

## AutoNetBayes

**AutoNetBayes** is a tool developed for conducting Bayesian network meta-analyses using the R programming language. It simplifies the process by allowing users to input data, configure a few commands, and let the system automatically perform the analysis. The results are then presented in structured tables and graphs.

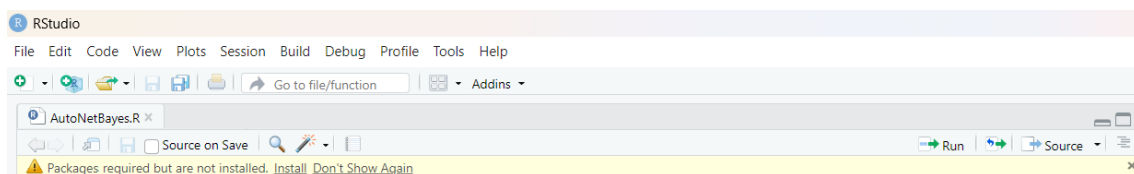
Initially, it is necessary to install R software and R-Studio platform, which can be downloaded from: <https://posit.co/download/rstudio-desktop/>. It is recommended to keep the R and Rstudio updated.

Once the software is installed, users should follow the steps outlined below that are exemplified using a network analysis of biological drugs:

### 1. Package Import

To run the software for the first time, some packages need to be installed: shinyjs[1], shiny[2], rio[3], gemtc[4], dplyr[5], purrr[6], tidyr[7], openxlsx[8], rsvg[9], svglite[10], network[11, 12], ggplot2[13], stringr[14], igraph[15], DT[16], tibble[17] and rjags[18].

When the code is opened, R will detect any missing packages and prompt the user to install them automatically by clicking "Install".



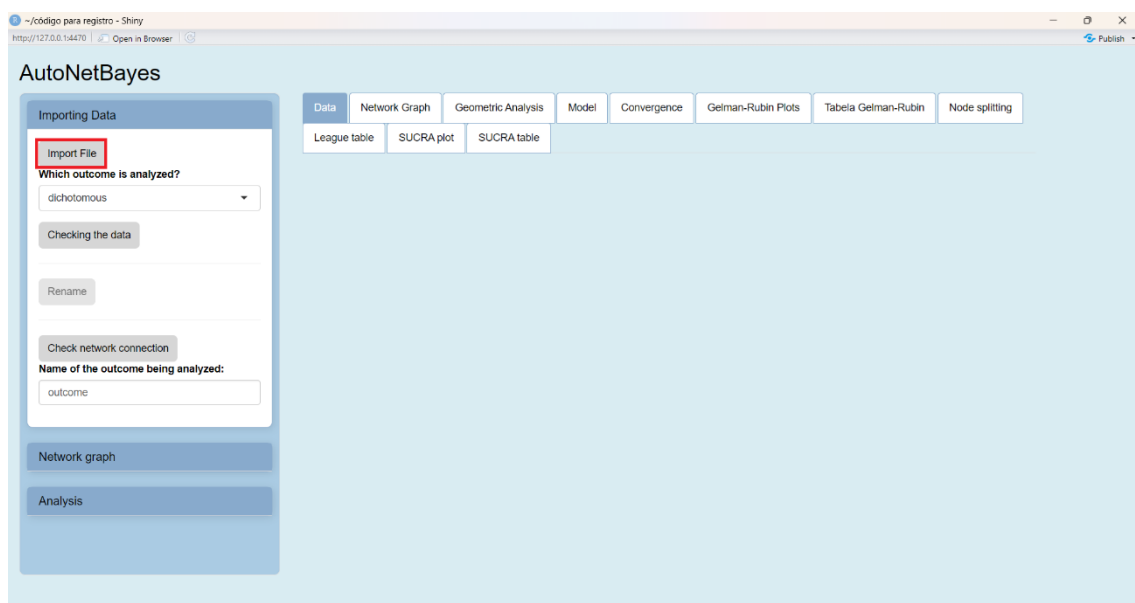
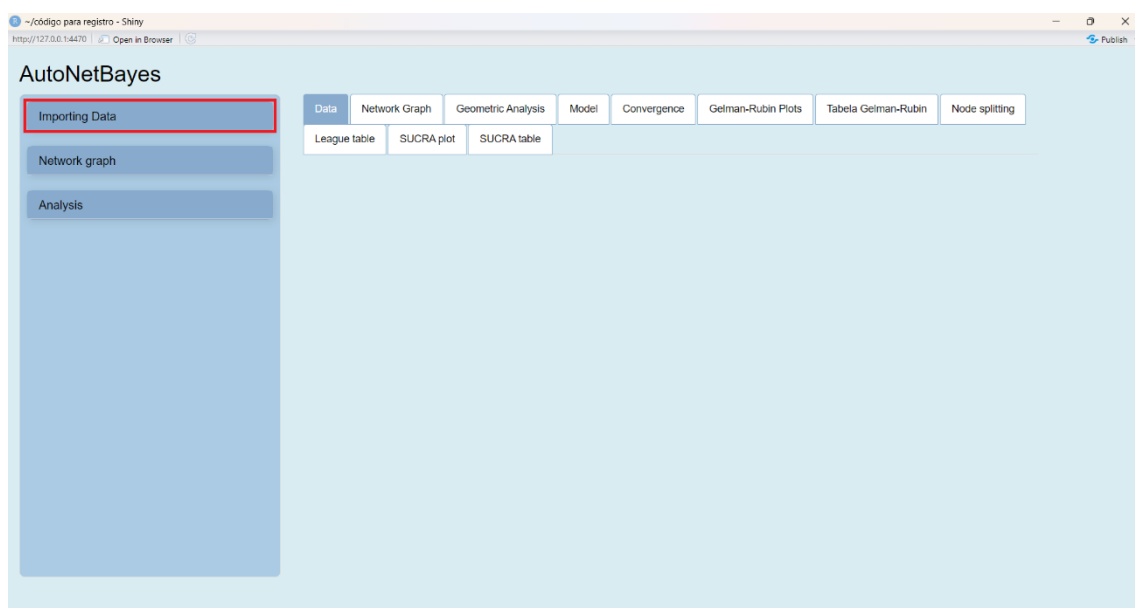
### 2. Start the analysis

