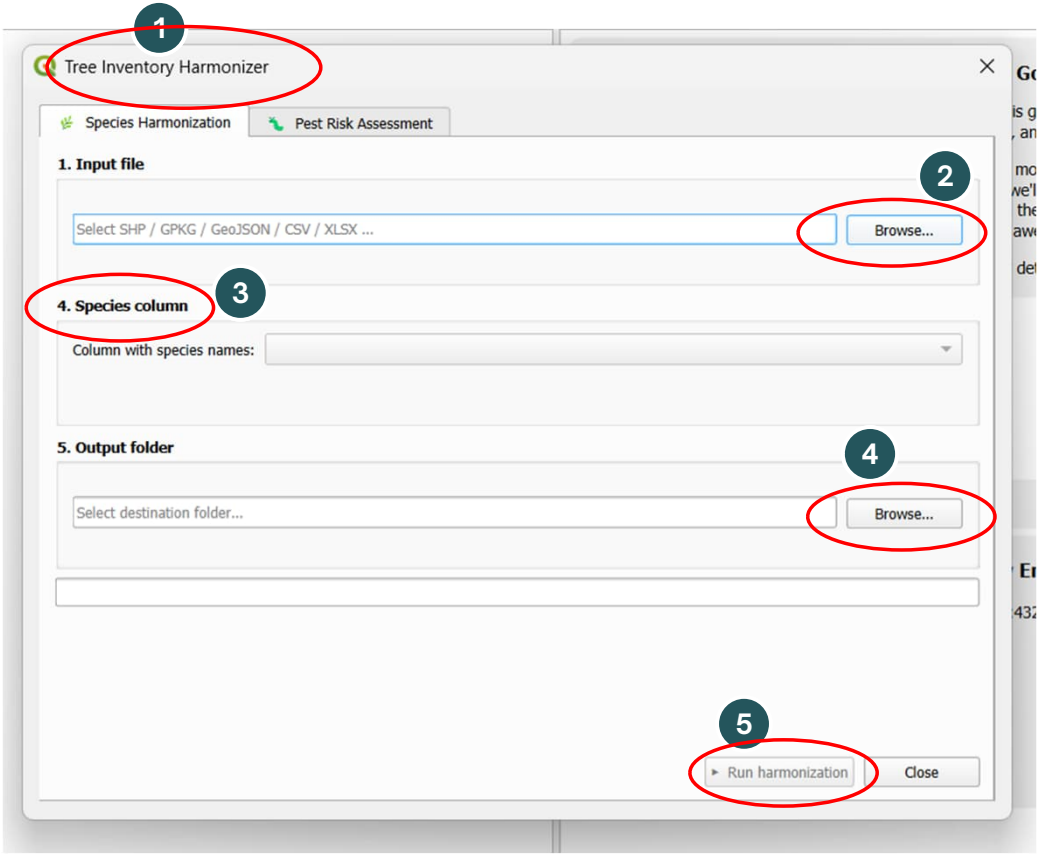
1. **Click the plugin button** in the toolbar. The 'Tree Inventory Harmonizer' window opens on the 'Species Harmonization' tab.

2. **Input file — 'Browse…'** and select your tree inventory. SHP, GPKG, GeoJSON, CSV and XLSX all work.

3. **Species column** — choose the column that holds the species names — the name you noted in Step P1.

4. **Output folder — 'Browse…'** and choose where the results should be written. This field is obligatory.

5. **Click 'Run harmonization'.** A progress bar runs to 100%. Large inventories take a minute or two.



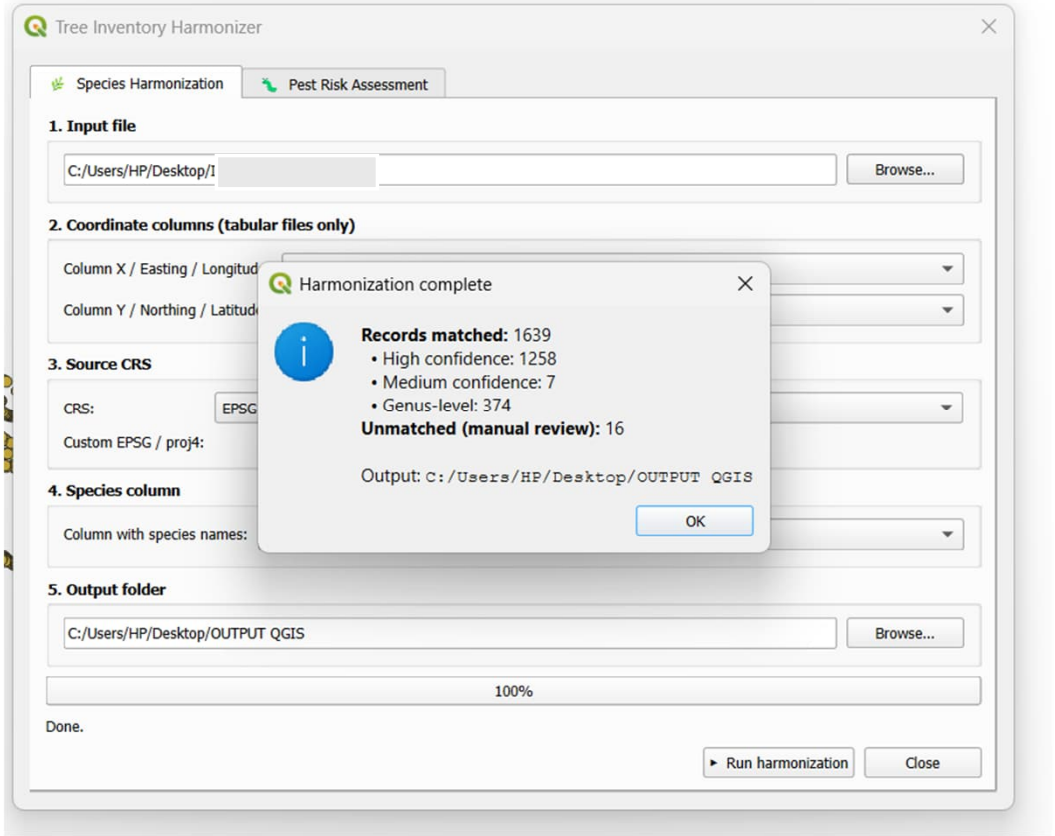
★ **Use an empty folder**

The plugin writes several files. Giving each city or each run its own folder keeps the outputs from overwriting one another.

Step A7

Read the harmonisation result

After harmonisation, the plugin reports how many records were matched and the confidence level of each match.



How to interpret the harmonisation results

Line	Meaning	Recommended action
High confidence	Exact match to an accepted species name, or an unambiguous correction.	None
Medium confidence	Match based on a synonym, cultivar suffix or likely spelling error.	Spot-check
Genus-level	Only the genus could be resolved; screening is therefore less specific.	Spot-check
Unmatched	No reliable match was found. These records are not included in pest–host screening.	Review

Unmatched records have not been screened

Unmatched records are not assigned a pest–host class because their species names could not be reliably resolved. Review these records before interpreting the screening results.

Pests included in the host screening

Each harmonised tree record is screened against 11 regulated pests after taxonomic name matching to the reference dataset.

PEST	COMMON NAME	ORGANISM GROUP
Agrilus planipennis	emerald ash borer	Insect
Anoplophora glabripennis	Asian longhorned beetle	Insect
Anoplophora chinensis	citrus longhorned beetle	Insect
Aromia bungii	red-necked longhorn beetle	Insect
Bursaphelenchus xylophilus	pine wood nematode	Nematode
Ceratocystis platani	canker stain of plane	Ascomycete
Dendrolimus sibiricus	Siberian silk moth	Insect
Phytophthora ramorum	sudden oak death	Oomycete
Popillia japonica	Japanese beetle	Insect
Rhynchophorus ferrugineus	red palm weevil	Insect
Xylella fastidiosa	olive quick decline	Bacteria

Watch out Absence of a match should not be interpreted as absence of risk.

