Notes for Ha’s Analysis:

* Make sure sessionInfo() is at the bottom of each script.

**0\_preprocessing:**

- had no issues running any code saved the PCA and tree to compare with Ha’s:

Chart, scatter chart

Description automatically generated

Chart, histogram

Description automatically generated

**1.1\_timepointSpecificGenes:**

- no issues running the scripts.

- results have ‘\_KK’ suffix

**1.2\_timepointSpecificGeneValidation**

Overall: All of the results I got matched Ha’s. Didn’t find any major bugs. Each section was well documented.

- changed a couple of paths from ‘Z:/hhvu/…’ to ‘Files/’

- Lines 143-149: RclusTool package ran on XQuartz window.

Chart, line chart

Description automatically generatedChart, line chart

Description automatically generatedChart, line chart

Description automatically generated

**2.1\_getAbundances**

* Add installation steps for the required packages.
* Changed the path to .h5 files to a path to .tsv files.

**2.2\_networkAnalysis**

- results look good.

- STRINGDB/Cytoscape/GLay:

- use version 11.0b in StringDB -> it will give different results. I would highlight this or change the link you have on your html.

- I built the networks 3 different times for each timepoint to look at the differences between GLay. When I ran on my laptop I got relatively the same subnetworks each time, but on my lab desktop they were different. ( I have included pictures of the sizes of my networks below ). I know Ha is aware of this difference and has looked into why GLay could be producing different results.

Table

Description automatically generated

Graphical user interface, table

Description automatically generated

PCE:

Chart

Description automatically generatedChart, waterfall chart

Description automatically generatedChart

Description automatically generatedA picture containing chart

Description automatically generatedA picture containing graphical user interface

Description automatically generatedChart, waterfall chart

Description automatically generatedChart, histogram, waterfall chart

Description automatically generated

- GENIE3:

- Version 1.16.0 -> be careful of the version because it will produce different results.

- Genie3 networks are slightly different due to different weights being calculated and therefore being ranked differently. We also noticed that GENIE3 performs differently on different systems. We don’t believe this changes the overall results of Ha’s analysis but may be something to note down in the RMD/HTML file.

- my GENIE3 networks are in GENIE3 folder with \_KK. Ha finished checking these scripts. I didn’t run PCE results again for this.

**3.1\_deconvolutionAnalysis:**

- output from deconvolution: Files/deconvolution\_422.errors

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3.2\_NetworkAnnotation:

- See PCE results above.

- Webgestalt results are found in PlacentaOntology folder.