After running the '# import AutoNetBayes' step, the panel opens automatically. If the user closes the panel and needs to reopen it, they can simply run the '# run AutoNetBayes' step.

The code will prompt the user to select a data file (in **xlsx** or **csv** format) using the **file.choose()** function. The dataset for each study intervention should be structured so that each set of information occupies a row. The file must include the information described on item 3 - Import dataset.

### 3. Import dataset

In the left-side panel, by selecting "Importing Data", the user can select a file in xlsx or csv formats and import it by clicking on "Import File".



The data for each intervention in the study should be organized so that each set of information occupies one row. The file should contain the following columns:

- **Study Identification:** Column named **study**

*In the case of crossover studies, name the different periods with equal numbers followed by different letters (e.g., 1A and 1B)*

- **Treatments:** Column named **treatment**. Do not use special characters or spaces in the names of interventions.
- **Number of Participants:** Column named **sampleSize**.
- **Outcomes:**
  - **Dichotomous:** Column **responders** (number of patients with the outcome).

study	treatment	sampleSize	responders
1	NNC2mg_kgSC	40.00	10.00
1	PBO	38.00	6.00
2	PBO	37.00	15.00
2	AMI0_4mgPO	39.00	11.00
3	RIS600mgIV	336.00	152.00
3	RIS1200mgIV	339.00	142.00
3	PBO	175.00	43.00

- **Continuous:** Column **mean** (mean) and **std.dev** (standard deviation).

study	treatment	sampleSize	mean	std.dev
1	PBO	55	20.00	29.00
1	SEM60mgIV	46	18.00	36.00
1	SEM60mgIVx3	51	21.00	36.00
2	UST130mgIV	209	29.10	33.82
2	UST6mg_kgIV	209	25.30	36.05
2	PBO	209	14.70	26.96
3	UST130mgIV	245	18.10	28.02
3	UST6mg_kgIV	249	22.10	28.59
3	PBO	247	11.90	26.51

- **Survival:** Column **responders** (number of patients with the outcome) and, if applicable, column **exposure**.

study	treatment	sampleSize	responders	exposure
1	NNC2mg_kgSC	40.00	10.00	100.1
1	PBO	38.00	6.00	105.3
2	PBO	37.00	15.00	104.6
2	AMI0_4mgPO	39.00	11.00	103.2
3	RIS600mgIV	336.00	152.00	101.5
3	RIS1200mgIV	339.00	142.00	103.8
3	PBO	175.00	43.00	104.9

## Choosing the Outcome

The user should provide the name of the outcome being analyzed, which will be used to name all files generated during the analysis.

## 4. Data verification

Once the data has been imported, it will be displayed in the 'Data' tab within the main panel:

The screenshot shows the AutoNetBayes web application interface. On the left, there is a sidebar with the title 'AutoNetBayes' and a section 'Importing Data'. This section includes buttons for 'Import File', 'Checking the data', 'Rename', 'Check network connection', and 'Analysis'. Below these is a text input field for 'Name of the outcome being analyzed:' with the value 'outcome'. The main panel has a top navigation bar with tabs: 'Data' (selected), 'Network Graph', 'Geometric Analysis', 'Model', 'Convergence', 'Gelman-Rubin Plots', 'Tabela Gelman-Rubin', and 'Node splitting'. Below the navigation bar, there are sub-tabs: 'League table', 'SUCRA plot', and 'SUCRA table'. A 'Show' dropdown is set to '50' and 'entries'. A search bar is present. The main content area displays a table with the following data:

study	treatment	sampleSize	responders
1	NNC0142-0002	40	10
1	Placebo	38	6
2	Placebo	37	15
2	Amiselimod	39	11
3	Risankizumab	675	294
3	Placebo	175	43
5	Risankizumab	40	32
5	Placebo	40	23
6	Ustekinumab	418	148
6	Placebo	209	41
50	Placebo	176	52
50	Upadacitinib	350	173
7	Placebo	171	36
7	Upadacitinib	324	126
8	Secukinumab	39	4

Next, the user must select the type of outcome to analyze, choosing from dichotomous, continuous or survival variables. Once selected, the uploaded data

can be reviewed by clicking 'checking the data' in the left-hand panel:

AutoNetBayes

Importing Data

Import File

Which outcome is analyzed?

dichotomous

Checking the data

Rename

Check network connection

Name of the outcome being analyzed:

outcome

Network graph

Analysis

Data

League table

SUCRA plot

SUCRA table

Model

Convergence

Gelman-Rubin Plots

Tabela Gelman-Rubin

Node splitting

Show 50 entries

Search:

study	treatment	sampleSize	responders
1	NNC0142-0002	40	10
1	Placebo	38	6
2	Placebo	37	15
2	Amiselimod	39	11
3	Risankizumab	675	294
3	Placebo	175	43
5	Risankizumab	40	32
5	Placebo	40	23
6	Ustekinumab	418	148
6	Placebo	209	41
50	Placebo	176	52
50	Upadacitinib	350	173
7	Placebo	171	36
7	Upadacitinib	324	126
8	Secukinumab	39	4

If the dataset contains all the required columns, the message **"All columns are correct!"** will be displayed. If one or more columns are missing from the imported spreadsheet, the user can specify the correct column name by clicking "Rename". Upon successful renaming, the message **"Columns have been renamed successfully!"** will appear.