Reference taxonomy

126 families

540 genera

2,219 species

TREE NAME → REFERENCE TAXONOMY → 11 SELECTED PESTS → PEST–HOST MATCH

How this affects the result

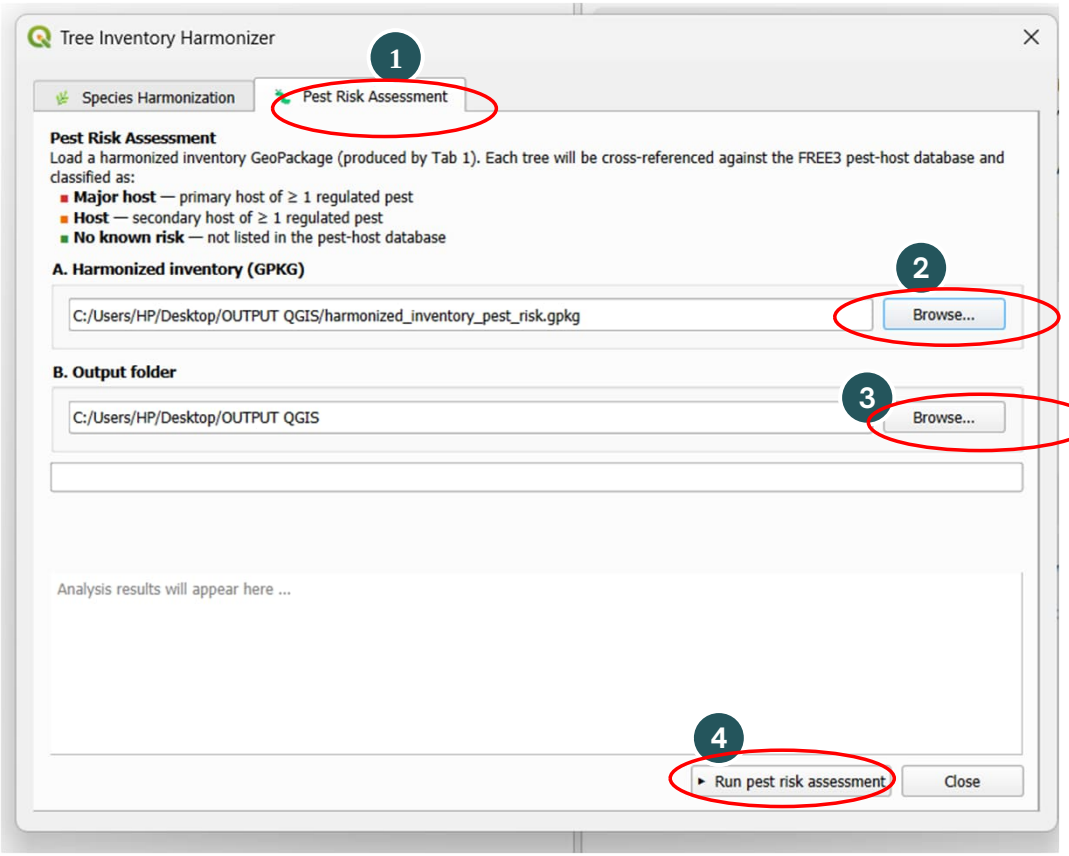
Only the pests listed here are included in the screening. An unresolved tree name, or the absence of a pest from the screening list, should therefore not be interpreted as evidence of no phytosanitary risk.

Step A8

Run the pest risk assessment

1. **Open the 'Pest Risk Assessment' tab** at the top of the plugin window.
2. **Harmonized inventory (GPKG) — 'Browse…'** and select harmonized_inventory.gpkg from the output folder you chose in step A6.
3. **Output folder — 'Browse…'** and choose where the risk results should be written.
4. **Click 'Run pest risk assessment'.** Every tree is cross-referenced against the FREE3 pest-host database and given a screening class.

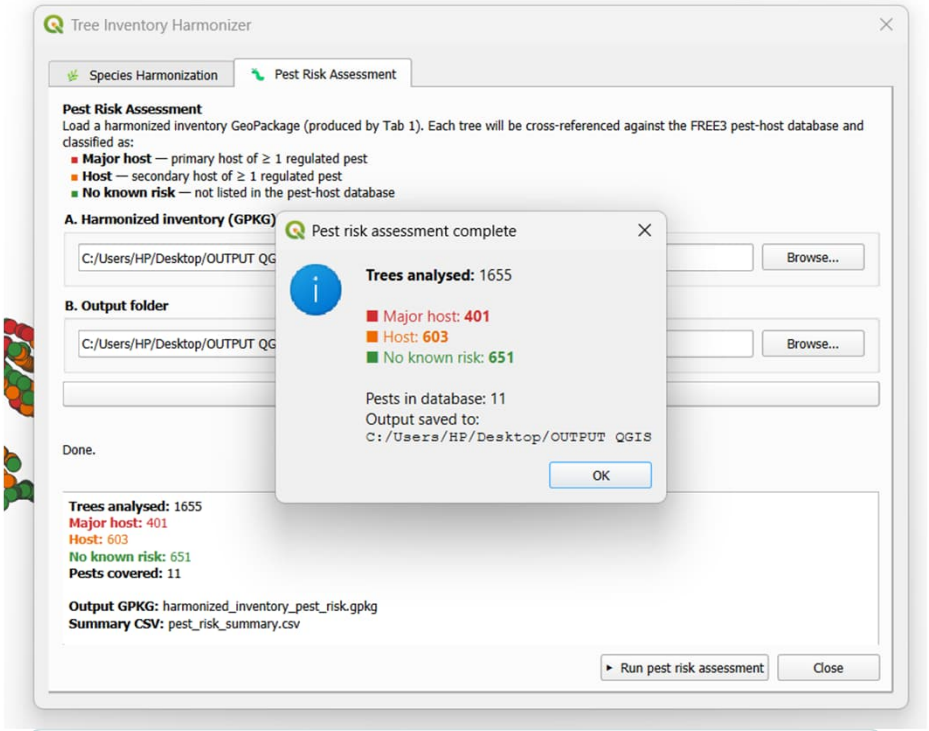
> **! Use the gpkg, not your original file**
> This tab only accepts the harmonised GeoPackage produced by the first tab. Pointing it at your original inventory will fail, because the harmonised species names are not in that file.



Step A9

Read the risk summary

The plugin summarises the screening results and adds a colour-coded layer to the QGIS map.



Check the totals add up

Major host + Host + No known risk should equal the total number of trees analysed. If not, repeat Step A8.

The three screening classes

Major host

Primary host of at least one regulated pest.
Highest priority for further inspection and monitoring.

Host

Secondary host of at least one regulated pest.
Potentially relevant for monitoring, depending on the pest and local context.

No known risk

Not listed as a host in the FREE3 pest–host database.
This does not mean that the species is pest-free or risk-free.

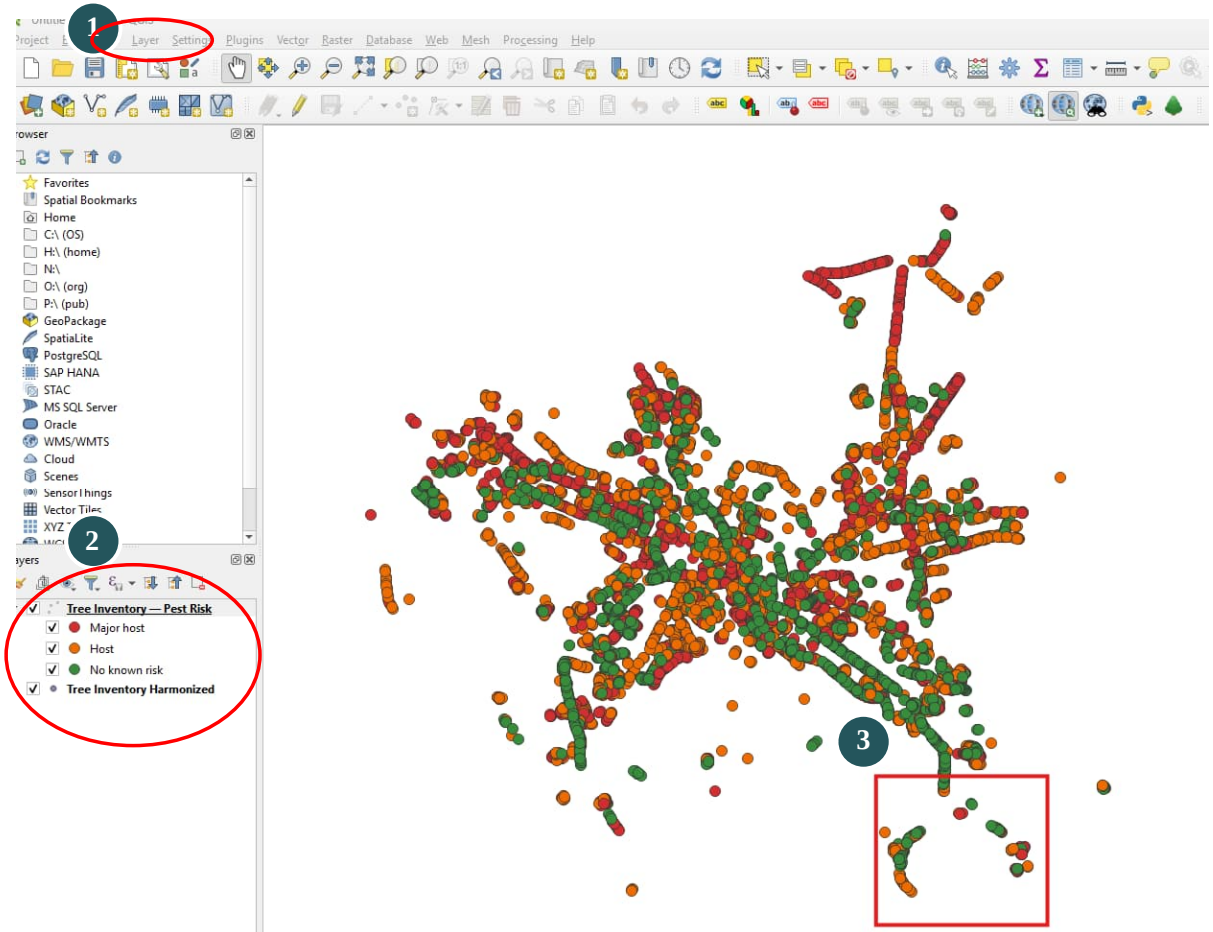
‘No known risk’ means ‘not listed in the database’

Interpret this category as absence of a known pest–host match in the database, not as evidence that the tree is safe from pests.

