

# santaR Graphical User Interface

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The *santaR* package is designed for the detection of significantly altered time trajectories between study groups, in short time-series. The graphical user interface implements all of *santaR*'s functions.

The GUI is to be preferred to understand the methodology, select the best parameters on a subset of the data before running the command line, or to visually explore results.

This vignette will:

- Detail the step-by-step use of the graphical user interface using an example dataset.

## Example Data

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This vignette employ the `.csv` and `.RData` files generated from *acuteInflammation* in the vignette [how to prepare input data for santaR](#).

## Getting Started

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The graphical user interface is started as follow:

```
library(santaR)

santaR_start_GUI(browser = TRUE)
# To exit press ESC in the command line
```

The graphical interface is divided in 4 main tabs, Import, DF search, Analysis and Export.

# Import

The first input format is a .csv file containing as *rows* the observations (samples) and as *columns* the variables as well as metadata.

The screenshot shows the 'Import' section of a Shiny application. The 'Input Type' is set to 'CSV'. A file named 'acuteInflammation\_GUI\_demo.csv' has been uploaded. The 'Header' checkbox is checked. The 'Separator' is set to 'Comma' and the 'Quote' is set to 'Double Quote'. Below these settings, a table preview is shown with 15 columns: 'time', 'ind', 'group', 'var\_1', 'var\_2', 'var\_3', 'var\_4', 'var\_5', 'var\_6', 'var\_7', 'var\_8', 'var\_9', 'var\_10', 'var\_11', 'var\_12', and 'var\_13'. The table contains 13 rows of data.

time	ind	group	var_1	var_2	var_3	var_4	var_5	var_6	var_7	var_8	var_9	var_10	var_11	var_12	var_13
0	ind_1	Group1	-0.34	-0.64	-0.22	1.90	-0.35	-0.12	-0.09	1.04	-0.33	-0.10	-0.42	0.29	-0.06
0	ind_2	Group2	-0.34	-0.64	-0.22	1.90	-0.35	-0.12	-0.09	1.04	-0.33	-0.10	-0.42	0.29	-0.06
0	ind_3	Group1	-0.41	-0.64	-0.51	-1.03	-0.93	-0.37	-0.83	-0.42	-1.20	-0.47	-0.81	-1.15	-0.74
0	ind_4	Group2	-0.41	-0.64	-0.51	-1.03	-0.93	-0.37	-0.83	-0.42	-1.20	-0.47	-0.81	-1.15	-0.74
0	ind_5	Group1	-0.41	-0.64	-0.40	-0.65	-0.50	-0.37	-0.54	-0.14	-0.89	-0.47	-0.51	-0.27	-0.37
0	ind_6	Group2	-0.41	-0.64	-0.40	-0.65	-0.50	-0.37	-0.54	-0.14	-0.89	-0.47	-0.51	-0.27	-0.37
0	ind_7	Group1	-0.41	-0.64	-0.36	-0.57	-0.43	-0.34	-0.51	0.11	-0.35	-0.47	-0.45	-0.16	-0.21
0	ind_8	Group2	-0.41	-0.64	-0.36	-0.57	-0.43	-0.34	-0.51	0.11	-0.35	-0.47	-0.45	-0.16	-0.21
4	ind_1	Group1	-0.30	0.57	0.91	0.48	0.54	0.24	1.19	0.56	-0.12	-0.47	0.25	-0.08	-0.30
4	ind_2	Group2	-0.30	0.57	0.91	0.48	0.54	0.24	1.19	0.56	-0.12	-0.47	0.25	-0.08	-0.30

Columns corresponding to metadata are selected: the metadata describe the individual ID and collection time corresponding to each observation, with optionally class information for identification of inter-class differential trajectories.

