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anvis

Automated Network VISualisation software

Connecting WUR data

Objective

The aim of this project is to provide a legible network visualisation tool using machine learning techniques to minimise the user's manual curation process.

Method

Networks are visualised in cartesian space to communicate the functions of the entire system. In order to avoid making the graphs too complicated, we reckon with the user's interests as user-defined node classifications. We further manipulate the topology of the figure using machine learning/AI techniques (Regressions and Sigmoid functions) to create data-driven visuals.

Results

We created a network visualisation software package in Bioconductor (R) that can be used in any user-defined data analysis pipeline. This package generates multiple human-readable co-ordinate visual representations of networks without the requirement of any manual curation. The package can produce networks that can be either directly visualised in R (using igraph) or using external software (Cytoscape) or exported to commonly used formats preserving network layouts such as graphNEL, igraph and xgmml that can be imported into tools of user's choosing. This provides researchers an open-source software to create human-interpretable visuals of networks describing complex systems without any manual curation using AI/DS techniques.

Impact

The use of big data and modeling of complex systems have become commonplace in most scientific disciplines, however, communicating results in a concrete way is a very time-consuming challenge. Our method of network visualisation should allow the user to isolate important information from the noise and help communicate the relevant states of the system. Apart from being a visual aid, we believe the software has the potential to be a reliable decision-making tool to determine further analysis
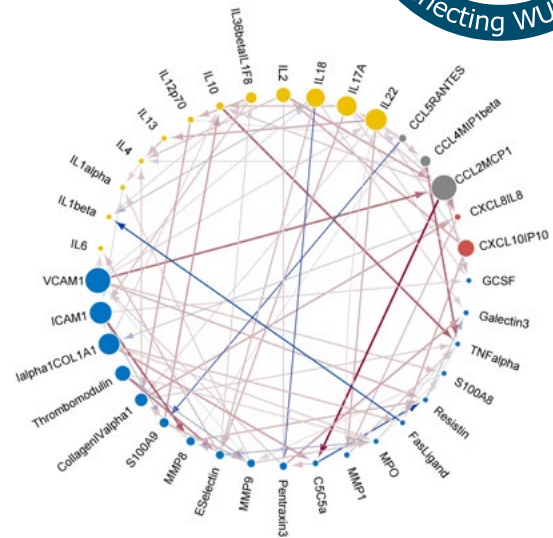

Figure1 The main function of the software outputs an automated visualisation that highlights the important variables and associations/interactions between those variables.

in any user-defined analysis pipeline. This software will speed up the process of interpreting results from network inference algorithms and related network differential/ similarity analysis.

Future plans

First, we will submit the finished package to Bioconductor (R) for being published as an open-source software. Since Bioconductor peer reviews the software packages, it is expected to take around 6 months for the package to be available on Bioconductor.

Second, we have uncovered interesting scientific finding by working with AEW (WUR) group using paleo-climate data. This finding will be used as an example for the utility of the software in the form of a publication/application note.

Further information

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Github: https://github.com/VanderJag/anvis.git

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