Step A10

Read the risk map

The plugin adds a layer called ‘Tree Inventory - Pest Risk’ allowing you to explore spatial patterns across the inventory.



1. **Find the new layer** in the *Layers* panel. It appears above the harmonised inventory.

2. **Read the legend** under the layer name: *Major host*, *Host* and *No known risk*.

3. **Look for spatial clusters** of red and orange trees. These may indicate areas where pest–host associations are concentrated.

Too many points to interpret?

Temporarily hide the ‘No known risk’ class in the layer legend to make spatial patterns among matched host trees easier to see.

Colour vision

Red, orange and green can be difficult to distinguish for some readers. When exporting figures, identify the classes in the caption as well as by colour.

Step A11

Zoom in

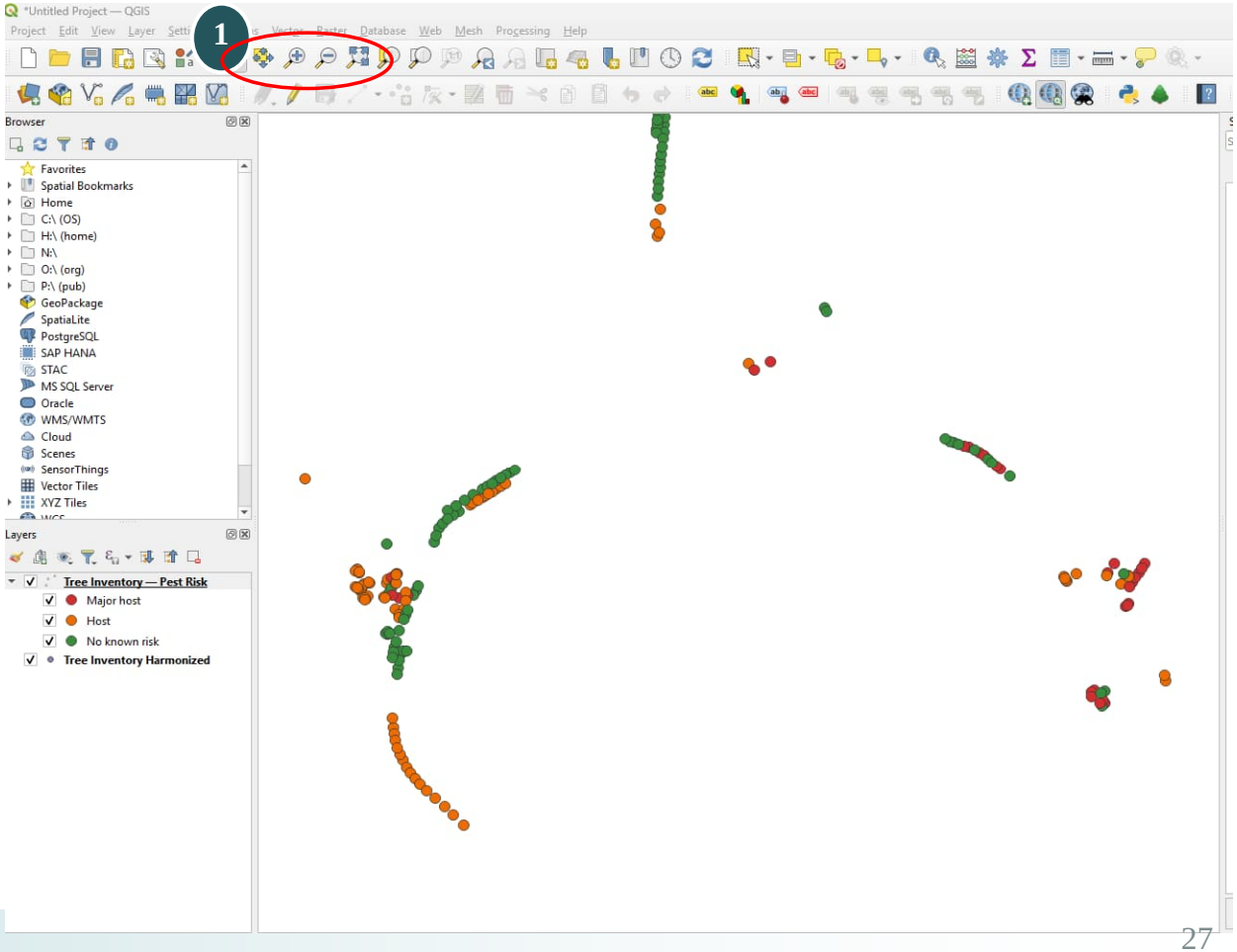
Zoom in to examine local clusters and individual trees.

1 **Scroll the mouse wheel** over the map to zoom in or out, or use the zoom buttons in the QGIS toolbar. **Hold down the mouse wheel** and drag to pan across the map. **Zoom in until individual trees are clearly visible.**
This makes local spatial patterns easier to examine.

Get back to the whole city
Right-click the layer in the 'Layers' panel and choose 'Zoom to Layer(s)' to fit the full inventory in the window again.

Add a background map

Streets and parks make clusters easier to read. See Step A12.

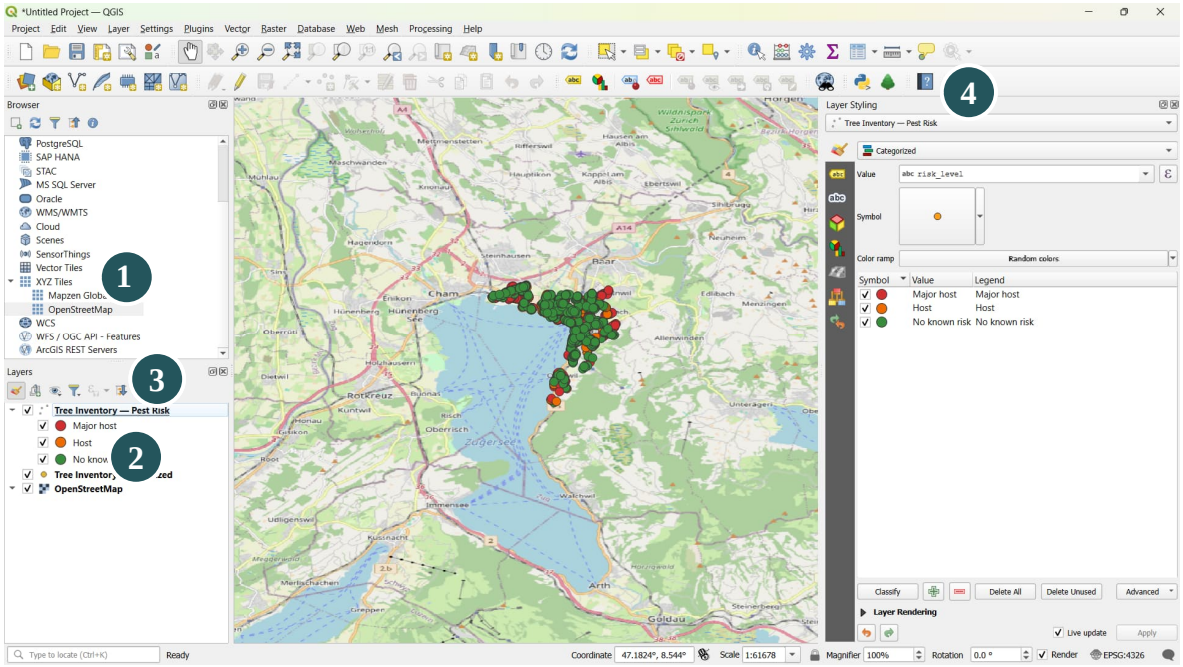


Step A12

Add a basemap

A basemap provides spatial context and helps you relate tree locations to streets, parks and other features.

1. **In 'Browser', open 'XYZ Tiles'** and double-click 'OpenStreetMap'.
2. **Drag 'OpenStreetMap' to the bottom** of the 'Layers' panel, below both tree layers.
3. **If the trees disappear,** right-click the tree layer and choose 'Zoom to Layer(s)'.
4. **Reduce the basemap opacity** select 'OpenStreetMap' in the Layer Styling panel, open 'Transparency' and set 'Global Opacity' to 50–60%.