AutoNetBayes

Importing Data

Import File

Which outcome is analyzed?

dichotomous

Checking the data

select the column for study

id

Rename

Check network connection

Name of the outcome being analyzed:

outcome

Network graph

Analysis

Data

League table

SUCRA plot

SUCRA table

Model

Convergence

Gelman-Rubin Plots

Tabela Gelman-Rubin

Node splitting

Show 50 entries

Search:

id	treatment	sampleSize	responders
1	NNC0142-0002	40	10
1	Placebo	38	6
2	Placebo	37	15
2	Amiselimod	39	11
3	Risankizumab	675	294
3	Placebo	175	43
5	Risankizumab	40	32
5	Placebo	40	23
6	Ustekinumab	418	148
6	Placebo	209	41
50	Placebo	176	52
50	Upadacitinib	350	173
7	Placebo	171	36
7	Upadacitinib	324	126
8	Secukinumab	39	4

AutoNetBayes

Importing Data

Import File

Which outcome is analyzed?  
dichotomous

Checking the data

select the column for study

Rename

Check network connection

Name of the outcome being analyzed:  
outcome

Network graph

Analysis

Data Network Graph Geometric Analysis Model Convergence Gelman-Rubin Plots Tabela Gelman-Rubin Node splitting

League table SUCRA plot SUCRA table

Show 50 entries Search:

study	treatment	sampleSize	responders
1	NNC0142-0002	40	10
1	Placebo	38	6
2	Placebo	37	15
2	Amiselimod	39	11
3	Risankizumab	675	294
3	Placebo	175	43
5	Risankizumab	40	32
5	Placebo	40	23
6	Ustekinumab	418	148
6	Placebo	209	41
50	Placebo	176	52
50	Upadacitinib	350	173
7	Placebo	171	36
7	Upadacitinib	324	126
8	Secukinumab	39	4

## • Verifying and Adjusting Columns in the Dataset

In this tab, the user can also check that if all the interventions are connected to the main network by selecting the "Check network connection" option:

AutoNetBayes

Importing Data

Import File

Which outcome is analyzed?  
dichotomous

Checking the data

select the column for study

Rename

Check network connection

Name of the outcome being analyzed:  
outcome

Network graph

Analysis

Data Network Graph Geometric Analysis Model Convergence Gelman-Rubin Plots Tabela Gelman-Rubin Node splitting

League table SUCRA plot SUCRA table

Show 50 entries Search:

study	treatment	sampleSize	responders
1	NNC0142-0002	40	10
1	Placebo	38	6
2	Placebo	37	15
2	Amiselimod	39	11
3	Risankizumab	675	294
3	Placebo	175	43
5	Risankizumab	40	32
5	Placebo	40	23
6	Ustekinumab	418	148
6	Placebo	209	41
50	Placebo	176	52
50	Upadacitinib	350	173
7	Placebo	171	36
7	Upadacitinib	324	126
8	Secukinumab	39	4

When checking the network connectivity, if all interventions are properly connected, the message **"All interventions are connected to the network! You can continue with the analysis"** will be displayed.

If the data forms more than one disconnected network, the network meta-analysis will not be possible. In this case, attempting to run the analysis will result in the error message **"Error when running the analysis. Check the data and try again."**. In this case, the user must reconfigure the spreadsheet and re-import the data.

If there are disconnected interventions, the message **"⚠ There are disconnected interventions in the network: [name of the disconnected interventions]. Verify the data before continuing with the analysis"** will be displayed. To solve this issue, the user must reconfigure the spreadsheet and re-import the data.

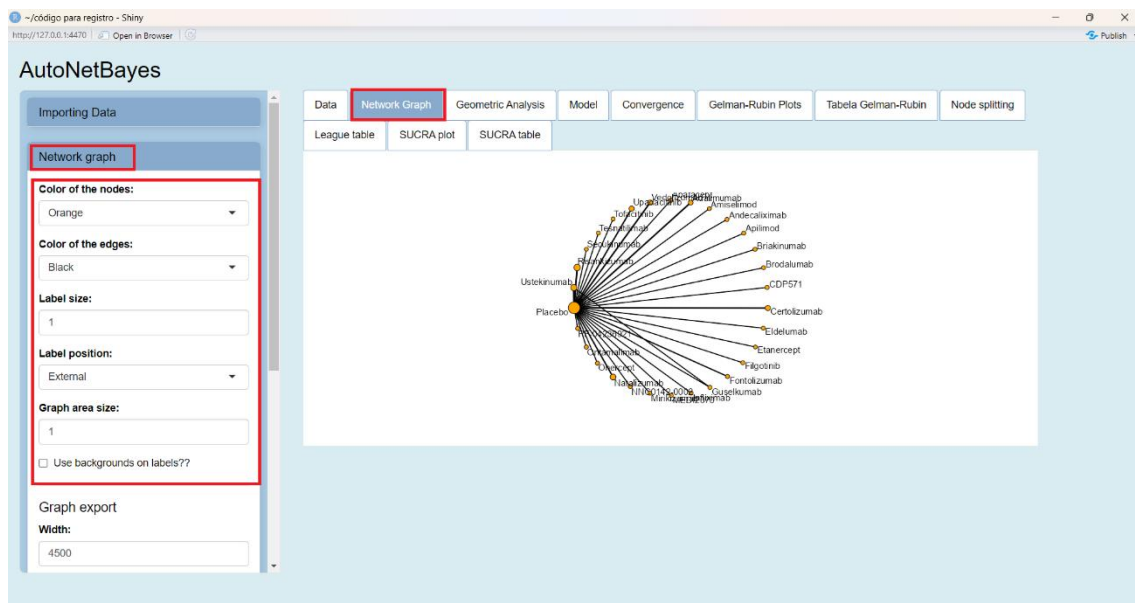
This tab also allows the user to specify a name of the result to be analyzed. If defined before running the analysis, this name will be automatically used for naming the exported files.

