

# ggPlantmap: an R package for the graphic mapping of plant images.

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## Summary

The development of single-cell techniques revolutionized the field of plant biology. It enabled the characterization of cell-specific events in a wide range of species and allowed us to gain novel insights of minute biological processes occurring in complex plant tissues (Cuperus, 2022; Libault et al., 2017). Such novel approach is greatly improving our understanding of plant development, evolution, and physiology. As these techniques gain more attention within the plant research community, there is a rising need for the development of specialized visualization tools that can effectively explore the rich and complex data they produce.

ggPlantmap is an open-source R package with the goal of facilitating the generation of informative ggplot maps from plant images to explore quantitative cell type-specific data. When combined with external quantitative data, ggPlantmap can be used for the visualization and displaying of spatial profiles in distinct parts/cells of the plant (Figure 1). The conceptual workflow is like other ggplot based geographic map packages, such as ggmap (Kahle and Wickham, 2013).

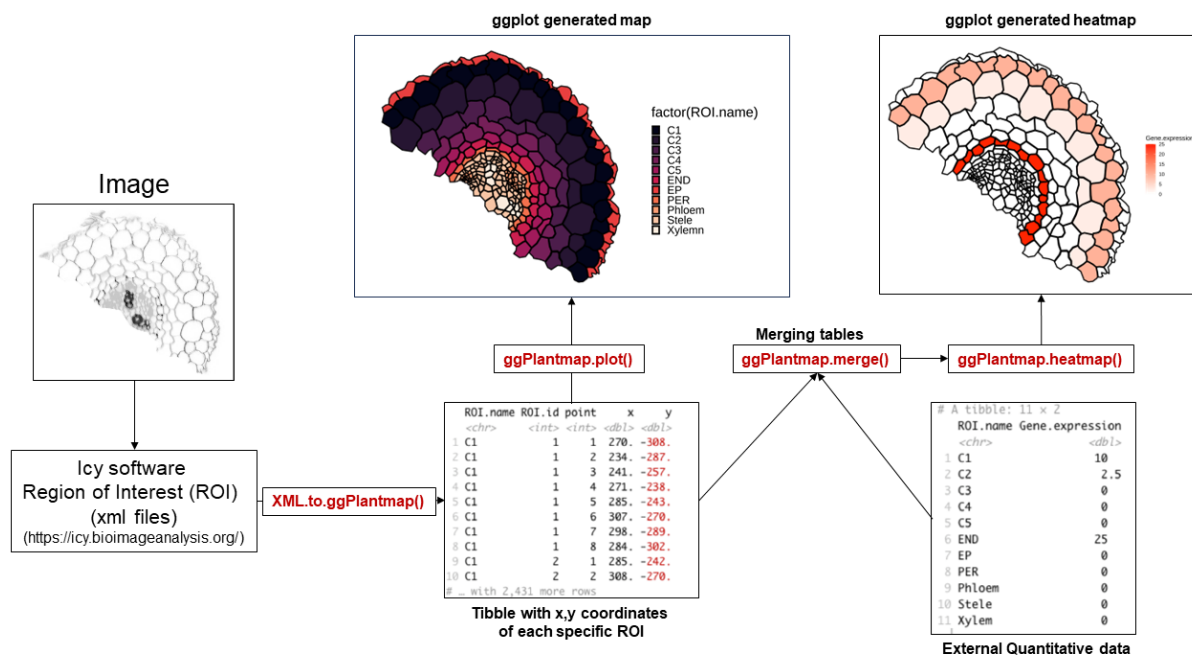


Figure 1: **General overview of the ggPlantmap workflow.**

Included in the package there is a set of pre-loaded maps created from previously published plant images that can be directly inserted into a ggplot coding workflow (Table 1, Figure 2). ggPlantmap enables users to plot heatmap signatures of gene expression or any other spatial quantitative data onto plant images providing a customizable and extensible platform for visualizing and analyzing spatial quantitative patterns within specific plant regions (Figure 1). This package uses the flexibility of the well-known ggplot2 R package (Wickham, 2011) to allow users to tailor maps to their specific research questions.