Layer order

Top: Tree Inventory — Pest Risk

Middle: Tree Inventory Harmonized

Bottom: OpenStreetMap

Watch out Do not press 'Classify' while editing the layer style, as this may replace the existing red, orange and green screening colours.

Step A13

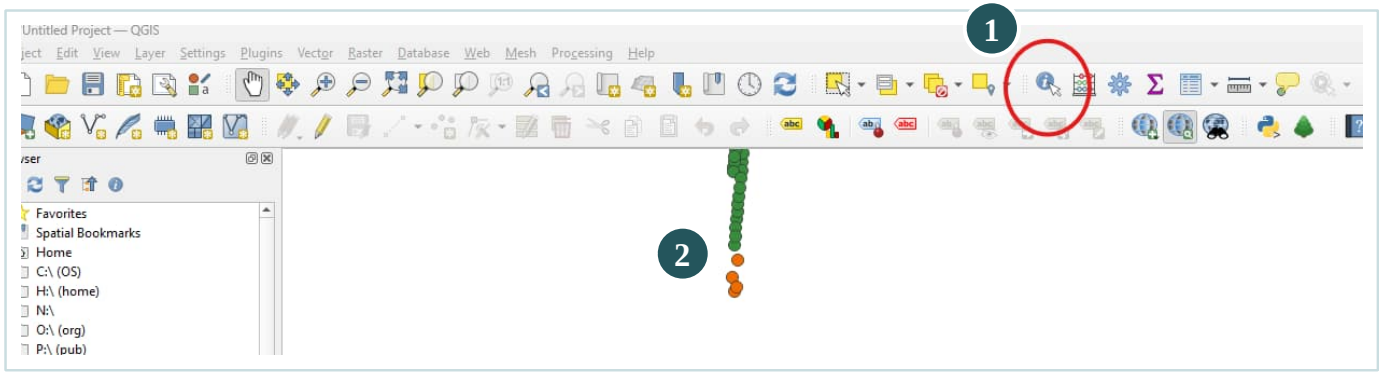
Look up an individual tree

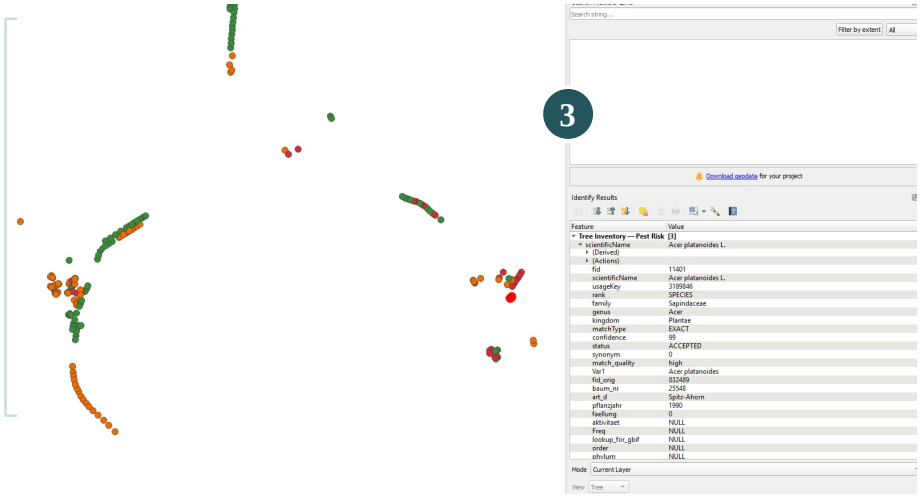
Click a tree on the map to view its attributes, harmonised name and pest–host screening information.

1. **Click the 'Identify Features' tool in the QGIS toolbar.**

2. **Click any tree on the map.** The 'Identify Results' panel opens at the side.

3. **Review the attributes**, including the original record, harmonised species name, match confidence, screening class and associated pests.





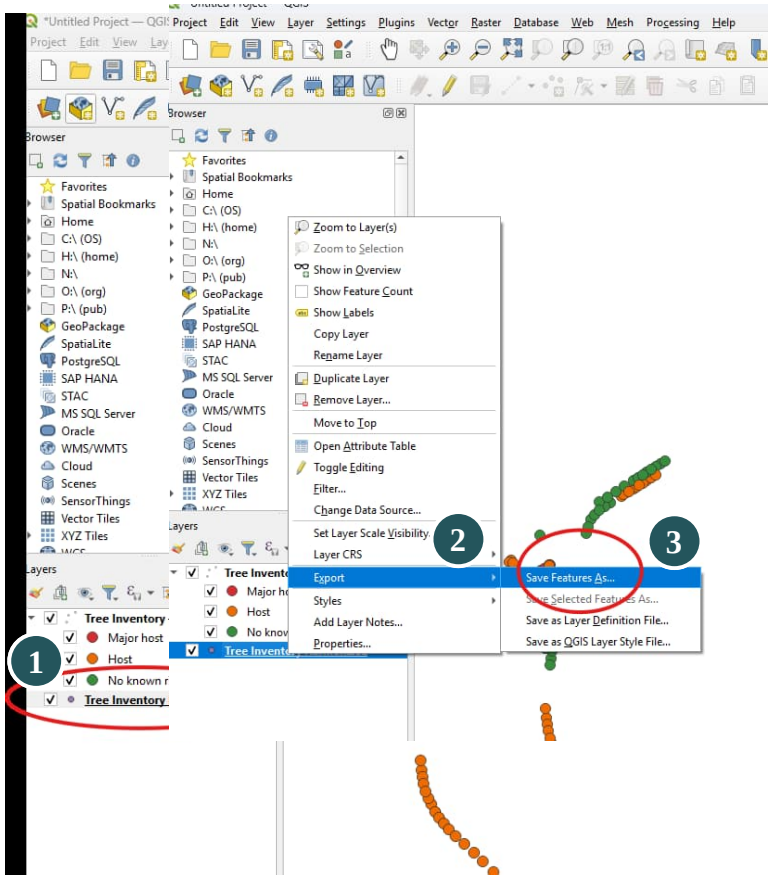
Checking an uncertain match

To verify a medium-confidence or genus-level match, click the tree and compare the original species name with the harmonised name.

Export the harmonised inventory (1 of 2)

The Shiny app accepts CSV files only, so the harmonised layer must first be exported from QGIS.

1. **In the 'Layers' panel, right-click 'Tree Inventory Harmonized'.**
2. **Hover over 'Export'** in the context menu.
3. **Click 'Save Features As…'** The 'Save Vector Layer as…' dialog opens. Continue on the next page.



! Select the correct layer

Export 'Tree Inventory Harmonized', not 'Tree Inventory — Pest Risk'. The harmonised layer is the standard input for the Shiny app. If you also want to retain the screening classes, export the pest-risk layer separately and use clear file names.

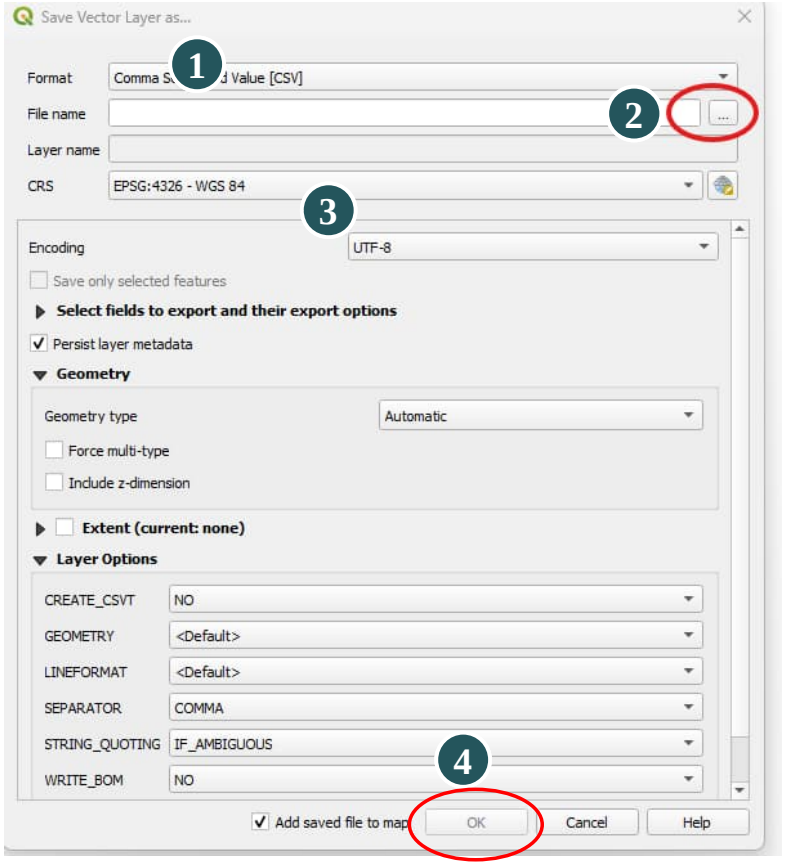
Export the harmonised inventory (2 of 2)

1. **Set 'Format' to 'Comma Separated Value [CSV]'.** This is required for the Shiny app.