The screenshot shows the AutoNetBayes web application. On the left, the 'Importing Data' sidebar is active, showing the 'Name of the outcome being analyzed' field set to 'outcome'. The main panel displays a table of study data with columns for study, treatment, sampleSize, and responders.

study	treatment	sampleSize	responders
1	NNC0142-0002	40	10
1	Placebo	38	6
2	Placebo	37	15
2	Amisellimod	39	11
3	Risankizumab	675	294
3	Placebo	175	43
5	Risankizumab	40	32
5	Placebo	40	23
6	Ustekinumab	418	148
6	Placebo	209	41
50	Placebo	176	52
50	Upadacitinib	350	173
7	Placebo	171	36
7	Upadacitinib	324	126
8	Secukinumab	39	4

## 5. Network Plot Configuration

The Network Graph tab on the left-side panel allows the user to customize the graph displayed in the Network Graph tab of the main panel:

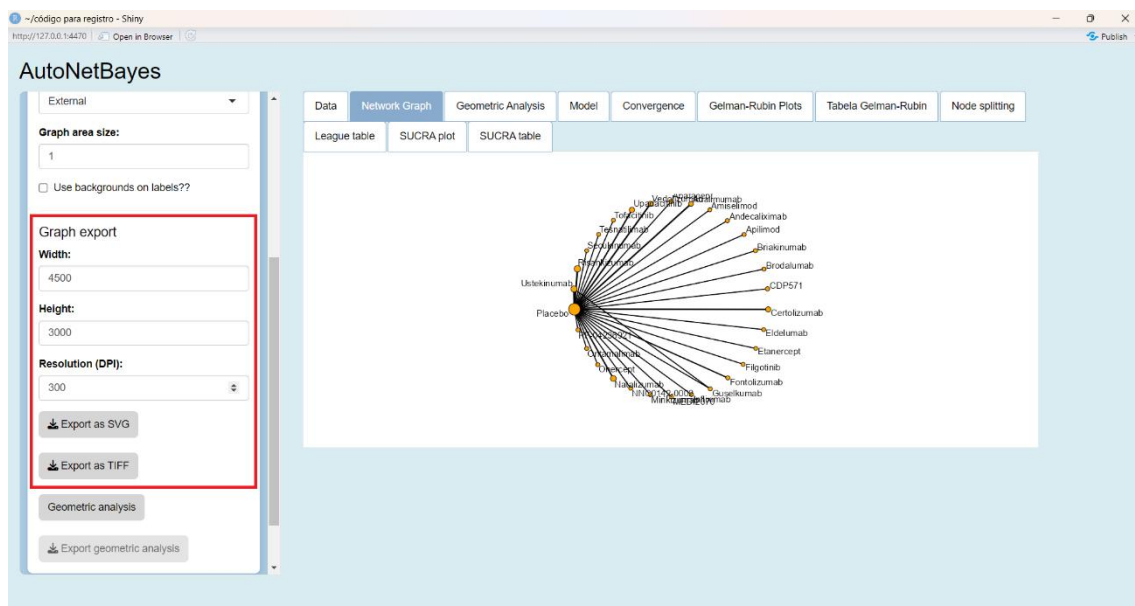


The customization options are:

- **Node Color:** Choose from 11 options (orange, light blue, dark blue, green, red, gray, purple, black, yellow, pink, aqua).
- **Edge Color:** Choose from 11 options (black, orange, light blue, dark blue, green, red, gray, purple, yellow, pink, aqua)
- **Label Size:** Numeric value that defines the text size (default: 1).
- **Distance between Labels and Nodes:** Value that adjusts the separation between the nodes and their labels (default: 1).
- **Plot Area Size:** Recommended value greater than 1, depending on the number of nodes (default: 1).
- **Label Position:** Choose from 6 positions (Extenal, below, left, above, right, center)
- **Label Background:** Choose between "Yes" or "No". If "Yes", select the color (orange, light blue, dark blue, green, red, gray, purple, white, yellow, pink, aqua) and background size (default: 1).