The screenshot shows the 'santaR' Shiny application interface. At the top, there is a navigation bar with 'santaR', 'About', 'Import', 'DF search', 'Analysis', and 'Export'. Below this, a message says 'Import a .csv file, a .RData with 2 data.frames, or a fully fitted dataset.' The 'Input Type' section has three radio buttons: 'CSV' (selected), 'RData', and 'Fitted Data'. On the left, a sidebar contains 'Import', 'CSV' (highlighted), '.RData', 'Fitted Data', 'View Input', and 'View Input'. A green success message reads 'Success: Input data generated'. Below this, there are 'File' and 'Columns' buttons. The main area contains instructions: 'Assign each columns to either data or metadata, select time and individual and generate the input dataset. All variables in Data will be fitted.' There are two columns: 'Data' and 'Metadata'. The 'Data' column lists 'var\_1' through 'var\_10'. The 'Metadata' column lists 'time', 'ind', and 'group'. Two arrows point from 'var\_7' and 'var\_8' in the 'Data' column to the 'Metadata' column. Below these columns are two dropdown menus: 'Time' (set to 'time') and 'Individual' (set to 'ind'). A 'Generate Input' button is at the bottom.

Additionally, data previously imported as well as fitting results (in `.RData` format) can be loaded for further analysis or plotting (see the **Export** section for more details).

The screenshot displays the SantaR Shiny application interface. At the top, a navigation bar includes 'santaR', 'About', 'Import', 'DF search', 'Analysis', and 'Export'. Below this, a header text reads: 'Import a .csv file, a .RData with 2 data.frames, or a fully fitted dataset.' The 'Input Type' section has three radio buttons: 'CSV', 'RData' (which is selected), and 'Fitted Data'. On the left sidebar, the 'Import' section is active, with sub-options for 'CSV', '.RData' (highlighted), and 'Fitted Data'. Below these are 'View Input' and 'View Input' links. A green 'Success' message box states 'Input data generated'. The main content area instructs the user to 'Select a .RData file containing 2 data.frame *inData* (variables to fit) and *inMeta* (metadata) containing observations as rows and variables/metadata as columns.' Under 'Choose a .RData File', a file named 'acuteinflammation\_GUI\_demo.rdata' is shown with a 'Browse...' button and an 'Upload complete' status. Below this, the 'Variables loaded:' field shows 'chr [1:2] "inMeta" "inData"'. There are two dropdown menus: 'Time' set to 'time' and 'Individual' set to 'ind'. A 'Generate Input' button is located at the bottom of the main content area.

## DF Search (optional)

### Note:

The single parameter to be set by the user is the number of **degrees of freedom ( $df$ )** to fit the spline model. The  $df$  controls how closely the curve models the input data-points.

Once the  $df$  is chosen for a dataset (a given number of time-points and missing values), it can be kept constant whichever the question to investigate (the metadata and group comparison).

Some indications based on simulated data and diverse datasets can guide the selection of  $df$ :

- $df$  controls the “complexity” of the model employed. A substantial difference can be found when going from 2 to 10, but very little change will take place when going from 10 to 50 (the model only gets more complex, but the general shape won’t change).
- More time points do not automatically require a higher  $df$ . More inflexions (more complex shape) could require a higher  $df$  if the number of points is sufficient (and the sampling frequency high).
- A lower  $df$  value is often more suited and generalisable (less over-fitted).
- If the  $df$  is for example 10, all individuals trajectories with less of 10 time-points cannot be fitted and will be rejected.
- On simulated data, the results ( $p$ -values) are resilient to most values of  $df$ , however the plots can look dramatically different.
- Trying multiple values of  $df$  on a subset of variables (using the GUI) and then selecting the fit that approximate the time evolution the best without over-fitting:
  - $df = 5$  is a good starting point in most cases (even more so if there is less than 10 time-points)
  - If the number of time-points is large and the curves seem very under-fitted,  $df$  can be increased to 6, 7 or more. Values higher than 10 should rarely be required and will provide with a diminishing return.  $df = \text{number of time-points}$  will result in a curve passing through all points (over-fitted).
  - If the number of points is lower or the trajectories seem over-fitted,  $df$  can be decreased to 4 or 3. (3 will be similar to a second degree polynomial, while 2 will be a linear model)
  - If the plots “look right” and don’t seem to “invent” information between measured data-points, the  $df$  is close to optimal.