2. **Click the '…' button next to 'File name'** and choose where to save the file.

3. **Keep the default settings**, including UTF-8 encoding and EPSG:4326.

4. **Click 'OK'.** Your harmonised inventory is now saved as a .csv and is ready for Part B.



Name the file so you can find it again

Something like city_harmonized_2026.csv. You will be picking this file out of a list in Step B5.

Note

Special characters in species names survive the export as long as encoding stays UTF-8.

Tool 1 output files

The plugin creates four main output files. This table summarises what each file contains and how it is used.

FILE	MADE IN	WHAT IT CONTAINS	USE IT FOR
harmonized_inventory.gpkg	Step A6	The inventory with harmonised species names and match-confidence information added to each record.	Input to step A8
harmonized_inventory_pest_risk.gpkg	Step A8	The harmonised inventory with screening classes and associated pests added to each tree.	Pest–host map and inspection in QGIS
pest_risk_summary.csv	Step A8	Summary counts by screening class and pest for the full inventory.	Reporting and summary statistics
harmonized_inventory.csv	Step A14	The harmonised inventory exported as a CSV file.	Input for the Shiny app

Gpkg?

A GeoPackage (.gpkg) is a single-file format for storing spatial features and their attributes. Unlike a shapefile, which consists of several separate files, a GeoPackage keeps the full layer in one file.

Keep the run together

Keep the output folder together with a copy of the input file and the date of the analysis. This makes it easier to reproduce the results later if needed.

Part B

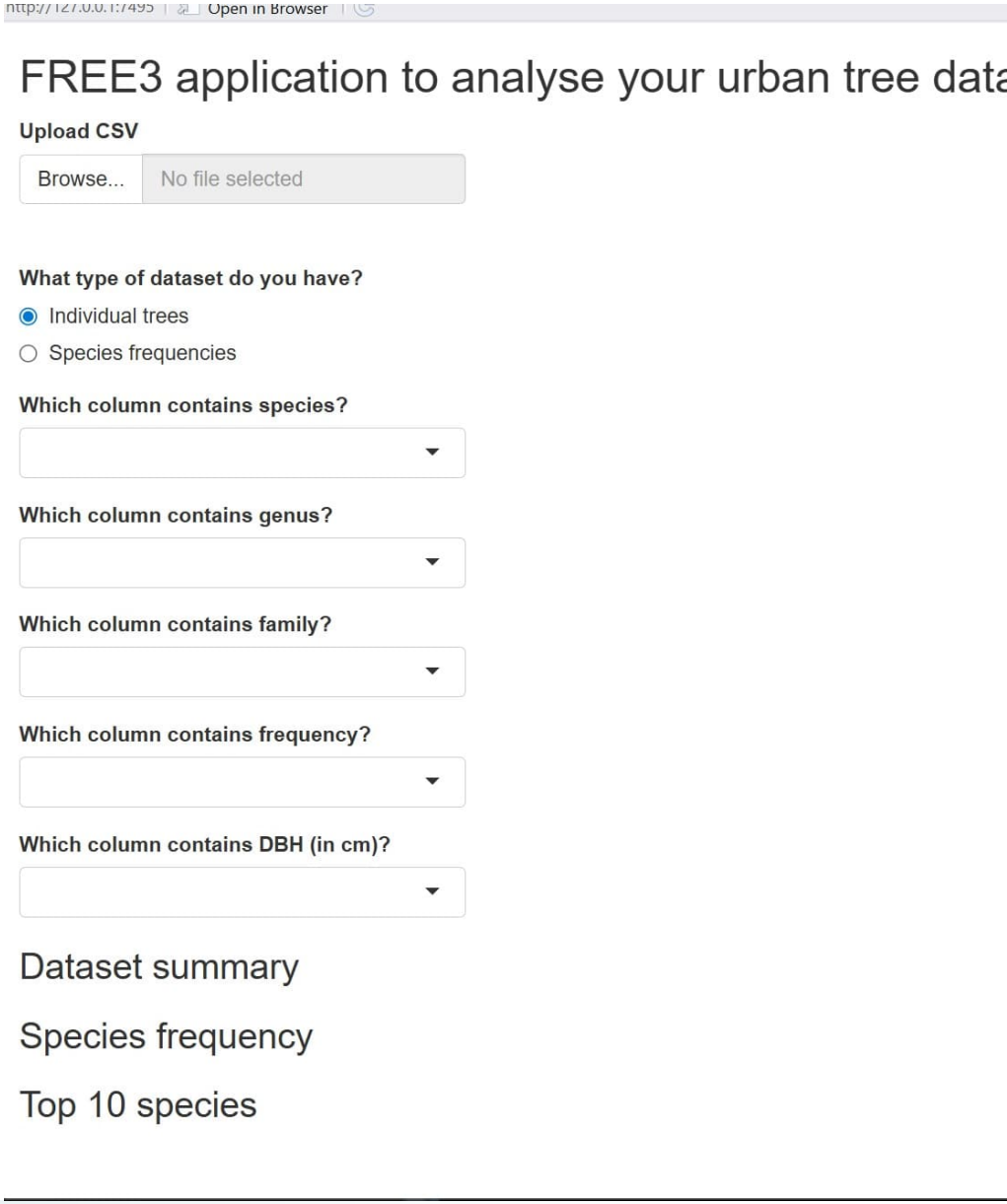
The Shiny app

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.

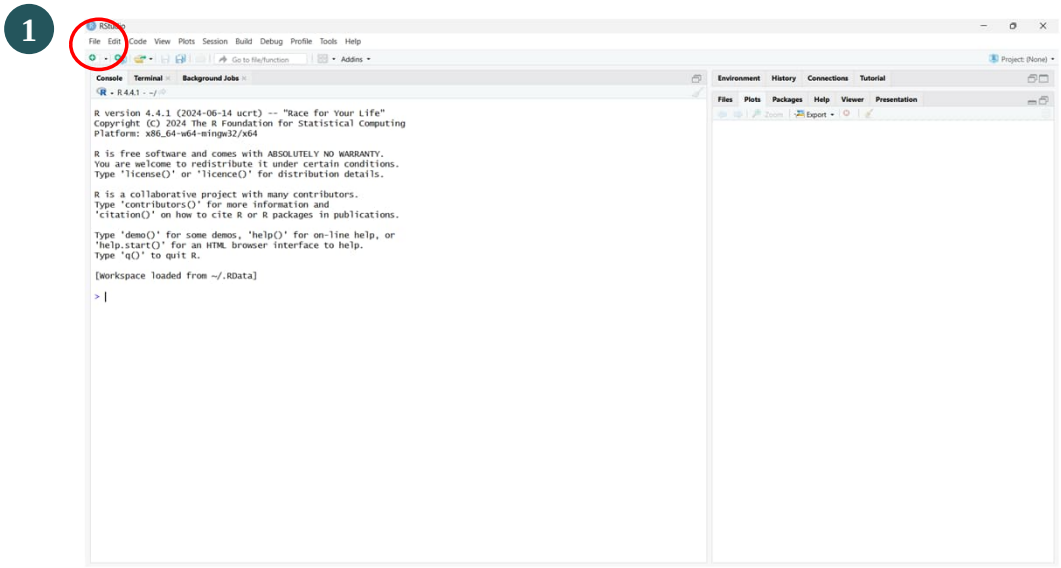
Step B2

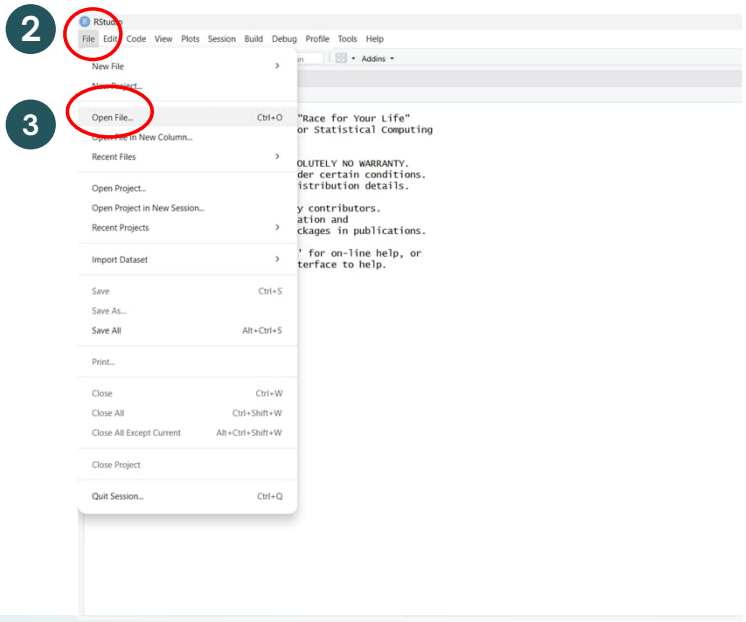
Open the app file in RStudio

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.