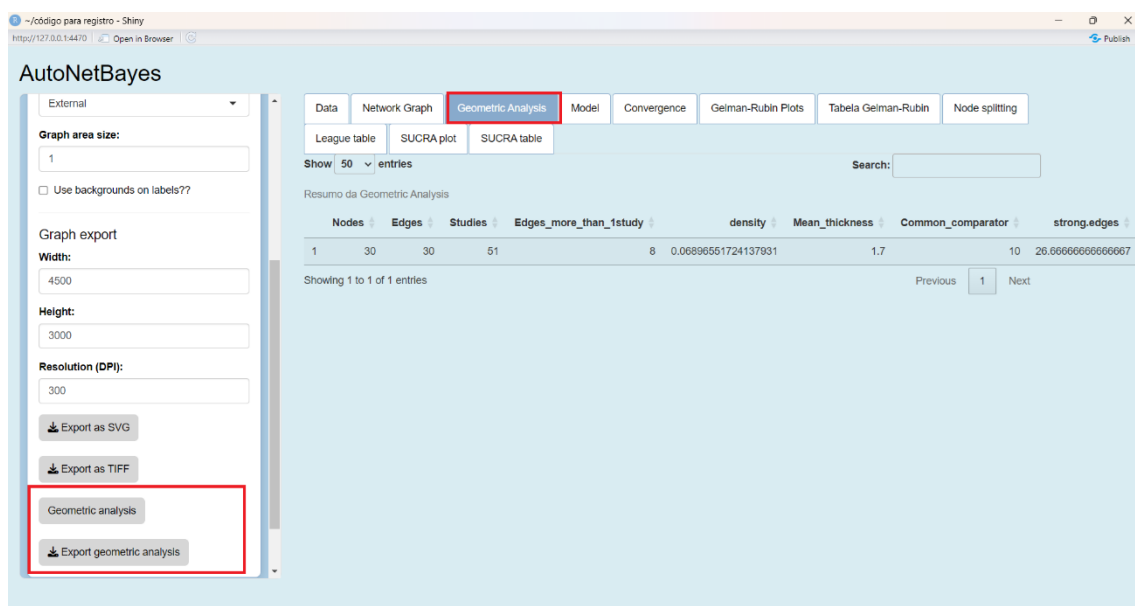
After customization, the user can export the graphics in SVG or TIFF format at 300 dpi. The SVG format allows the user to adjust the graphic elements using vector editing programs (e.g., Inkscape®):





## 6. Geometric Network Analysis

The code allows the user to analyze the geometric parameters of the network, as described by TONIN et al.[19]. To perform this analysis, select the "Geometric Analysis" option within the "Network Graph" tab in the left-side panel. The results will be displayed in the "Geometric Analysis" tab of the main panel:



## 7. Model Parameters Configuration

In the “Analysis” tab on the left-hand panel, the user must select the type of outcome to be calculated by the model, based on the type of variable previously selected (dichotomous, continuous or survival):

**AutoNetBayes**

**Analysis**

Configure model

Select the type of result:

Odds Ratio

Risk Ratio

Thinning Factor:

25

Number of Iterations:

5000

Run analysis

Export results

Export model summary to .txt

Download Traceplot in TIFF

Download densplot in TIFF

Geometric Analysis

League table SUCRA plot SUCRA table

Show 50 entries

Search:

Resumo da Geometric Analysis

Nodes	Edges	Studies	Edges_more_than_1study	density	Mean_thickness	Common_comparator	strong_edges
1	30	30	51	8	0.06896551724137931	1.7	10

Showing 1 to 1 of 1 entries

Previous 1 Next

Next, the user must provide the parameters for building the model:

**AutoNetBayes**

**Analysis**

Configure model

Select the type of result:

Odds Ratio

Number of Adaptations:

1000

Thinning Factor:

25

Number of Iterations:

5000

Run analysis

Export results

Export model summary to .txt

Download Traceplot in TIFF

Download densplot in TIFF

Geometric Analysis

League table SUCRA plot SUCRA table

Show 50 entries

Search:

Resumo da Geometric Analysis

Nodes	Edges	Studies	Edges_more_than_1study	density	Mean_thickness	Common_comparator	strong_edges
1	30	30	51	8	0.06896551724137931	1.7	10

Showing 1 to 1 of 1 entries

Previous 1 Next

- **Adaptation:** The number of times the algorithm will adjust its parameters (default: 1000).
- **Thinning factor:** Controls the number of samples that will be retained in the analysis, discarding some to reduce autocorrelation between consecutive samples (default: 25).

- **Number of iterations:** The number of times the algorithm will perform the sampling process during the analysis to estimate the posterior distributions of the parameters (default: 5000).

## 8. Model Execution

At this step, selecting "Run Analysis" will generate the model using the previously specified settings and perform the convergence assessment, inconsistency analysis, and league table generation:

AutoNetBayes

Analysis

Configure model

Select the type of result:

Odds Ratio

Number of Adaptations:

1000

Thinning Factor:

25

Number of Iterations:

5000

Run analysis

Export results

Export model summary to .txt

Download Traceplot in TIFF

Download densplot in TIFF

Data Network Graph Geometric Analysis Model Convergence Gelman-Rubin Plots Tabela Gelman-Rubin Node splitting