It does not seem to be possible to automatically select the degree of freedom. A choice based on visualisation of the splines while being careful with over-fitting, keeping in mind the “expected” evolution of the underlying process seems the most reasonable approach.

Even if automated approaches cannot reliably select a number of degree of freedom to em-

ploy, **DF search** implements some of these approaches and multiple tools to help guide optimal *df* selection.

The screenshot shows the SantaR Shiny application interface. The browser address bar indicates the URL is `http://127.0.0.1:4009`. The application title is `~/R/win-library/3.4/santaR/shiny-GUI/SANTA-App - Shiny`. The navigation menu includes `santaR`, `About`, `Import`, `DF search`, `Analysis`, and `Export`. The main content area is titled `About DF search` and contains the following text and list:

The single parameter to be set by the user is the number of degrees of freedom (*DF*) to employ. The *DF* parameter controls how closely the curve (spline) fits the input data. It is necessary to ensure that the curve is not over-fitting or under-fitting the data. This parameter is dependent on the study design (*number of time-points, sampling rate, time-scale of the function of time under study*) and therefore only needs to be selected once per dataset.

Some indications based on simulated data and diverse datasets can guide the selection of *DF*:

- *DF* controls the "complexity" of the model employed. A substantial difference can be found when going from 2 to 10, but very little change will take place when going from 10 to 50 (the model only gets more complex, but the general shape won't change).
- More time points do not automatically require a higher *DF*. More inflexions (*more complex shape*) could require a higher *DF* if the number of points is sufficient (and the sampling frequency high).
- A lower *DF* value is often more suited and generalisable (less over-fitted).
- If the *DF* is for example 10, all individual trajectories with less of 10 time-points cannot be fitted and will be rejected.
- On simulated data, the results (*p-values*) are resilient to most values of *DF*, however the plots can look dramatically different.
- Try multiple values of *DF* on a subset of variables (using the GUI) and then select the fit that approximate the time evolution the best without over-fitting:
  - *DF*=5 is a reasonable starting point in most cases (*even more so if there less than 10 time-points are available*).
  - if the number of time-points is large and the curves seem very under-fitted, *DF* can be increased to 6, 7 or more. Values higher than 10 should rarely be required and will provide with a diminishing return. *DF*=*number of time-points* will result in a curve passing through all points (*over-fitted*).
  - if the number of time points is lower or the trajectories seem over-fitted, *DF* can be decreased to 4 or 3. (3 will be similar to a second degree polynomial, while 2 will be a linear model).
  - if the plots "*looks right*" and don't seem to "*invent*" information between measured data-points, the *DF* is close to optimal.

While it does not seem to fully automate the selection of the number of degrees of freedom, *DF Search* implements visualisation approaches to assist in the selection of an adequate *DF* to apply across all variables for a given dataset:

**Eigen-trajectories estimation**

- A PCA extracts the eigen-trajectories across all variables. The *DF* that will best fit that subset of eigen-trajectories is expected to be satisfactory for all trajectories in the dataset.
- Set parameters on the left and press the run button to generate the eigen-trajectories

**Auto-Fit**

- Auto-Fit returns the optimal *DF* based on different goodness of fit metrics.

**Parameter Evolution**

- Plot the evolution of different goodness of fit metrics for all possible *DF*.
- Set parameters and press the *update step* button to calculate the metrics.

**Plot Fit**

- Plot eigen-trajectories fitted with a selected *DF* (left panel).
- Set parameters (automatic fitted spline in red) and press the *update* button to generate the plot.

Auto-Fit uses principal component analysis (PCA) to extract latent trajectories and generate eigen-trajectories that are subsequently assessed for optimal  $df$  using various goodness-of-fit metrics.