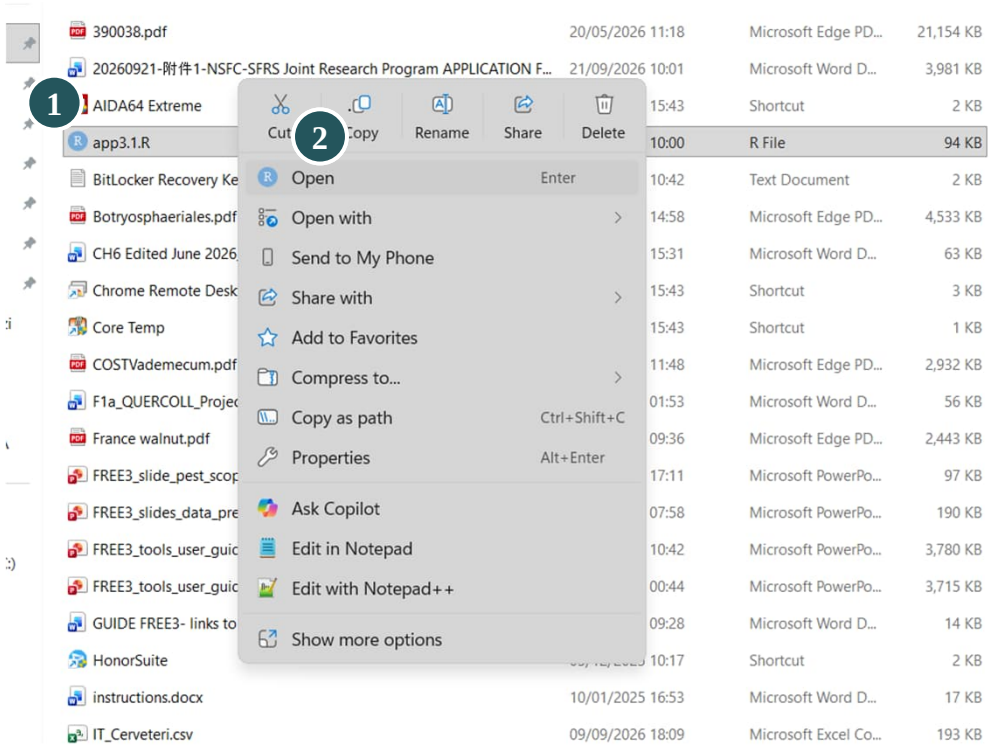
> **★** **Next time**
>
> After the file has been opened once, you can access it from 'File' › 'Recent Files'.

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.

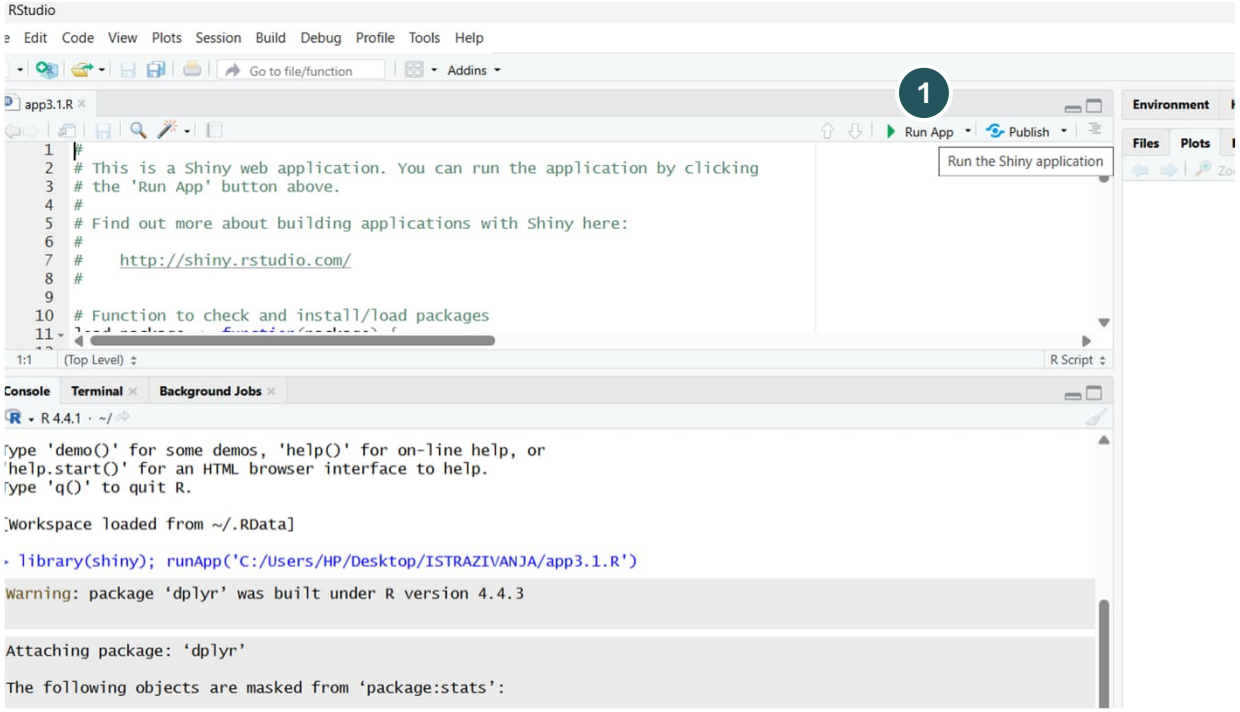
The app has not started yet

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.