League table SUCRA plot SUCRA table

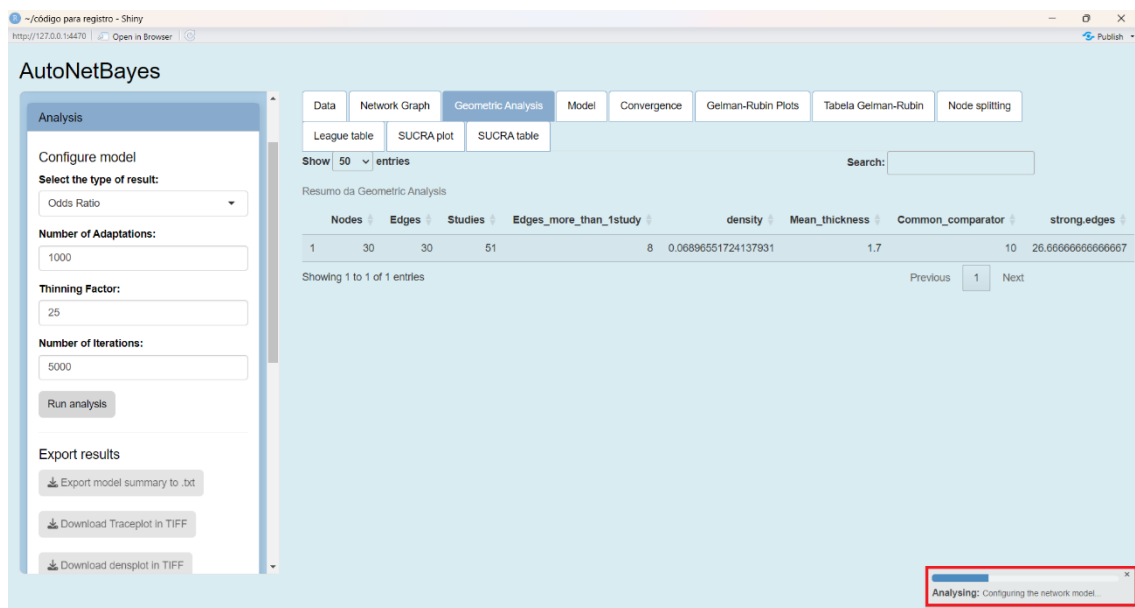
Show 50 entries Search:

Resumo da Geometric Analysis

Nodes	Edges	Studies	Edges_more_than_1study	density	Mean_thickness	Common_comparator	strong.edges
1	30	30	51	8	0.06806551724137931	1.7	10

Showing 1 to 1 of 1 entries Previous 1 Next

The progress of this step can be tracked by the progress bar in the lower right corner of the panel:



At the end of the analysis, the message " **Analysis successfully completed!**" will be displayed. The system then generates a summary of the model data, including convergence plots (trace plot and dens plot), Gelman-Rubin\* plots and table, the node-splitting\*\* table, and the Ranked List. Each of these results is presented in a separate tab within the main window and can be exported in the following formats: .txt (analysis summary), TIFF (graphs) and .xlsx (tables).

The screenshot shows the AutoNetBayes web application with the 'Model' tab selected. The 'League table' sub-tab is active, displaying the following table:

	Mean	SD	Naive SE	Time-series SE
d.Placebo.Abatacept	-0.31486	0.41627	0.014717	0.040796
d.Placebo.Adalimumab	1.34714	0.23329	0.008248	0.027790
d.Placebo.Amiselinod	-0.51341	0.46984	0.016611	0.048591
d.Placebo.Andecaliximab	0.27279	0.52896	0.018702	0.064226
d.Placebo.Aplimod	-0.60845	0.38743	0.013698	0.028694
d.Placebo.Briakinumab	0.98690	0.54195	0.019161	0.058350
d.Placebo.Brodalumab	2.01745	1.65614	0.058553	0.517093
d.Placebo.CDP571	-0.01759	0.23787	0.008410	0.014505
d.Placebo.Certolizumab	0.18369	0.13155	0.004651	0.009037
d.Placebo.Eldelumab	0.38163	0.43163	0.015260	0.044720
d.Placebo.Etanercept	0.81225	0.78851	0.027878	0.096901
d.Placebo.Filgotinib	1.13202	0.42865	0.015155	0.054477
d.Placebo.Fontolizumab	0.39663	0.39829	0.014082	0.045563
d.Placebo.Guselkumab	1.41571	0.27483	0.009717	0.027084
d.Placebo.Infliximab	2.58157	1.02635	0.036287	0.167717
d.Placebo.MEDI2070	0.48721	0.55743	0.019708	0.064244
d.Placebo.Mirikizumab	1.31661	0.47022	0.016625	0.042540
d.Placebo.Natalizumab	0.46890	0.12858	0.004546	0.007735
d.Placebo.NNK0142_0002	0.64863	0.58432	0.020659	0.083128
d.Placebo.Onercept	0.82178	0.37481	0.013223	0.034217
d.Placebo.Ontamalimab	0.29567	0.36139	0.012777	0.029906

\* If the error "Error in gelman.preplot(x, bin.width = bin.width, max.bins = max.bins, : Insufficient iterations to produce Gelman-Rubin plot" is displayed in the Gelman-Rubin plot tab, the user must rerun the analysis with a larger number of interactions.

\*\* If there are no loop comparisons involving more than one study, it will not be possible to perform the node splitting analysis. In this case, the message "No loop comparison with more than one study found. It was not possible to perform Node Splitting." will appear in the Node Splitting tab of the main panel.