ggPlantmap	Species	Tissue	Reference
ggPm.At.roottip.crossection	Arabidopsis thaliana	Root	(Sotta and Fujiwara, 2017)
ggPm.At.roottip.longitudinal	Arabidopsis thaliana	Root	(Rahni and Birnbaum, 2019)
ggPm.At.3weekrosette.topview	Arabidopsis thaliana	Rosette	(Nguyen and McCurdy, 2015)
ggPm.At.leafepidermis.topview	Arabidopsis thaliana	Leaf	(Guo et al., 2021)
ggPm.At.leaf.crossection	Arabidopsis thaliana	Leaf	(Tsukaya, 2013)
ggPm.At.seed.devseries	Arabidopsis thaliana	Seed	(Belmonte et al., 2013)
ggPm.At.earlyembryogenesis.devseries	Arabidopsis thaliana	Embryo	(Wendrich and Weijers, 2013)
ggPm.At.shootapex.longitudinal	Arabidopsis thaliana	Shoot Apex	(Fuchs and Lohmann, 2020)
ggPm.At.inflorescencestem.crossection	Arabidopsis thaliana	Stem	(Shi et al., 2021)
ggPm.Sl.root.crossection	Solanum lycopersicum	Root	(Ron et al., 2014)
ggPm.At.leaf.topview	Arabidopsis thaliana	Leaf	(Vanhaeren et al., 2015)
ggPm.At.rootlong.longitudinal	Arabidopsis thaliana	Root	(Shahan et al., 2022)
ggPm.At.rootmatur.crossection	Arabidopsis thaliana	Root	(Shahan et al., 2022)
ggPm.At.flower.diagram	Arabidopsis thaliana	Flower	(Taiz et al., 2015)
ggPm.At.lateralroot.devseries	Arabidopsis thaliana	Lateral Root	(Torres-Martinez et al., 2019)
ggPm.Ms.root.crossection	Medicago sativa	Root	Unpublished

Table 1: List of pre-loaded ggPlantmap in the package and their references

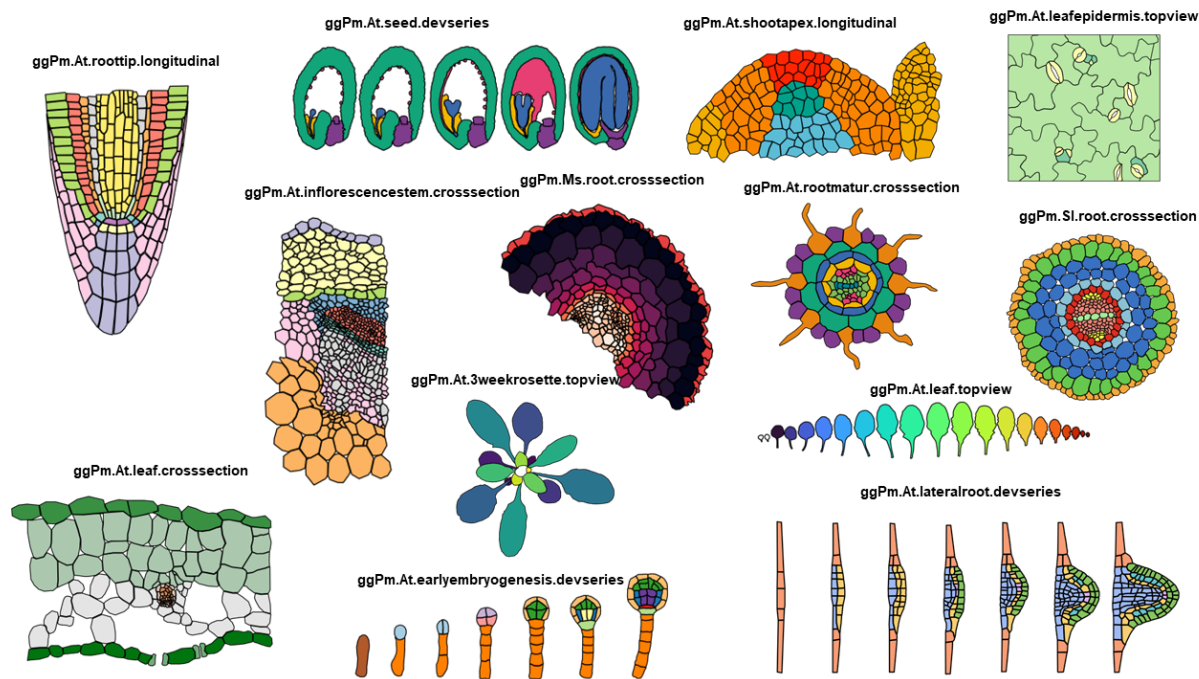


Figure 2: Examples of ggplots generated from pre-loaded ggPlantmaps.

