Proteomics Exercise Part 3

1. Open this GeneName identifier file "ProteomicsDemoList2.txt." This file has 45 identifiers.

Go to the UniProt website and repeat the steps outlined in Part 1 of this exercise to map them to UniProt Identifiers. Then return for the next steps.

2. You should be able to generate an annotated file of 45 UniProt proteins.

3. Go to www.reactome.org. Select the "Analyze Data" option.

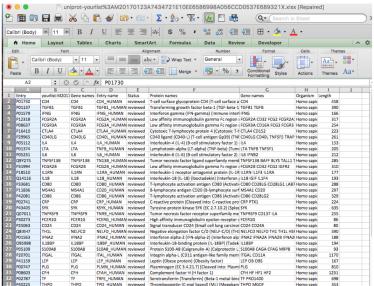
4. Copy/Paste your Accession list into the box. You can add a header line at the top following a # symbol.

Select "Continue."

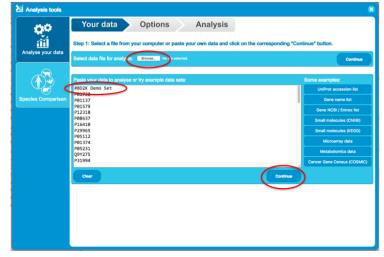
On the next page, select "Analyze" (all IDs are for Human).

5. The display should look similar to this image. You can change color profile settings as shown if you want to see overview better. I use barium salts. The darker the color, the more significant the pathway.

[no image]







Note: some IDs were not found. You can ignore these—not all gene/proteins exist in a defined pathway yet.

The central image is an overview display of all their pathways so you can quickly see what pathways your genes fall into. On the left you have all the pathways in their hierarchy. Note that Reactomes pathways are organized in a loose hierarchy (not all pathways resources do this).

On the bottom you have the analysis results pane, which is similar to the GO analysis we did and shows an over-representation of genes in a pathway compared to random results with the number of entities (proteins/genes) found, expected, and p-value, etc.

You can adjust pane sizes as needed. See <u>Reactome</u> tutorials for full details on the interface.

6. Note: the 3 panes are linked. If I click on one pathway, the other panels change also.

Hover over a term on the analysis results pane, and you will see it highlighted on the overview pane. Click on it, and the overview and hierarchy pane change to zoom in on more details.

7. In the analysis results pane, select "Hemostasis."

In the hierarchy pane we see the pathway we selected highlighted. Hemostasis is a high-level pathway in the hierarchy under which more specific pathways are grouped.

8. Select "Description," and you get a description of the pathway with references about what this top level pathway is about.

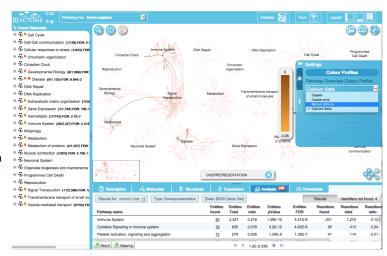
Hemostasis is a physiological response that culminates in the arrest of bleeding from an injured vessel.

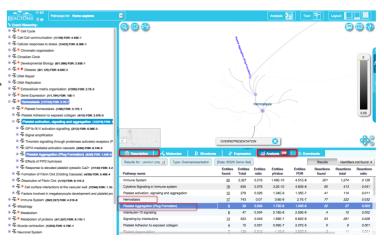
9. Select "Analysis" to go back to Analysis results.

Select "Platelet Aggregation (Plug Formation)" and you see in the hierarchy pane that it is one of the more specific pathways in the "Hemostasis" hierarchy under "Platelet activation, signaling and aggregation," which is also highlighted and on our list of significant hits.

Note: Results here are slightly different in order of significance than in the demo video as the Reactome database and pathways has been updated since the demo video was recorded. Slight changes like this are normal if the resources are improving themselves. It is important to note the database version and date you are using for any analysis you want to publish.

10. Double-click on the hemostasis pathway in the "Analysis" pane. Now you see 7 boxes in graphics pane illustrating that hemostasis is really a high-level collection of more detailed pathways related to hemostasis.





[no image]

[no image]

[no image]

The brown shading illustrates the proportion of genes/protein in our list that is in a pathway.

"Platelet Adhesion to exposed collagen" seems to have the most shading. Double click on it to see details.

Now we see some details of the pathway. Again, the brown shading shows genes that are in our list. The orange/pink color illustrates were in the cell certain reactions occur, cytosol, nucleus, membrane, extracellular, etc. Not all are shown in all pathways.

11. Now you see the pathway and reactions in more detail.

Open the pathway in the hierarchy pane and to see each reaction and click on the reaction "vWF binds to Collagen." This will zoom into the reaction. Adjust panes as needed.

Hover over "VWF" (von Willebrand Factor), one of the proteins in our list in the extra cellular space.

Double-click on the VWF box, and we see the reaction it participates in. VWF binds to Collagen type 1 to make collagen IV vWF complex, which then binds to another complex called GPIb-IX-V complex to form the GPIb-IX-V:vWF:Collagen IV complex on the plasma membrane.

Hover over GPIb-IX-V:vWF:Collagen IV complex or other box and you see an arrow on the right. Click to see the contents of the molecule or complex and which molecules are in our list (highlighted in brown) and which are missing (in blue). You can also see if the complex is involved in another pathway or other interactions.

Note: Red numbers on VWF (or other proteins) indicates that there are 4 proteins known to interact with the molecule in the IntAct database. More information can be found in the demo video.

Please investigate other options on the interface and/or take the tour or other tutorials Reactome offers.

Now lets take a quick look at the "Interaction of GPVI and FceRI gamma" reactions in this pathway. Click on the reaction "Interaction of GPVI and FceRI gamma" in the hierarchy pane.

12. Now lets take a quick look at the "Interaction of GPVI and FceRI gamma" reactions in this pathway.

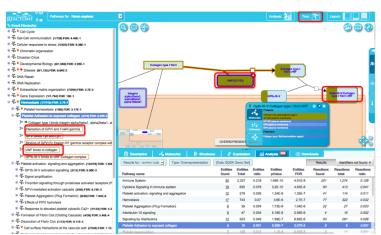
Click on the reaction "Interaction of GPVI and FceRI gamma" in the hierarchy pane.

You can go through the individual steps of the reaction on your own.

13. Now let's look at the description for this reaction by clicking on the "Description" button.

Glycoprotein VI (on our list) was identified as a collagen receptor from studies of patients with a GPVI deficiency. GPVI-deficient platelets lack collagen-induced





[no image]

aggregation and the ability to form thrombi (blood clots) on a collagen surface under flow conditions. GPVI complexes with the Fc epsilon R1 receptor gamma chain, with a possible stochiometry of two GPVI molecules and one FceRI gamma-chain dimer (Jung & Moroi 2008). GPVI binding to FcR gamma is necessary for high affinity GPVI binding to collagen.

Note: Publications are provided.

14. Go back to the analysis results.

This gives you a flavor of the level of detail you can get from a Reactome pathway analysis. Obviously many hours maybe needed to investigate this more, but let's back up and look at the big picture again.

Review the other significant hits on the "Analysis" pane and "Hierarchy" panes. What biological processes are related to this gene list? Lots of pathways related to hemostasis, platelets and immune system processes.