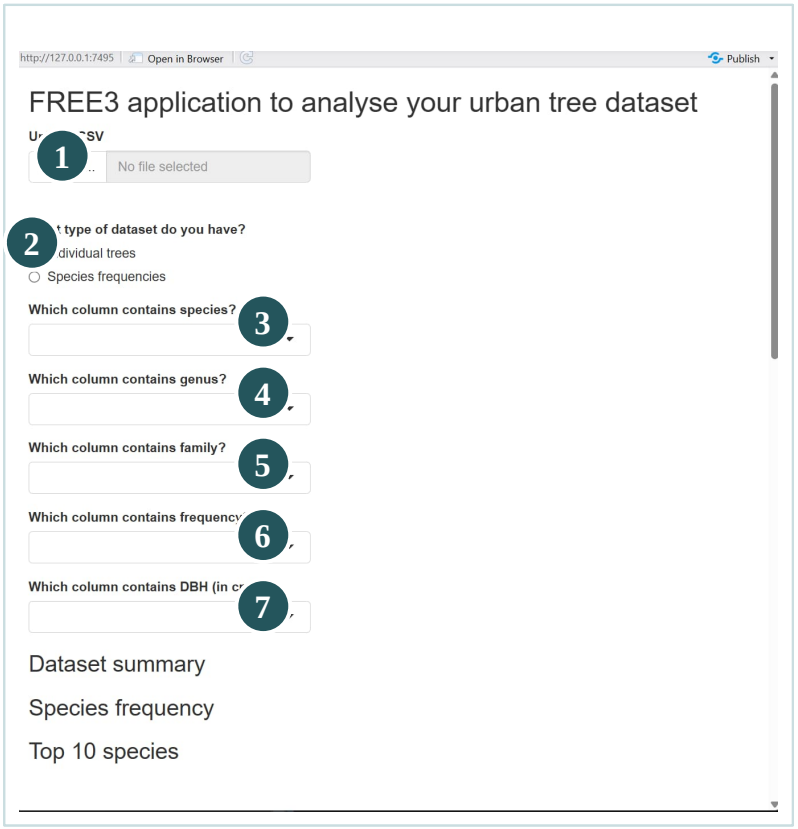
! **Keep RStudio open**

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**

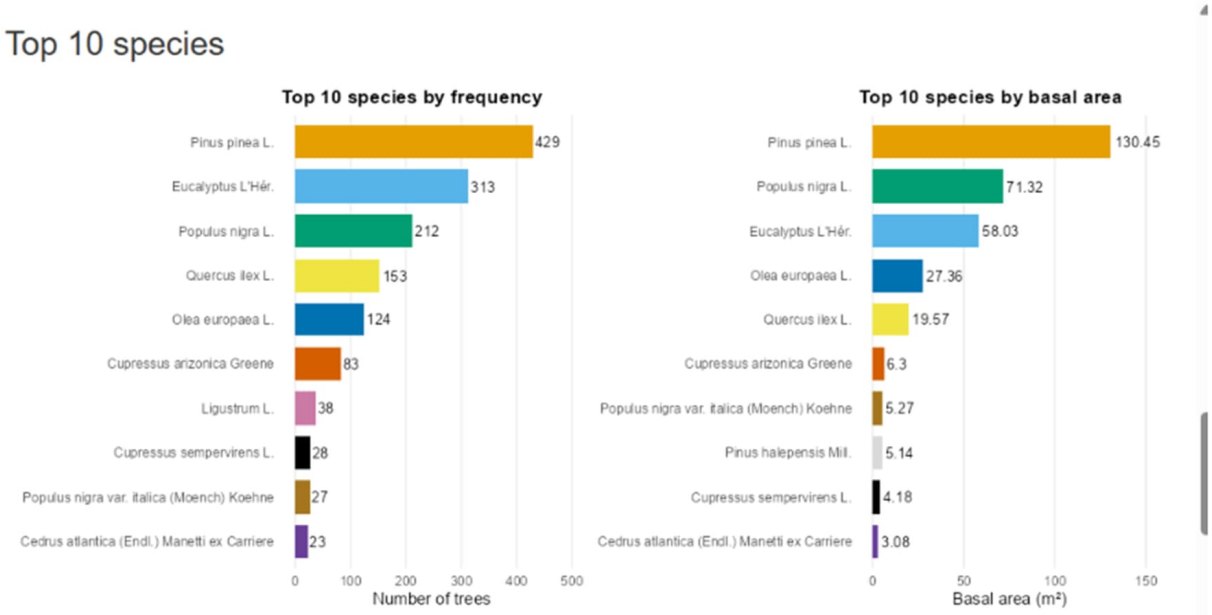
Tree count shows species abundance, while basal area indicates structural dominance. Common species do not necessarily contribute the most basal area.

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**

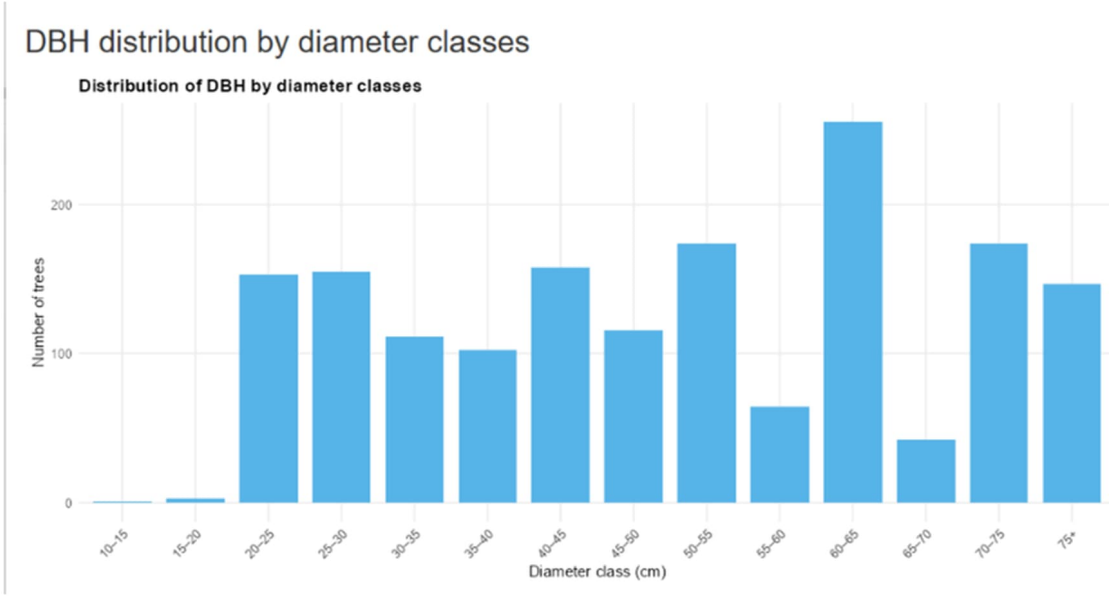
Tree size structure, possible recruitment gaps and historical planting patterns.

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.

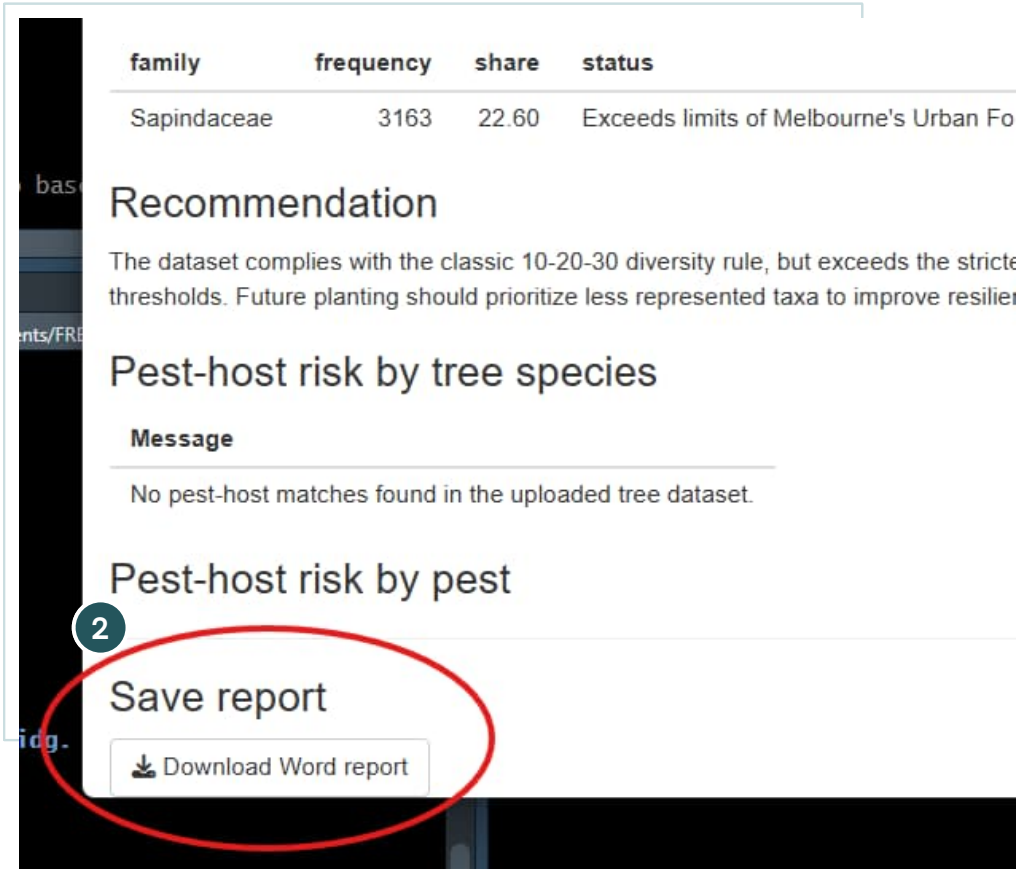
Pest-host risk by pest

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.

Your inventory table

Steps 1–2. Start from your own file; fix only what the check finds.

	Where you are	Click or choose	You should see
1	Your inventory file	**Open it** › **find the species column** (note its name)	You know your column names
2	Same file	Check: header in row 1 · one tree per row · species in its own column · DBH in cm	All yes? Go straight to row 6
3	Data ribbon **if needed**	**Filter** › **arrow on species header** › **(Blanks)** › **delete those rows**	No rows without a species name
4	DBH column **if needed**	Numbers only, in centimetres. From mm: ÷ 10. From circumference: ÷ π.	Numbers aligned to the right
5	Template **optional**	**Open FREE3_inventory_template.xlsx** › **click A2** › **Paste Values**	Your data under 8 headers
6	File menu	**Save As** › **Excel Workbook (*.xlsx)** › **name it** (keep the original)	A new .xlsx next to the original

✓ **You are done when** One sheet, header in row 1, one tree per row, every row has a species, DBH is a number in cm.

QGIS plugin

Steps 3–7. Rows 1–2 are needed only once per computer.

	Where you are	Click or choose	You should see
1	QGIS menu bar Once only	**Plugins** › **Manage and Install Plugins…**	The Plugins window opens
2	Plugins window, left list Once only	**Install from ZIP** › **‘…’** › tree_inventory_harmonizer_….zip › **Install Plugin** › **Yes**	A green tree icon in the toolbar
3	QGIS toolbar	**Green tree icon**	Tree Inventory Harmonizer window
4	Species Harmonization tab	**Input file: Browse…** (your inventory) › **Species column** (from your P1 notes) › **Output folder: Browse…** › **Run harmonization**	Progress bar to 100 %, then a match summary
5	Match summary	Note the number of ‘Unmatched’ records; spot-check ‘Medium’ and ‘Genus-level’.	Unmatched records are not screened
6	Pest Risk Assessment tab	**Browse…** (harmonized_inventory.gpkg) › **Output folder: Browse…** › **Run pest risk assessment**	New red / orange / green layer
7	Map	**Identify Features tool** › **click a tree**	Harmonised name, class and pests
8	Layers panel	**Right-click ‘Tree Inventory Harmonized’** › **Export** › **Save Features As…**	The ‘Save Vector Layer as…’ dialog
9	Save dialog	**Format: Comma Separated Value [CSV]** › **File name: ‘…’** › **OK**	A .csv in the folder you chose

✓ **You are done when** you have a CSV of the harmonised inventory — that file goes into the Shiny app.