In addition to the pre-loaded maps, we documented the workflow and functions for plant researchers to create their own ggPlantmap. The creation of new ggPlantmaps is based on the manual segmentation of plant shapes into distinct Regions of Interest (ROIs) using the open-source software for image analysis Icy (De Chaumont et al., 2012). With our described method, users can generate new ggPlantmaps without the necessity of high-resolution images and advanced coding skills. The ggPlantmap package is an open-source project, encouraging community contributions and creation of maps that will be continuously loaded into the package. We encourage users to extend its functionality to meet specific research requirements and to better display plant biological data. Its compatibility with R, one of the most comprehensive programming languages in plant biology, makes it a versatile and accessible tool for the plant science community.

## Statement of Need

Understanding the spatial distribution of gene expression patterns or any other quantitative data within plant tissues and cells is fundamental to understand the complex and intricate events in plant biology. The Plant eFP (Expression, Function, and Protein Localization) Browser (Winter et al., 2007) has been an extremely valuable resource for researchers seeking to visualize gene expression data in the context of plant tissues across many different plant species (Winter et al., 2007). Although widely used by the plant research community, the Plant eFP browser lacks open and user-friendly tools for the creation of customized expression maps independently. Plant biologists with less coding experience can often encounter challenges when attempting to incorporate their own spatial quantitative data or explore specific aspects of gene expression within plant tissues. To address this issue, we created ggPlantmap to allow plant researchers to create ggplot maps from plant images, like the Plant eFP Browser, with minimal knowledge in the R language (Figure 3). In this sense, ggPlantmap can play an important role in the plant science toolbox by offering an open, accessible, and customizable solution for creating quantitative image maps from plant images. By providing researchers with the means to independently generate maps from plant images, we aim to empower plant scientists to explore the visualization and communication of plant research in creative and exciting ways. We hope that ggPlantmap can assist the plant science community, fostering innovation and improving our understanding of plant development and function.

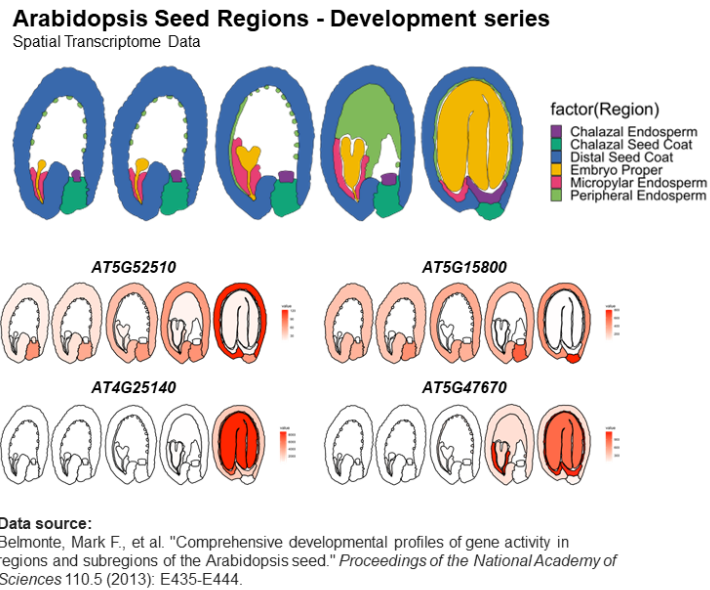


Figure 3: **Example of a heatmap generated from a ggPlantmap.** Data source: Belmonte et al., 2013

## Functionality

The package is available on GitHub under the MIT License at <https://github.com/leonardojo/ggPlantmap>. We also created a detailed [user guide](#) through all the available functionality of ggPlantmap. We also created a [walkthrough document](#) to guide users on creating their own ggPlantmap. The following few examples demonstrate the simplicity of using ggPlantmap.

### • Installation

**## Installing devtools**

```
install.packages("devtools")
library(devtools)
```

**## Installing ggPlantmap**

```
install_github("leonardojo/ggPlantmap")
library(ggPlantmap)
```

- Pre-loaded ggPlantmaps

```
library(ggPlantmap)
ggPm.summary$ggPlantmap.name

## [1] "ggPm.At.roottip.crosssection"
## [2] "ggPm.At.roottip.longitudinal"
## [3] "ggPm.At.3weekrosette.topview"
## [4] "ggPm.At.leafepidermis.topview"
## [5] "ggPm.At.leaf.crosssection"
## [6] "ggPm.At.seed.devseries"
## [7] "ggPm.At.earlyembryogenesis.devseries"
## [8] "ggPm.At.shootapex.longitudinal"
## [9] "ggPm.At.inflorescencestem.crosssection"
## [10] "ggPm.Sl.root.crosssection"
## [11] "ggPm.At.leaf.topview"
## [12] "ggPm.At.rootelong.longitudinal"
## [13] "ggPm.At.rootmatur.crosssection"
## [14] "ggPm.At.flower.diagram"
## [15] "ggPm.At.lateralroot.devseries"
## [16] "ggPm.Ms.root.crosssection"
```