The screenshot shows the 'About DF search' section of the santaR application. The sidebar on the left contains several controls: 'Number of Principal Components' set to 6, 'Scaling' set to 'UV scaling', 'PCA Method' set to 'NIPALS', and 'Parallelisation' checked. Below these is a 'Run!' button. The main content area has a navigation bar with 'About', 'Auto-fit', 'Parameter Evolution', 'Plot fit', and 'Missing value'. The 'About DF search' section explains that the user sets the number of degrees of freedom (DF) to control how closely the spline fits the data. It provides a list of guidelines for selecting DF based on data characteristics and offers instructions on how to use the 'Auto-Fit', 'Parameter Evolution', and 'Plot Fit' features.

**About DF search**

The single parameter to be set by the user is the number of degrees of freedom ( $DF$ ) to employ. The  $DF$  parameter controls how closely the curve (spline) fits the input data. It is necessary to ensure that the curve is not over-fitting or under-fitting the data. This parameter is dependent on the study design (*number of time-points, sampling rate, time-scale of the function of time under study*) and therefore only needs to be selected once per dataset.

Some indications based on simulated data and diverse datasets can guide the selection of  $DF$ :

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**Auto-Fit**

- Auto-Fit returns the optimal  $DF$  based on different goodness of fit metrics.

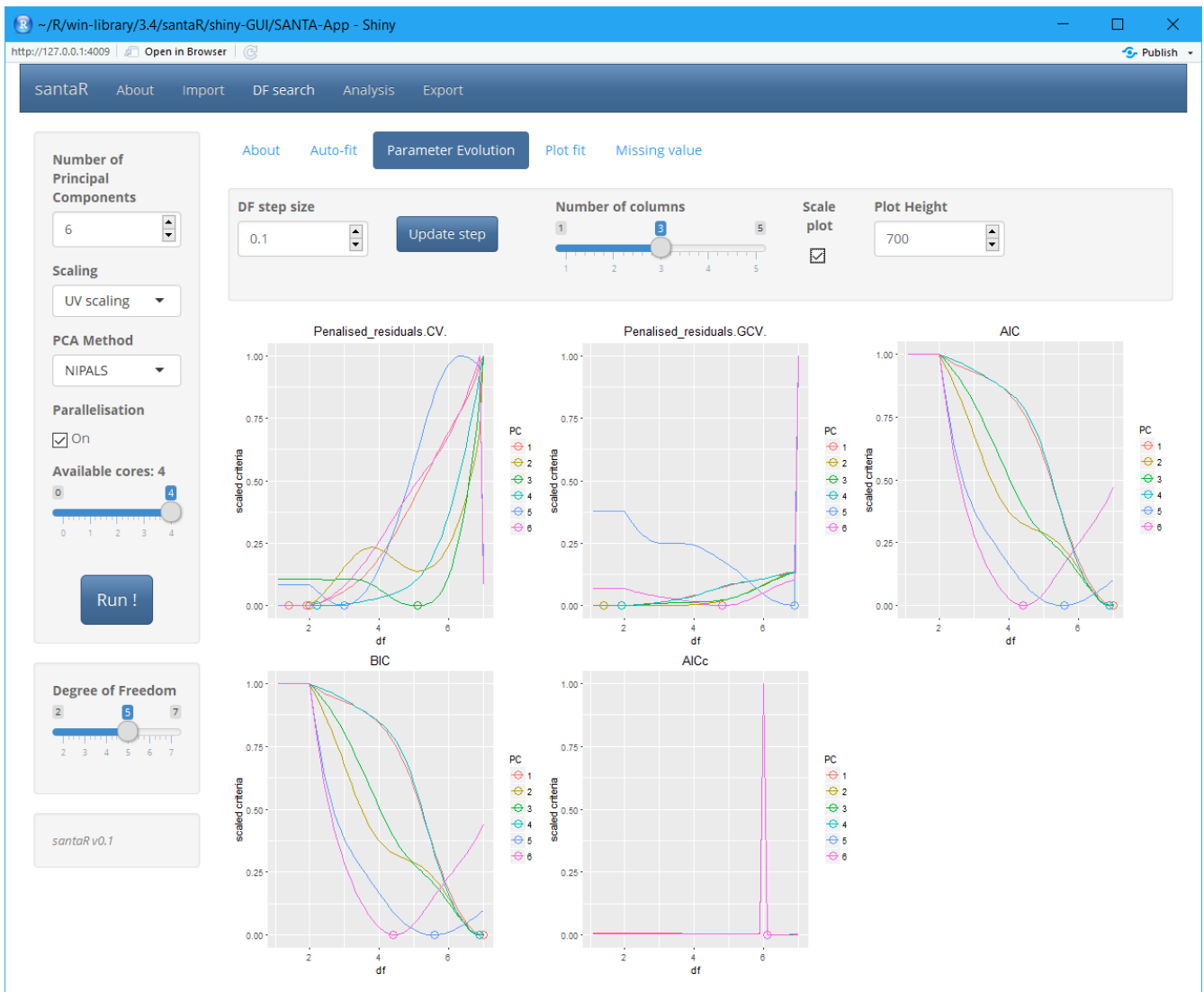
**Parameter Evolution**

- Plot the evolution of different goodness of fit metrics for all possible  $DF$ .
- Set parameters and press the *update step* button to calculate the metrics.

**Plot Fit**

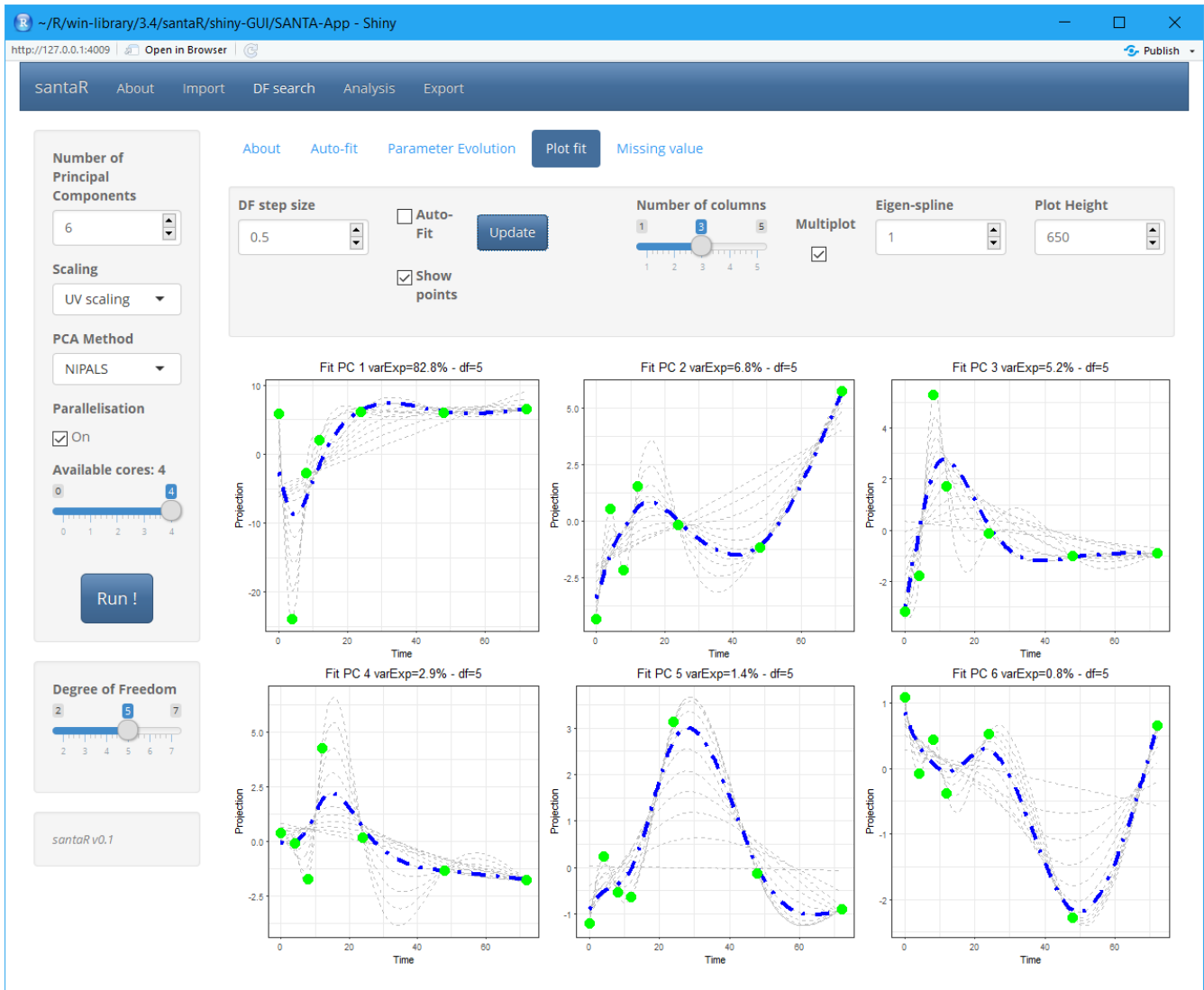
- Plot eigen-trajectories fitted with a selected  $DF$  (left panel).
- Set parameters (automatic fitted spline in red) and press the *update* button to generate the plot.

