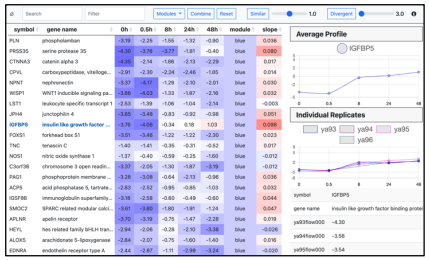
Profiler User Guide

USER GUIDE FOR *FLOW PROFILER*

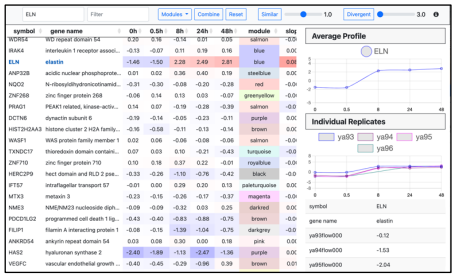
The Flow Profiler platform can be downloaded directly into any laptop or desk computer. It will improve accessibility and analysis capabilities of the generated flow data. The platform functions in chrome or firefox and can display the data as a table or plots and with some analysis functionalities.

You can click on specific modules to see genes that behave in a similar manner. Here the blue module was selected. You can then look at the transcriptional profile of any specific gene in the table and its plot to the right. The plot shows expression levels in each timepoint after flow exposure and the average value of available samples (the values shown in the table at columns 0h, 0.5h, 8h, 24h and 48h). Origin and slope values of this curve are also shown in the last columns of the table. The example on the right shows IGBP5 selected (as per the blue color on the table). On the right portion of the program and below the average plot, each individual sample (ya93, ya94, ya95, ya96) is displayed with another plot where each sample has its own curve (you can temporarily mask a curve on that plot by clicking on its name above the plot). Before any new selection – press the “reset” box.



Search: In the search bar you can type a gene name and hit [ENTER] when you’re done. The first match will be selected, be patient as the search will take a few seconds, you can see a glowing circle on the left of the search field while the program is working ongoing. If no hit is found in the table, the circle will be crossed out.

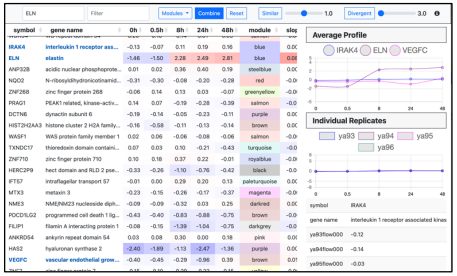
In the example on the right, the gene entered: Elastin shows transcriptional increase after 8h of flow.



For a new search – remember to first press the “Reset” function to clear the previous search.

Filter: In the filter box you can type text, and as soon as you type, the text will be looked up in the table, using the gene symbol, description, and module columns. Every line without a match will be masked, and you’ll see the filtered total entries number at the bottom of table reflecting the new displayed total. You can also use the “Modules” dropdown list to filter on the selected modules (you can select multiple modules and you need to re-click on a selected module to deselect it). You can combine both filter bar and modules dropdown list.

Combine: The combine tool allows displaying simultaneously multiple gene profiles in the same plot. Push the button to activate the “combine mode”. In that mode, each time you click on a gene in the table, that gene profile will be added to the plot. Re-click on a selected gene in the table to remove it from the plot. Push the “Combine” button again to leave the “combine mode”.



Note that when you use the search bar in combine mode, the first match will be automatically added to the plot. The example on the right shows IRAK4, ELN and VEGFC combined.

Hitting the “Reset” button will deselect all genes in the table and clear the plot. You can also temporarily mask a curve on the plot by clicking on its name above the plot.

Similar: This tool allows to find the most similar gene profiles compared to a selection of one or more profiles.

Figure 2-figure supplement 3

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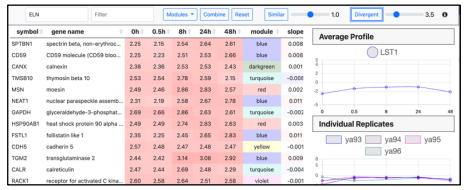
The similarity is defined by a value between 0 and 2, that you can select using the slider next to the “Similar” button. Then a range is defined for each available timepoint (the average value of the selection plus and minus the similarity value). When you hit the “Similar” button, all gene profiles in the table with all their timepoint in this range will be filtered, and you will see the filtered total entries number at the bottom of table reflecting the new displayed total. On the example above, the request was to find genes with a similar profile as ELN (upregulated by flow). Note that the “Similar” filter had to be adjusted to 1.6 to identify 11 transcripts out of 12,645.

Note that if the plot displays multiple gene profiles (using the “Combine” button), they are all considered for the similarity computation (using average value of all displayed profile for each timestamp).

Divergent: This tool allows to find the most divergent gene profiles compared to a selection of one or more profiles. The divergence is defined by a value between 3 and 5, that you can select using the slider next to the “Divergent” button. Then a range is defined for each available timepoint (the average value of the selection plus and minus the similarity value). When you hit the “Divergent” button, all gene profiles in the table with all their timestamp outside this range will be filtered, and you will see the filtered total entries number at the bottom of table reflecting the new displayed total. Note that if the plot displays multiple gene profiles (using the “Combine” button), they are all considered for the divergence computation (using average value of all displayed profile for each timepoint).



Draw: You can click on the plot to draw one or multiple coordinates, generating a custom profile. That custom profile can be alone (if you drawn on an empty plot when no gene is selected in the table) or combine to one or more gene profiles (if they are selected in the table). Thecu stom profile is considered by the “Similar” and “Divergent” tools. It means that, for example, if you are looking for genes with a specific behaviour, you can just draw the desired curve and hit the “Similar” button. In the example above, transcripts increased from 8 to 24h were requested using a “Similar” button with 1.6 stringency. Note that this custom curve can be partially drawn (missing some timestamp), those missing timestamp will just not be considered in the similarity/divergence computation. Use the “Reset” button if you want to clear your custom curve.