

OMIC TOOLS 12/20

Yusuke Kijima

CONTENTS

1. GeneWeaver

Web-based genomeic functional analysis tool enabling analysis across multiple species

2. PIANO

Convenient R package for GSA (Gene Set Analysis)

1. GeneWeaver

- What can we do with GeneWeaver?
 - Web-based easy GSA (Gene Set Analysis)
- Good
 - Easy analysis and abundant gene sets
- Bad
 - In fish, only zebrafish is available

1. GeneWeaver

How to use?

- Upload gene data

	gene	log2(fold_change)
1	Mir3597-1	-5.27725
2	Stpg1	-5.11362
3	Tnfr-ucg	-5.09248
4	Cacng8	-5.19032
5	Mir127,Mir431,Mir127-1,Mir18a	-5.18569
6	RGD1563748	-5.17924
7	Mir17-1,Mir18a	-5.01784
8	Col1a1	-4.46493
9	Cilp2	-4.11309
10	LCC102554942	-3.85932
11	Mir125b1,Vof16	-3.84164
12	Mir337,Mir493,Mir125b1	-3.77587
13	Twist2	-3.46401
14	Col1a2	-3.43137
15	LCC102551675	-3.42102
16	Tnfr-ocg	-3.35484
17	-	-3.32197
18	Kera	-3.31149
19	Gria2	-3.26845
20	Hmgb4	-3.18514
21	Fmod	-3.05833
22	Col11a1	-2.98085
23	Cpz	-2.9522
24	-	-2.90851
25	Comp	-2.90213
26	Chad	-2.89435



Gene name
and fold change

Gene List

Provide a list of genes to associate with the descriptive info from above.

Species:

Gene Identifiers:

Input Gene List*:

The species that the gene identifiers are coming from.

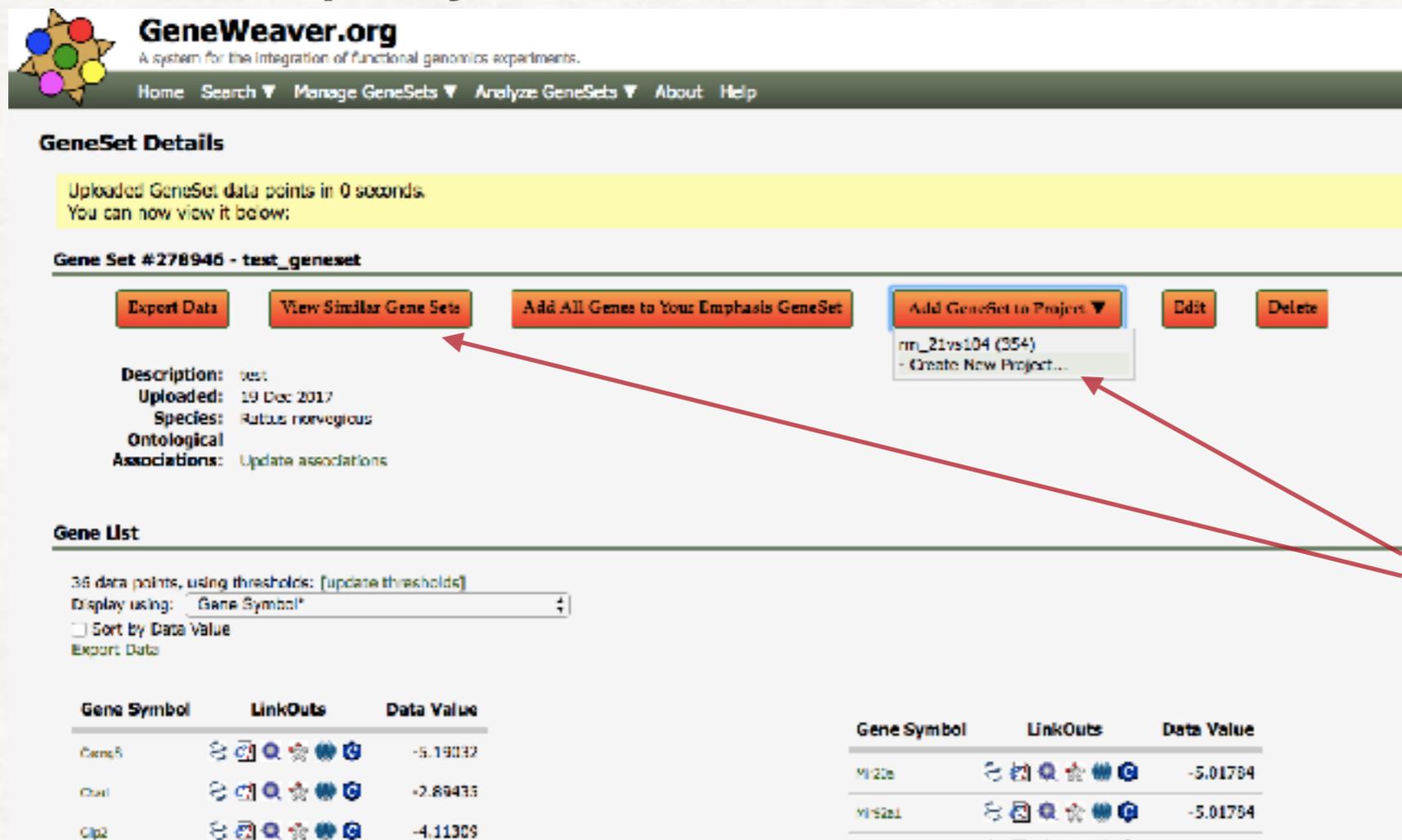
Switch to file upload

- ✓ -- please select --
- Mus musculus
- Homo sapiens
- Rattus norvegicus
- Danio rerio
- Drosophila melanogaster
- Macaca mulatta
- Caenorhabditis elegans
- Saccharomyces cerevisiae
- Gallus gallus
- Canis familiaris

1. GeneWeaver

How to use?