- `ggPlantmap.plot()` - Plotting your `ggPlantmap`

```
library(ggPlantmap)
```

```
ggPlantmap.plot(ggPm.At.inflorescencestem.crossection,ROI.name)
```

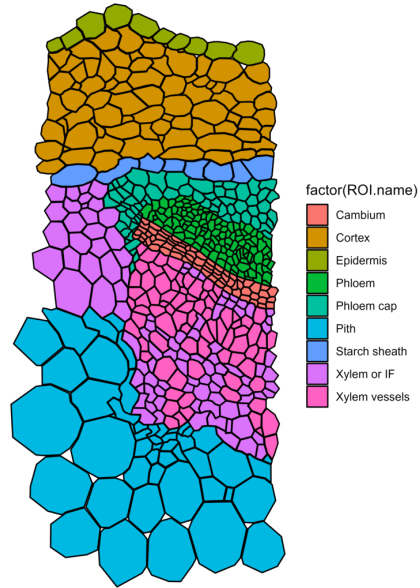


Figure 4: `ggPlantmap` plotted from `ggPm.At.inflorescencestem.crossection`. The column `ROI.name` was used to color map the `ggPlantmap`.

- ggPlantmap.merge() - Combining a ggPlantmap with external quantitative data

```
library(ggPlantmap)
## Expression sample data
ggPm.tomatoatlas.expression.sample

## A tibble: 7 x 2
##   Cell.layer SCR.expression
##   <chr>          <dbl>
## 1 Epidermis      1.24
## 2 Cortex         1.17
## 3 Endodermis    75.8
## 4 Phloem         0.44
## 5 Procambium    0.95
## 6 Pericycle     0.95
## 7 Xylem         2.78

## Combining with the tomato root ggPlantmap
ggPlantmap.merge(ggPm.Sl.root.crosssection,
  ggPm.tomatoatlas.expression.sample,
  id.x="ROI.name",
  "Cell.layer")

## A tibble: 4,314 x 6
##   ROI.name ROI.id point      x      y SCR.expression
##   <chr>    <int> <int> <dbl> <dbl>          <dbl>
## 1 Exodermis      1     1  615. -370.           0
## 2 Exodermis      1     2  601. -349.           0
## 3 Exodermis      1     3  598. -327.           0
## 4 Exodermis      1     4  617. -312.           0
## 5 Exodermis      1     5  636. -307.           0
## 6 Exodermis      1     6  651. -310.           0
## 7 Exodermis      1     7  671. -327.           0
## 8 Exodermis      1     8  684. -343.           0
## 9 Exodermis      1     9  676. -354.           0
## 10 Exodermis     1    10  668. -365.           0
## with 4,304 more rows
```



- `ggPlantmap.heatmap()`

```
library(ggPlantmap)

## Combining with the tomato root ggPlantmap
ggPlantmap.expression <- ggPlantmap.merge(ggPm.Sl.root.crosssection,
  ggPm.tomatoatlas.expression.sample,
  id.x="ROI.name",
  "Cell.layer")
ggPlantmap.heatmap(ggPlantmap.expression,SCR.expression) +
  scale_fill_gradient(low="green",high="red",na.value="green")
```

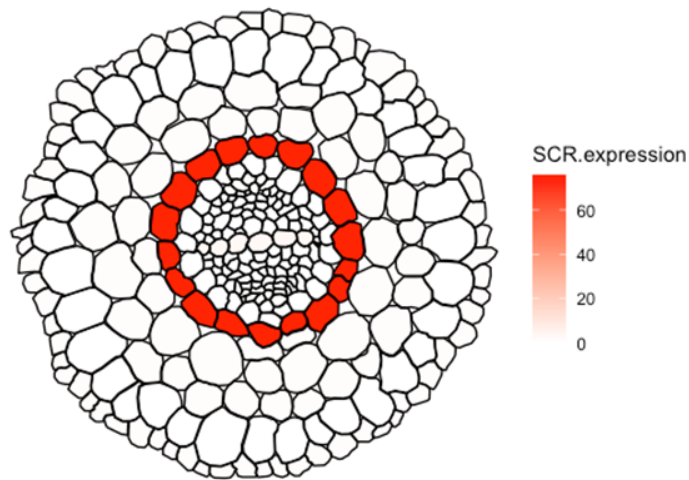


Figure 5: **Sample for ggPlantmap heatmap.** Expression of tomato SCARECROW (SCR) in distinct cell types of the tomato root. Data obtained from Kajala et al., 2021.

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