

Introduction

Automated Workflows

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Outline

- Automated analysis workflows in R
- Three examples of how to use pathway information from COVID19 disease map / WikiPathways
- Can be extended to all WikiPathways pathways!

Setup

- Each workflow comes with an .Rmd file
- The data.zip files contains all required files for all three workflows
→ put all .Rmd files in the same folder as the extracted data folder
- **Process:**
 - Read the description of the section
 - Check if you need to change/write any code
 - Run the code block
 - Answer the questions > technical and biological
 - Move to next section

Setup

- We will work in breakout rooms with 2-3 people each
- Turn on the video, share the screen and discuss!
- Use the “Ask for help” button if you need input or help from one of the instructors and we will join the breakout room when someone is available

Workflow 1

Enrichment analysis
Pathway visualization
Drug-target extension



Transcriptomics data analysis

- Dataset: NHBE cells infected with SARS-CoV-2 vs. mock

| Steps | R-packages | Cytoscape apps |
|---|----------------------------------|----------------|
| Differential gene expression analysis (COVID19 vs. non-COVID19) | DESeq2 EnhancedVolcano | |
| Integration pathway content from Disease Map and WikiPathways (complete human collection) | rWikiPathways clusterProfiler | |
| Over-representation analysis | clusterProfiler | |
| Visualization of enrichment result | ggplot2 | |
| Pathway visualization in Cytoscape (make sure Cytoscape is open!) | RCy3 | WikiPathways |
| Network view of the pathway and extension with drug-target information | RCy3 | CyTargetLinker |

Workflow 2

Protein-protein interaction network

Network visualization

Extension with pathway information



Protein-protein interaction network

- Dataset: NHBE cells infected with SARS-CoV-2 vs. mock

| Step | R-packages | Cytoscape apps |
|--|------------|----------------|
| Select up- and down-regulated genes | | |
| Build PPI network with STRING | RCy3 | stringApp |
| Network visualization | RCy3 | |
| Extension with COVID19 pathway information | RCy3 | CyTargetLinker |

Workflow 3

Pathway crosstalk analysis (topology)

Proteomics data visualization

Animation

Enhanced visualization



Pathway crosstalk analysis

- Dataset: Multi-organ proteomic landscape of COVID19
 - <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7794601/>

| Step | R-packages | Cytoscape apps |
|--|--|------------------|
| Create COVID19 pathway crosstalk network (pathway-gene network) | clusterProfiler rWikiPathways RCy3 | |
| Network visualization | RCy3 | |
| Animation of proteomics data (lung, liver, kidney as examples!) – covid / non-covid for each organ | RCy3 | CyAnimator |
| Enhanced visualization (heatmap) to compare tissues | RCy3 | EnhancedGraphics |

Questions?

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