Parameter evolution plots the evolution of these metrics across the range of possible  $df$  for each latent trajectory.





To select the most suitable  $df$  parameter, **Plot fit** generates a visualisation of the fit on each latent projection at automatically and manually selected  $df$  values.



Finally **Missing value** highlight the number of trajectories that would have to be excluded as they contain less time-points than the  $df$  selected.

# Analysis

With the data imported and a pertinent  $df$  value selected, **Analysis** regroups the fitting, visualisation and identification of variables significantly altered between groups.

**Fit** handles parameter selection as well as downstream computation. Calculation of inter-group differential evolutions can be performed with either initial class information or an advance option generated new grouping (e.g., including / combining / excluding input groups). The user can control the number of permutations and bootstrap rounds for significance and group mean curve confidence band calculation. The sub-sampling or the area between group mean curves can be altered to favour calculation speed at the expense of numerical precision. **Parallelisation** enables the selection of the number of CPU cores to employ for computation. **View Input** presents the dataset as fitted.

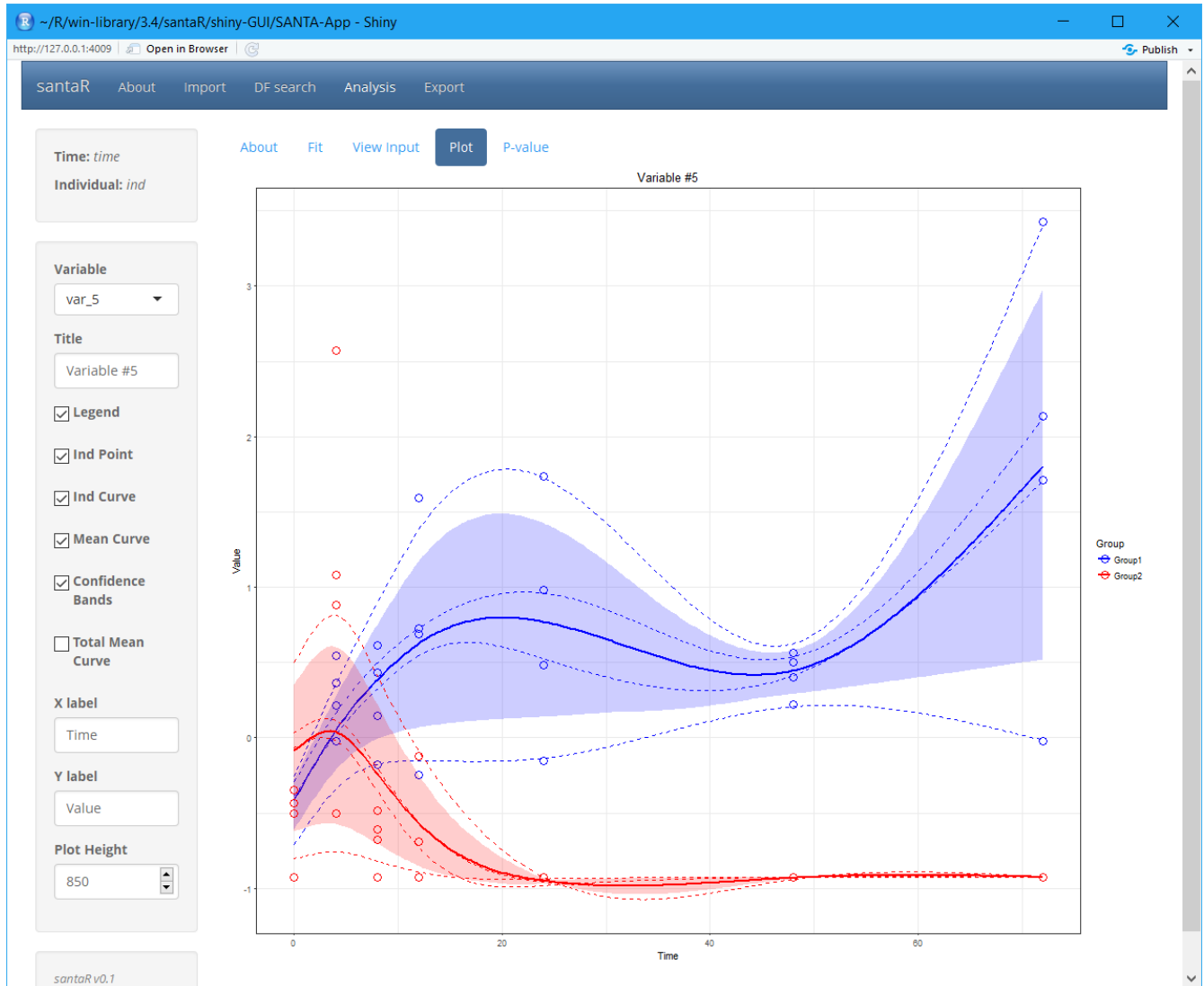