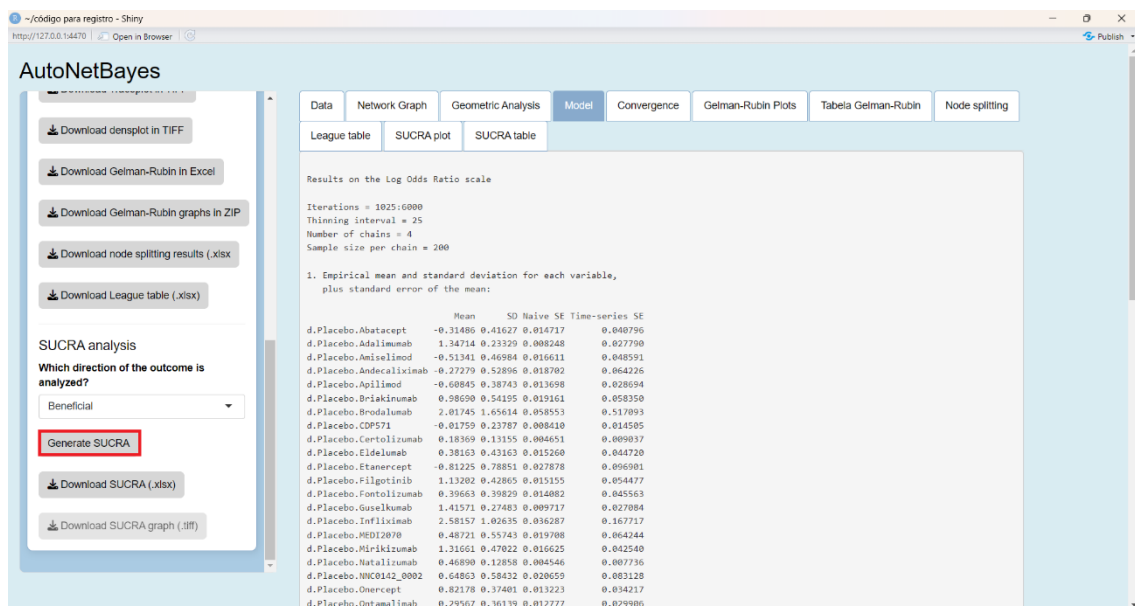
## 9. SUCRA Analysis

For the SUCRA analysis, the user must specify the direction of the outcome (beneficial or harmful) and then click "Generate SUCRA" in the "Analysis" tab on the left-hand panel:

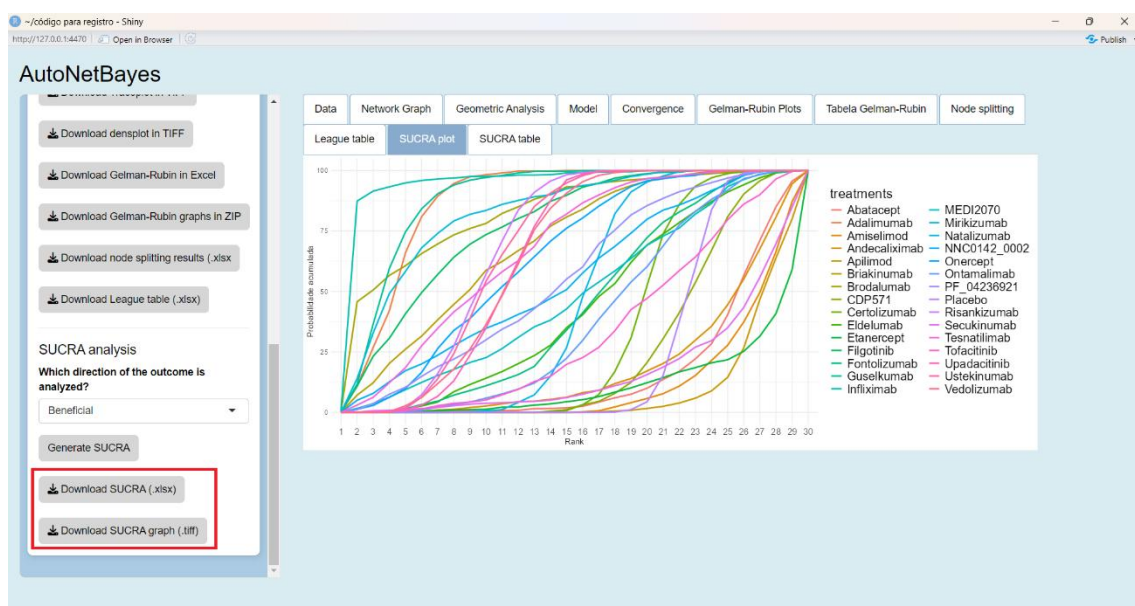
The screenshot displays the AutoNetBayes web application interface. On the left-hand panel, under the "Analysis" tab, the "SUCRA analysis" section is highlighted with a red box. It contains a dropdown menu labeled "Which direction of the outcome is analyzed?" with "Beneficial" selected. Below this are buttons for "Download SUCRA (.xlsx)" and "Download SUCRA graph (.tiff)".

The main panel shows the "Model" tab selected, displaying "Results on the Log Odds Ratio scale". It includes summary statistics: Iterations = 1025:6000, Thinning interval = 25, Number of chains = 4, and Sample size per chain = 200. Below this is a table of empirical mean and standard deviation for each variable.

	Mean	SD	Naive SE	Time-series SE
d.Placebo.Abatacept	-0.31486	0.41627	0.014717	0.048796
d.Placebo.Adalimumab	1.34714	0.23329	0.008248	0.027790
d.Placebo.Amiselmod	-0.51341	0.46984	0.016611	0.048591
d.Placebo.Andecaliximab	-0.27279	0.52896	0.018702	0.064226
d.Placebo.Aplimod	-0.60845	0.38743	0.013698	0.028694
d.Placebo.Briakinumab	0.98690	0.54195	0.019161	0.058350
d.Placebo.Brodalumab	2.01745	1.65614	0.050553	0.517093
d.Placebo.CDP571	-0.01759	0.23787	0.008410	0.014505
d.Placebo.Certolizumab	0.18369	0.13155	0.004651	0.009037
d.Placebo.Eldelumab	0.38163	0.43163	0.015260	0.044720
d.Placebo.Etanercept	-0.81225	0.78851	0.027878	0.096901
d.Placebo.Filgotinib	1.13202	0.42865	0.015155	0.054477
d.Placebo.Fontolizumab	0.39663	0.39829	0.014082	0.045563
d.Placebo.Guselkumab	1.41571	0.27483	0.009717	0.027004
d.Placebo.Infliximab	2.58157	1.80635	0.036287	0.157717
d.Placebo.MED12070	0.48721	0.55743	0.019788	0.064244
d.Placebo.Mirikizumab	1.31661	0.47022	0.016625	0.042540
d.Placebo.Natalizumab	0.46890	0.12858	0.004546	0.007736
d.Placebo.NMC0142_0002	0.64863	0.58432	0.020659	0.083128
d.Placebo.Onercept	0.82178	0.37401	0.013223	0.034217
d.Placebo.Ortanalimab	0.29567	0.36139	0.012777	0.029906