- Create project



GeneWeaver.org
A system for the integration of functional genomics experiments.

Home Search Manage GeneSets Analyze GeneSets About Help

GeneSet Details

Uploaded GeneSet data points in 0 seconds.
You can now view it below:

Gene Set #278946 - test_geneset

Export Data View Similar Gene Sets Add All Genes to Your Emphasis GeneSet Add GeneSet to Project Edit Delete

Description: test
Uploaded: 19 Dec 2017
Species: Rattus norvegicus
Ontological Associations: Update associations

Gene List

36 data points, using thresholds: [update thresholds]
Display using: Gene Symbol*
 Sort by Data Value
Export Data

Gene Symbol	LinkOuts	Data Value
Gene5		-5.19132
Gene1		-2.89435
Gene2		-4.11309

Gene Symbol	LinkOuts	Data Value
Mi22b		-5.01784
Mi22l		-5.01754

We can search similar gene sets and create projects for further analysis.

1. GeneWeaver

How to use?

- Create project

Analyze GeneSets Help | Feedback

Analysis Tools

- MSim Graph**
Bridges-based analysis is used to generate hierarchical maps of gene set interactions.
- GeneSet Graph**
Visualize the Gene-Geneset graph.
- Jaccard Overlap**
This tool compares the Jaccard Coefficient (a measure of similarity) for multiple gene sets.
- GeneSet Clustering**
Jaccard Distance (a measure of dissimilarity) is used to cluster GeneSets.
- ABBA Gene-Centered Search**
Find GeneSets most closely associated with your gene(s) of interest.
- Boolean Algebra**
Derive a new set back to integrate multiple GeneSets.
- Combine GeneSets**
Advanced tool to combine multiple GeneSets into a single association matrix.

rm_21vs104 - 354 GeneSets Favorite Guide

test1220 - 1 GeneSets Rename Guide

Add notes

Tbx1 16 Genes GS2789M6: test_geneSet Refresh

Add Selected to Project... Remove Selected Share with: Private

Adding some gene sets to the project, and then some statistical analysis is available.

1. GeneWeaver

How to use?

- Similar gene sets search

[← Back to GeneSet details](#)

Similar GeneSets: Select All

					Gene Similarity (Jaccard)		
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Tier I	Human	GC	426 Genes	GS196302: GO:0031012 extracellular matrix	0.079687
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Tier I	Mouse	GC	336 Genes	GS193273: GO:0005578 proteinaceous extracellular matrix	0.078995
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Tier I	Human	GC	362 Genes	GS110217: GO:0005578 proteinaceous extracellular matrix	0.077653
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Tier I	Mouse	GC	377 Genes	GS179537: GO:0031012 extracellular matrix	0.077052
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Tier I	Human		192 Genes	GS227358: MSigDB GeneSet - HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	0.070093
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Tier I	Mouse	GC	436 Genes	GS181450: GO:0014120 extracellular matrix part	0.065728
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Tier I	Human	GC	470 Genes	GS201254: GO:0014120 extracellular matrix part	0.063079
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Tier I	Rat		225 Genes	GS224301: Insulin dependent diabetes mellitus QTL 18 (iddm18 Published QTL Chr 6)	0.061994
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Tier I	Rat		247 Genes	GS224760: Colorectal carcinoma resistance QTL 5 (Colo5 Published QTL Chr 6)	0.059917
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Tier I	Human		254 Genes	GS232404: PC GeneSet - "extracellular matrix organization" pathway genes	0.059003
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Tier I	Human		257 Genes	GS240120: [MeSH] Basement Membrane : D001485	0.058704
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Tier I	Rat		204 Genes	GS224657: Insulin dependent diabetes mellitus QTL 29 (iddm29 Published QTL Chr 6)	0.057884
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Tier I	Rat		203 Genes	GS224725: Experimental allergic encephalomyelitis QTL 9 (Eae9 Published QTL Chr 6)	0.057423
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Tier I	Mouse	GC	107 Genes	GS181440: GO:0005581 collagen	0.057085
<input checked="" type="checkbox"/>	<input checked="" type="checkbox"/>	Tier I	Human		73 Genes	GS238431: [MeSH] Tendons : D013710	0.056475

We can search similar gene sets with our uploaded gene sets.

2. Piano

- What can we do with piano?
 - Flexible GSA
 - Analysis from raw output of microarray to advanced GSA plot.
- How to use?

2. Piano

- Good
 - Many species available
 - Complicated plot with brief command.
- Not good
 - A bit R skills are needed.
 - Microarray is now not mainstream, so we cannot make fully use of the benefit.