The screenshot displays the 'Fit' tab of the santaR Shiny application. The interface includes a navigation bar with 'About', 'Fit', 'View Input', 'Plot', and 'P-value' tabs. On the left, there are input fields for 'Time: time', 'Individual: ind', and 'santaR v0.1'. The main panel contains several configuration sections:

- Degree of Freedom:** A slider set to 5, with a range from 2 to 7.
- Parallelisation:** A checked checkbox, 'Available cores: 4' (slider set to 4), and an unchecked 'Force parallelisation' checkbox.
- Confidence Bands:** A checked checkbox, 'Number of bootstrap rounds (Conf. band)' set to 1000, and 'Number of permutation rounds (p-value)' set to 1000.
- Group:** A dropdown menu set to 'group', a table of 'Unique groups', and an unchecked 'Advanced' checkbox.
- P-value Dist:** A checked checkbox, 'P-value Fit' (unchecked), and 'Sub-sampling p-Dist' set to 5000.

A 'Run !' button is located at the bottom center of the configuration panel.

group	nb_ind
Group1	4
Group2	4

Plot enables the interactive visualisation of the raw data points, individual trajectories, group mean curves and confidence bands for all variables, which subsequently can be saved as an image figure to disk.



If inter-group differential evolution has been characterised, **P-value** summarise in tables all significance testing - providing multiple options for false discovery correction (e.g., Benjamini-Hochberg, Benjamini-Yekutieli and Bonferroni) as well as confidence intervals on the  $p$ -values.

