



lincsccloud > Tools and Apps > Interpreting Results

Query App Results

This page is dedicated to aid in interpreting results from the [LINCSCLOUD Query App](#). For information on how the application works and the underlying algorithms, please see our [support page](#).

The Query App takes as input one or two gene sets and computes the connectivity between these sets with all of the gene expression signatures in the LINC database. There are a number of different results generated by the Query App, each of which is accessible from an index page, as listed in the examples below.

The Query Title

Query Results

GS638200 MEK inhibitor GS6212 treated A375 clones (30nM at 24h) vs. DMSO treated

23-May-2014 1:29 PM

The input query was matched against 476,251 signatures derived from 1,208,088 experiments (Database version A2, release May 04 2014).

The results are shown in two formats:
1. A summary report listing perturbagens ranked by the strength and consistency of their connectivity to the input query, aggregated across cell types and experimental conditions.
2. A detailed view comprising the full list of connectivity scores between the input query and 476,251 signatures.

Help on interpreting these results is available in the [lincsccloud knowledge base](#).

Summary Report

- View Summary
- Download summary

Detailed Results

- Preview of top 2000 connections
- Download full result (476251 connections)

Inputs

- Up geneaset (139 features)
- Down geneaset (140 features)
- View Parameters

The name you assigned your query and the time at which it was run are displayed at the top of the page.

Summary Report

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12/1/15, 2:12 PM

Query Results

GS638200 MEK inhibitor GS6212 treated A375 clones (30nM at 24h) vs. DMSO treated

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The tool outputs a summary report like the one seen below. This report can be viewed by clicking the 'View Summary' link or by clicking the download icon to download the report as a text file.

1

Compound Connections

Rank	Comp ID	Comp Name	Score	Score	Score	Score	Score	Score
1	800-43700010	AP-1	100	100	100	100	100	100
2	800-43700010	AP-1	100	100	100	100	100	100
3	800-43700010	AP-1	100	100	100	100	100	100
4	800-43700010	AP-1	100	100	100	100	100	100
5	800-43700010	AP-1	100	100	100	100	100	100
6	800-43700010	AP-1	100	100	100	100	100	100
7	800-43700010	AP-1	100	100	100	100	100	100
8	800-43700010	AP-1	100	100	100	100	100	100
9	800-43700010	AP-1	100	100	100	100	100	100
10	800-43700010	AP-1	100	100	100	100	100	100
11	800-43700010	AP-1	100	100	100	100	100	100
12	800-43700010	AP-1	100	100	100	100	100	100
13	800-43700010	AP-1	100	100	100	100	100	100
14	800-43700010	AP-1	100	100	100	100	100	100
15	800-43700010	AP-1	100	100	100	100	100	100
16	800-43700010	AP-1	100	100	100	100	100	100
17	800-43700010	AP-1	100	100	100	100	100	100
18	800-43700010	AP-1	100	100	100	100	100	100
19	800-43700010	AP-1	100	100	100	100	100	100
20	800-43700010	AP-1	100	100	100	100	100	100

2

Gene Expression Connections

Rank	Comp ID	Comp Name	Score	Score	Score	Score	Score	Score
1	800-43700010	AP-1	100	100	100	100	100	100
2	800-43700010	AP-1	100	100	100	100	100	100
3	800-43700010	AP-1	100	100	100	100	100	100
4	800-43700010	AP-1	100	100	100	100	100	100
5	800-43700010	AP-1	100	100	100	100	100	100
6	800-43700010	AP-1	100	100	100	100	100	100
7	800-43700010	AP-1	100	100	100	100	100	100
8	800-43700010	AP-1	100	100	100	100	100	100
9	800-43700010	AP-1	100	100	100	100	100	100
10	800-43700010	AP-1	100	100	100	100	100	100
11	800-43700010	AP-1	100	100	100	100	100	100
12	800-43700010	AP-1	100	100	100	100	100	100
13	800-43700010	AP-1	100	100	100	100	100	100
14	800-43700010	AP-1	100	100	100	100	100	100
15	800-43700010	AP-1	100	100	100	100	100	100
16	800-43700010	AP-1	100	100	100	100	100	100
17	800-43700010	AP-1	100	100	100	100	100	100
18	800-43700010	AP-1	100	100	100	100	100	100
19	800-43700010	AP-1	100	100	100	100	100	100
20	800-43700010	AP-1	100	100	100	100	100	100