Shiny app

Steps 8–10. Keep RStudio open while the app is running.

	Where you are	Click or choose	You should see
1	Your computer Once only	Install R first, then RStudio Desktop. Default settings are fine.	RStudio starts without errors
2	RStudio menu bar	**File** › **Open File…** › **app3.1.R** (newest version) › **Open**	The script in the editor
3	Editor, top-right	**Run App**	Packages load; first time takes minutes
4	App window, top	**Upload CSV: Browse…** › **your CSV** (from QGIS, Step 7)	The file name next to Browse…
5	What type of dataset?	Choose Individual trees (one row per tree) or Species frequencies (one row per species with a count).	The matching option selected
6	Column drop-downs	**Species** (harmonised name) › **Genus** › **Family** › **Frequency** (counts only) › **DBH (cm)**	Results appear below the fields
7	Results, scrolling down	Dataset summary, species frequency, 10–20–30, Melbourne, DBH, pest–host.	Tree total matches your inventory
8	Bottom of the app	**Save report** › **Download Word report**	FREE3_report.docx in Downloads

✓ You are done when the Word report is in Downloads and the checklist ‘before you share’ is done.

The whole job on one page

Print this page and keep it next to the computer. Work down each column, left to right.

Your inventory table

Excel · Steps 1–2

1. **Open your file › find the species column**
2. Check: header in row 1, one tree per row, DBH in cm
3. Fix only what fails (P3–P4)
4. Template only if the table is messy
5. **File › Save As › Excel Workbook (*.xlsx)**

QGIS plugin

QGIS · Steps 3–7

1. **Plugins › Install from ZIP › .zip › Install** (once)
2. **Tree icon › Species Harmonization**
3. **Input file › Species column › Output folder** ›
4. **Run harmonization › check ‘Unmatched’**
5. **Pest Risk Assessment › .gpkg › Run**
6. **Right-click Tree Inventory Harmonized › Export › Save Features As… › CSV › OK**

Shiny app

RStudio · Steps 8–10

1. Install R, then RStudio (once)
2. **File › Open File… › app3.1.R › Run App**
3. **Upload CSV: Browse… › your CSV**
4. **Dataset type › Species › Genus › Family › DBH**
5. Scroll through the results
6. **Save report › Download Word report**

RESULT FREE3_report.docx in Downloads. Before sending it, go through ‘Before you share’.

Installation

QGIS, the plugin, R and RStudio.

Problem	Likely cause	Solution
The installer is blocked	Managed computer without administrator rights.	Ask IT to install QGIS 3.44 LTR, R and RStudio (see ‘Before you start’).
'Install from ZIP' rejects the file	The ZIP was extracted — some browsers (Safari) do this automatically — or the wrong file was chosen.	Select the original .zip. If only a folder exists, download the ZIP again.
Python error when the plugin starts	QGIS version not supported, e.g. QGIS 4.x.	Check Help › About. Install QGIS 3.44 LTR and the plugin again.
The tree button does not appear	QGIS was not restarted, or the plugin is not enabled.	Restart QGIS. Plugins › Manage and Install Plugins › Installed › tick 'Tree Inventory Harmonizer'.
'Run App' does nothing / R not found	R is missing, or RStudio was installed before R.	Install R, restart RStudio and open the script again.
Packages fail to install on first run	No internet, a firewall or no permission to write the package library.	Connect and retry. In the Console run install.packages("name") for the package named in the error.

Still stuck? Send the FREE3 team the error text, a screenshot and your QGIS / R version (Help › About).

QGIS plugin

Harmonisation, screening and the map.

PROBLEM	LIKELY CAUSE	SOLUTION
Species column list is empty or odd	Title rows above the header, or data not on the first sheet.	Header in row 1 of the first sheet (Step P2).
'Run harmonization' does nothing	No output folder was chosen.	Choose an output folder — the field is obligatory (Step A6).
Very high unmatched count	Wrong species column, or names mixed with other text.	Re-run Step A6 with the right column; move notes out of the species cells (Step P3).
Screening tab does not accept the file	The original inventory was selected.	Select harmonized_inventory.gpkg from the Step A6 output folder.
Every tree is 'No known risk'	Very few names were matched.	Check the counts from Step A7; usually the wrong column was selected.
Trees are missing, in the sea or at 0,0	x and y swapped, or coordinates not in WGS84.	x = longitude, y = latitude, decimal degrees (Step P3).
Red / orange / green colours are gone	'Classify' was pressed while styling the layer.	Remove the layer and run Step A8 again.

Still stuck? Send the FREE3 team the error text, a screenshot and your QGIS / R version (Help › About).

Shiny app and report

Running the app, uploading the CSV and downloading the report.

Problem	Likely cause	Solution
'Run App' button is missing	The file was not opened as an R script.	File › Open File… and select app3.1.R (Step B2).
App closes with red text in the Console	A package is missing or failed to load.	Read the package name in the error, install it, then Run App again.
App opens but stays empty	No CSV uploaded, or species column not mapped.	Complete the upload and species fields (Step B5).
Strange characters (Ã©, ?) in names	The CSV is not UTF-8.	Export again from QGIS with UTF-8 encoding (Step A14).
Tree total is wrong	Wrong dataset type, or frequency mapped for individual trees.	Check dataset type and leave frequency empty (Step B5).
A whole section is missing	A required column was not mapped.	See ‘Which columns are required for each analysis’.
App stops responding	RStudio was closed, or the Console is busy.	Keep RStudio open; press Stop in the Console and Run App again.

Still stuck? Send the FREE3 team the error text, a screenshot and your QGIS / R version (Help › About).

Data and results

When the numbers look wrong rather than the software.

Problem	Likely cause	Solution
DBH section missing although DBH exists	DBH is stored as text (‘34 cm’).	Numbers only, in cm (Step P4, line 4).
Basal area looks far too large	DBH was recorded in mm.	Divide by 10 (Step P4, line 5) and run the analysis again.
The same species appears twice	The original species column was mapped in the app.	Map the harmonised species column (Step B5).
10–20–30 only at species level	Genus and family columns are missing or not mapped.	Add or map them — see step P1 (slide 8).
Excel turned values into dates	Automatic formatting when pasting.	Undo, set the columns to ‘Number’, paste again (Step P4).
Fewer trees in the app than in Excel	Rows without species, or rows lost during cleaning.	Compare with the totals from Step A7 and with the original file.

Still stuck? Send the FREE3 team the error text, a screenshot and your QGIS / R version (Help › About).

Glossary — names and screening

Harmonisation

Matching inventory names to an accepted reference taxonomy, so spelling variants, synonyms and other inconsistencies are recognised consistently.

Match confidence

How reliably a name was matched: high, medium, genus-level or unmatched (Step A7).

Major host

A tree species identified as a primary host of at least one regulated pest.

No known risk

Not listed as a host in the FREE3 database for the 11 screened pests. It does not mean pest-free.

Reference taxonomy

The accepted list of families, genera and species (126 · 540 · 2,219) that inventory names are matched against.

Regulated pest

A pest subject to official control measures because of the damage it may cause. FREE3 screens 11 of them.

Host

A tree species identified as a secondary host of at least one regulated pest.

Pest–host association

A documented link between a tree species and a regulated pest that can use it as a host.

Reference (Glossary 2 of 2)

Glossary — diversity, data and files

DBH

Diameter at breast height — trunk diameter measured 1.3 m above ground. The app expects centimetres.

Basal area

Cross-sectional stem area at breast height, per tree or summed per species. A size-based measure of representation.

10–20–30 rule

Diversity guideline: no more than 10% of one species, 20% of one genus and 30% of one family.

Melbourne recommendations

A stricter benchmark: at most 5% per species, 10% per genus and 20% per family.

Dataset type

Individual trees: one row per tree. Species frequencies: one row per species with a count in a frequency column.

GPKG (GeoPackage)

An open, single-file format for spatial features and attributes. The plugin’s main spatial output.

CSV · UTF-8

CSV: a plain-text table, one row per line. UTF-8: the encoding that keeps characters such as ×, ä or ł intact.

CRS · WGS84

Coordinate reference system: how coordinates relate to places on Earth. WGS84 (EPSG:4326) is latitude/longitude.