The screenshot shows the 'P-value' tab in the santaR Shiny application. The interface includes a sidebar with 'Time: time' and 'Individual: ind', and a main panel with 'False Discovery Rate Correction' options:  Benjamini-Hochberg,  Benjamini-Yekutieli,  Bonferroni, and  Confidence Interval on p-value. Below this, there are tabs for 'Summary', 'All', 'P-value Dist', and 'P-value Fit'. The 'Summary' tab is active, displaying a table with the following data:

Test	Inf 0.05	Inf 0.01	Inf 0.001
dist	17	5	0
dist_BH	16	0	0

The screenshot shows the 'All P-value' tab in the santaR Shiny application. The interface is similar to the previous one, but the 'All' tab is active, displaying a table with 22 entries. The table has the following columns: var, dist, dist\_upper, dist\_lower, curveCorr, and dist\_BH. The first 10 entries are shown, and a search bar is available. The table data is as follows:

var	dist	dist_upper	dist_lower	curveCorr	dist_BH
var_15	0.002997003	0.008778565	0.001019262	0.1268472977	0.02874049
var_11	0.005994006	0.013020000	0.002748896	0.0568042969	0.02874049
var_8	0.006993007	0.014368956	0.003390296	-0.4678734702	0.02874049
var_6	0.007992008	0.015695799	0.004053809	-0.4766590516	0.02874049
var_3	0.009990010	0.018296616	0.005433704	-0.1309867342	0.02874049
var_5	0.010989011	0.019575399	0.006145277	-0.5634864236	0.02874049
var_1	0.012987013	0.022098179	0.007603209	-0.2429725171	0.02874049
var_16	0.012987013	0.022098179	0.007603209	0.5054671906	0.02874049
var_21	0.012987013	0.022098179	0.007603209	0.1461738945	0.02874049
var_2	0.014985015	0.024582471	0.009099629	0.0006571798	0.02874049

Showing 1 to 10 of 22 entries

# Export

The **Export** tab manages the saving of results and automated reporting. Fitted data is saved as a spline object, which contains all inputs and outputs, and subsequently downloaded as **.RData** file for future analysis, reproduction, or analysis of results.

**.csv** files containing significance testing results can also be generated and summary plot for each significantly altered variable automatically saved to disk for rapid evaluation.

The screenshot shows the 'Export Data' section of the SANTA App interface. It is divided into three main columns for saving different types of data:

- Save CSV imported data:** Create a .RData file with *inData* and *inMeta* for future import. All the data and metadata columns **as imported from a .csv** file will be available. The file name is `exportFromCSV`.
- Save input data as fitted:** Create a .RData file with *inData* and *inMeta* for future import. Only the data and metadata columns (*time/ind/group*) **used for fitting** are saved. The file name is `inputDataAsFitted`.
- Save fitted dataset:** Create a .RData file with *inSp* the fitting result for future analysis. The SANTAObjects also contain the calculated ConfBands and p-values. The file name is `fittedData`.

Each section has a 'Download' button. Below this is the 'Export P-values and Figures' section, which is noted as being possible only if Shiny is running on a local machine. It includes:

- Save P-values:** Stores all P-values calculated in multiple .csv file. ( default *summary\_pvalue-all.csv* ). It has a 'Summary file name' field with `summary` and three options for False Discovery Rate Correction:  Benjamini-Hochberg,  Benjamini-Yekutieli, and  Bonferroni. There is also a checked option for **Confidence Interval on p-value**.
- Save Figures:** Plots and save to disk all variables with a P-value inferior to a given cut-off. The 'P-value cut-off' is set to `0.05` and 'P-value dist' is `17 plots. Plot options include  Legend,  Confidence Bands, and  Total Mean Curve.`

A 'Target Folder' field contains `C:/result_TS_analysis` with a note to 'Select a target folder with write permission.' At the bottom, there are 'Save P-values' and 'Save plots' buttons.

## Final Note

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If a very high number of variables is to be processed, *santaR*'s command line functions are more efficient, as they can be integrated in scripts and the reporting automated.

## See Also

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- [Getting Started with santaR](#)
- [How to prepare input data for santaR](#)
- [santaR theoretical background](#)
- [Automated command line analysis](#)
- [Plotting options](#)
- [Selecting an optimal number of degrees of freedom](#)
- [Advanced command line options](#)