3

Overexpression Connections

Rank	Comp ID	Comp Name	Score	Score	Score	Score	Score	Score
1	800-43700010	AP-1	100	100	100	100	100	100
2	800-43700010	AP-1	100	100	100	100	100	100
3	800-43700010	AP-1	100	100	100	100	100	100
4	800-43700010	AP-1	100	100	100	100	100	100
5	800-43700010	AP-1	100	100	100	100	100	100
6	800-43700010	AP-1	100	100	100	100	100	100
7	800-43700010	AP-1	100	100	100	100	100	100
8	800-43700010	AP-1	100	100	100	100	100	100
9	800-43700010	AP-1	100	100	100	100	100	100
10	800-43700010	AP-1	100	100	100	100	100	100
11	800-43700010	AP-1	100	100	100	100	100	100
12	800-43700010	AP-1	100	100	100	100	100	100
13	800-43700010	AP-1	100	100	100	100	100	100
14	800-43700010	AP-1	100	100	100	100	100	100
15	800-43700010	AP-1	100	100	100	100	100	100
16	800-43700010	AP-1	100	100	100	100	100	100
17	800-43700010	AP-1	100	100	100	100	100	100
18	800-43700010	AP-1	100	100	100	100	100	100
19	800-43700010	AP-1	100	100	100	100	100	100
20	800-43700010	AP-1	100	100	100	100	100	100

to the gene expression signature derived by treating A375 cells with GSK212 at 30nM for 24 hours (relative to DMSO).

The tables list a number of metrics, each of which is described below:


Metric	Range	Description
cmap_id	n/a	A unique identifier for the given pertubagen
cmap_name	n/a	The common name for the pertubagen
score_best2	-100 to 100	The mean connectivity score across the two cell lines in which the pertubagen connected most strongly to the query
score_best4	-100 to 100	The mean connectivity score across the four cell lines in which the pertubagen connected most strongly to the query
score_best6	-100 to 100	The mean connectivity score across the six cell lines in which the pertubagen connected most strongly to the query
ncell	4 to 9	The number of cell lines over which the connectivity between the query and the pertubagen have been summarized

The different score metrics indicate how well a particular pertubagen connected to the query in the given best number of cell lines. In practice, we have found the **score_best4** metric to be a reasonable compromise between too many and too few cell types over which to summarize, and hence the tables are sorted by this value to start. The scores in these columns range from -100 (complete anti-connection) to 100 (complete connection). Positive values indicate that the perturbation gave a similar signature to the query, and negative values indicate that the perturbation gave a signature opposite to that of the query. -666 means that no information is available. We have generally found that scores with a magnitude of greater than **90** correspond to significant connections.

The underlying space of perturbagens in the summary report corresponds to the subset of perturbagens that have been profiled systematically across multiple cell types and have given reproducible signatures.

If we continue with the MEK inhibitor example above, we see in the 'Compound Connections' section that there are a number of compounds with strong positive connectivity scores, many of which are known MEK inhibitors (selumetinib, PD-0325901, UO126, AS-703026, PD-184352, known PI3-K inhibitor AS-605240 and known RAF inhibitor AZ-628). If we look in the 'Consensus Knockdown Connections' section, we also observe that knockdowns of known MEK pathway members (KRAS, MAP2K1) connect strongly to the query MEK inhibitor signature.

Detailed Results



Query Results

(GSE35200) MEK inhibitor GSK212 treated A375 clones (30nM at 24h) vs. DMSO treated

23-May-2014 1:29 PM

The input query was matched against 476,251 signatures derived from 1,328,088 experiments (Database version A2, release May 04 2014).

The results are shown in two formats:

1. A summary report listing pertubagens ranked by the strength and consistency of their connectivity to the input query, aggregated across cell types and experimental conditions.
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Inputs

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In addition to the summarized results described above, in which connections have been aggregated across cell types, it is also possible to view a detailed list of connections in which different cell types remain unaggregated. The top 2,000 connections can be previewed in the web browser by clicking the corresponding link, or a list of all connections can be downloaded as a text file by clicking the download icon.

The detailed report contains a number of fields, described in the table below:

Metric	Range	Description
rank	1 to 4,000	The rank by connectivity score of the particular signature
sig_id	n/a	A unique identifier for the signature
pert_id	n/a	A unique identifier for perturbation used to generate the signature
pert_iname	n/a	The common name for the perturbation
pert_type	n/a	A code for the type of perturbation. Please see this table for a list of all the pert_type values.
cell_id	n/a	The cell line in which the signature was generated
pert_time	3 to 144 h	The treatment time that generated the signature
pert_dose	n/a	The treatment dose that generated the signature
connectivity_score	-1 to 1	The integrated connectivity score for the query relative to the given signature.

up_score	-1 to 1	The connectivity score for the up-regulated genes in the query relative to the given signature.
down_score	-1 to 1	The connectivity score for the down-regulated genes in the query relative to the given signature.

Inputs



Lastly, the index page allows you to view and download the inputs and parameters for the query by clicking the links in this section.

[query_index_inputs.png](#) (90 KB)
[query_index_title.png](#) (90 KB)
[query_index_summary.png](#) (90 KB)
[query_index_detail.png](#) (90 KB)
[query_result_table_numbered.png](#) (200 KB)

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Comments



Jeanette McClintick

January 07, 2015 16:07

The reports on this page are unreadable. The columns identified by this knowledge base article no longer match the query report output. Is "score best 2" equivalent to "mean rank2". etc? What does a value of -666 mean. Reports are meaningless if you don't have a key to interpret them.