The results are displayed in the “SUCRA plot” and “SUCRA table” tabs in the main panel. These results can be exported using the “download SUCRA plot” (.tiff) and “download SUCRA” (.xlsx) buttons, respectively:



If additional analyses are desired, the code can be adapted or extended.

## Reference

- [1] D. Attali, shinyjs: Easily Improve the User Experience of Your Shiny Apps in Seconds, CRAN (Comprehensive R Archive Network), 2021.
- [2] W. Chang, J. Cheng, J.J. Allaire, C. Sievert, B. Schloerke, Y. Xie, J. Allen, J. McPherson, A. Dipert, B. Borges, Shiny: Web Application Framework for R., CRAN (Comprehensive R Archive Network), 2024.
- [3] C.-h.L. Chan, Thomas J.; Becker, Jason; Schoch, David rio: A Swiss-army knife for data file I/O, CRAN (Comprehensive R Archive Network), 2023.
- [4] G. van Valkenhoef, J. Kuiper, gemtc: Network Meta-Analysis Using Bayesian Methods, 2023.
- [5] H.F. Wickham, Romain; Henry, Lionel; Müller, Kirill ; Vaughan, Davis; Posit Software, dplyr: A Grammar of Data Manipulation, CRAN (Comprehensive R Archive Network), 2023.
- [6] H.H. Wickham, Lionel; Posit Software, purrr: Functional Programming Tools, CRAN (Comprehensive R Archive Network), 2025.
- [7] H.V. Wickham, Davis; Girlich, Maximilian; Ushey, Kevin; Posit Software, tidyr: Tidy Messy Data, CRAN (Comprehensive R Archive Network), 2024.
- [8] P.W. Schauburger, Alexander; Braglia, Luca; Sturm, Joshua; Garbuszus, Jan Marvin; Barbone, Jordan Mark; Zimmermann, David; Kainhofer, Reinhold, openxlsx: Read, Write and Edit xlsx Files, CRAN (Comprehensive R Archive Network), 2025.
- [9] J.B. Ooms, Salim, rsvg: Render SVG Images into PDF, PNG, (Encapsulated) PostScript, or Bitmap Arrays, CRAN (Comprehensive R Archive Network), 2025.
- [10] H.H. Wickham, Lionel; Pedersen, Thomas Lin; Luciani, T Jake; Decorde, Matthieu; Lise, Vaudor; Plate, Tony; Gohel, David; Qiu, Yixuan; Malmedal, Håkon; Posit, PBC, svglite: An 'SVG' Graphics Device, CRAN (Comprehensive R Archive Network), 2023.
- [11] C.T. Butts, network: A Package for Managing Relational Data in R, Journal of Statistical Software, 24 (2008) 1 - 36.
- [12] C.T. Butts, network: Classes for Relational Data, The Statnet Project (<http://www.statnet.org>), 2015.
- [13] H. Wickham, gplot2: Elegant Graphics for Data Analysis, Springer-Verlag, New York, 2016.
- [14] H.P.S. Wickham, PBC, stringr: Simple, Consistent Wrappers for Common String Operations, CRAN (Comprehensive R Archive Network), 2023.
- [15] G.N. Csárdi, Tamás; Traag, Vincent; Horvát, Szabolcs; Zanini, Fabio; Noom, Daniel; Müller, Kirill; Salmon, Maëlle; Antonov, Michael; Chan Zuckerberg Initiative, igraph: Network Analysis and Visualization, CRAN (Comprehensive R Archive Network), 2025.
- [16] Y.C. Xie, Joe; Tan, Xianying; Allaire, JJ; Girlich, Maximilian; Freedman Ellis, Greg; Rauh, Johannes; SpryMedia Limited; Reavis, Brian; Gersen, Leon; Szopka, Bartek; Pickering, Alex; Holmes, William; Marttila, Mikko; Quintero, Andres; Laurent, Stéphane; Posit Software, PBC, DT: A Wrapper of the JavaScript Library 'DataTables', CRAN (Comprehensive R Archive Network), 2024.
- [17] K.W. Müller, Hadley; Francois, Romain; Bryan, Jennifer; RStudio, tibble: Simple Data Frames, CRAN (Comprehensive R Archive Network), 2023.

- [18] M.S. Plummer, Alexey; Denwood, Matt, rjags: Bayesian Graphical Models using MCMC, CRAN (Comprehensive R Archive Network), 2025.
- [19] F.S. Tonin, H.H. Borba, A.M. Mendes, A. Wiens, F. Fernandez-Llimos, R. Pontarolo, Description of network meta-analysis geometry: A metrics design study, PLoS One, 14 (2019) e0212650.