

PRYNT (PRioritization bY protein NeTwork)

Introduction

The urinary proteome is a promising pool of biomarkers of kidney disease. However, the protein changes observed in urine only partially reflect the deregulated mechanisms within kidney tissue. In order to improve on the mechanistic insight based on the urinary protein changes, we developed a new prioritization strategy called PRYNT (PRioritization bY protein NeTwork) that employs a combination of two closeness-based algorithms, shortest-path and random walk, and the protein-protein interaction (PPI) network STRING. In order to assess the performance of our approach, we evaluated both precision and specificity of PRYNT in prioritizing kidney disease candidates. Using four urinary proteome datasets associated with kidney diseases, PRYNT prioritization performed better than the standard reference method used by biologists that prioritizes experimental observations based on their p-value. Moreover, PRYNT performed to a similar, but complementary, extent compared to the upstream regulator analysis from the commercial Ingenuity Pathway Analysis software. In conclusion, PRYNT appears to be a valuable freely accessible disease candidate prioritization tool for urinary proteome data and could be equally applied to other biofluids, molecular traits and diseases. The source code is freely available on GitHub at: <https://github.com/Boizard/PRYNT>.

Getting started

Install software

PRYNT Application is programmed with R software and the shiny package. It is necessary to install R (<https://cran.r-project.org/bin/windows/base/>) and Rstudio (<https://rstudio.com/products/rstudio/download/#download>). Then you have to install the shiny package on the Rstudio console.

```
install.packages("shiny")
```

Launch the application

To run the tool you have to boot shiny package and run Laboiz by writing the following the code lines in Rstudio.

```
library("shiny")  
  
runGitHub(repo = "PRYNT",username = "Boizard", subdir="AppPRYNT)
```

For the first launch, the software install packages and dependencies (last few minutes).

Input datas

Format of the input

The input of the algorithm is a set of deregulate proteins. There is a area of free text to enter proteins in the application (see screenshot below) each line containing a protein.

Application PRYNT

PRIoritization bY protein NeTwork

Prioritize disease candidates from urinary protein profile

List of deregulated proteins (one of each line)

KRT4
BLMH
SERPINA5
FXD2
GSTT1

Not found :

GSTT1

Run PRYNT

Under the text zone, in red character, is showing all identifier which are not present in Sring database.

Once the data is entered the Run button will launch PRYNT.

Example data

A dataset, 'data.txt', is available in the files as an example. This set of deregulated proteins is from the study Bakun et al. (PMID: 31018934) concerning the Urine proteome of autosomal dominant polycystic kidney disease patients.

Results

The results are present in a table (see screenshot below) with 3 attributes: **rank** of the protein according to the PRYNT score, **gene symbol** identified the protein, **score** is the result of the algorithm (see the publication for details).

The application table present as well a tool to research a protein in the entire list.

Results

Show 10 entries

Search:

rank	Gene symbol	score
1	CDC5L	6
2	MAPK14	36
3	FGA	96
4	ADRB2	108
5	TCHH	110
6	IQGAP1	162
7	MAPK11	272
8	KEAP1	312
9	FGB	330
10	F2	348

rank	Gene symbol	score
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Showing 1 to 10 of 7,548 entries

Previous	1	2	3	4	5
...	755	Next			