WORKSHOP Gene Set Analysis Approach CANB 7640

Aik Choon Tan, Ph.D. Associate Professor of Bioinformatics Division of Medical Oncology Department of Medicine aikchoon.tan@ucdenver.edu 9/18/2018 http://tanlab.ucdenver.edu/labHomePage/teaching/CANB7640/

GSEA GUI

http://www.broadinstitute.org/gsea/index.jsp

| 000 | CSEA v2.06 (Gene set enrichment analysis Broad Institute) | |
|---|---|-----|
| File Options Downloads Tools Hel | lp | |
| Steps in GSEA analysis | Home 🔣 Load data 🛪 🗱 Run Gsea 🗴 📲 Gsea 🗴 | > ▼ |
| | Load data: Import data into the application | |
| Load data | Method 3: drag and drop files here Supported file formats | |
| Run GSEA | Dataset: res or gct (Broad/MIT), pct (Stanford) txt (tab-delim text) Phenotype labels: cls | |
| eading edge analysis | Gene sets: gmx or gmt | |
| Gene set tools Chip2Chip mapping | | |
| 💓 Browse MSigDB | | |
| Analysis history | | |
| - GSEA reports Processes: click 'status' field for results | Clear Load these files! ⑦ More on file formats | |
| Name Status | Recently used files (double click to load, right click for more options) (Purge) Object cache (objects already loaded & ready for use, right click for more options) | |
| 2 I Gsea "Success 5 | /CELL_LINES/ENMD2076_CL_SvsR.cls /PDTX/ENMD2076_PDTX_SvsR.cls /RMA_GENES.CollapseDataset1377620563185/rma_collapsed_to_symbols.gct /CELL_LINES/ENMD2076_PDTX_SvsR.gt /CELL_LINES/ENMD2076_PDTX_SvsR.gt /LN4924/KEGG.101310_symbols.gmt /LN4924/KEGG.101310_symbols.gmt /CODES/kegg.082007.symbols.gmt /CESULTS/BIOCARTA.symbols.082007.gmt /RSSL_TS/ABIOCARTA.symbols.082007.gmt /SENvsRES/incl.nature.gmt /RIXGA/AMBION.gmt /SENvsRES/incl.nature.gmt /SENvsRES/incl.nature.gmt /RIXGA/ABIOCARTA.symbols.082007.gmt /RIXGA/AMBION.gmt /RIXGA/AMBION.gmt /RIXGA/AMBION.gmt /RIXGA/AMBION.gmt /RIXGA/AMBION.gmt /RIXGA/AMBION.gmt /RIXGA/AMBION.gmt /RIXGA/AMBION.gmt /RIXGA/AMBION.gmt /SENV-RES/incl.nature.gmt /RIXGA/AMBION.gmt /RIXGA/AMBION.gmt /RIXGA/AMBION.gmt /SENV-RES/incl.nature.gmt < | |
| | | |
| 5:17:15 PM + 4315 [INFO] Already a synch | ned dataset-template NO extracting done 392M of 600M | |

Loading Data into GSEA

| 000 | CSEA v2.06 (Gene | e set enrichment analysis –– Broad Institute) | | |
|--|---|--|---|---------------------------|
| File Options Downloads Tools Hel | p | | | |
| Steps in GSEA analysis | Home 🛛 🖸 Load data 🗻 🎇 Run Gsea 🛛 🖓 Gsea 🗴 | 🍯 Gsea 🛛 🖌 | | 4 4 4 |
| Load data | Load data: Import data into the application | | | |
| Load data | Method 1: | Method 3: drag and drop files here | Supported file formats | |
| Run GSEA | Browse for files | | Dataset: res or gct (Broad/MIT), pcl (Stanford) txt (tab-delim text) Phenotype labels: cls | |
| Leading edge analysis | Section 2: | | Gene sets: <i>gmx</i> or <i>gmt</i> | |
| Gene set tools | $\bigcirc \bigcirc \bigcirc$ | Open | | |
| Chip2Chip mapping | | example_datasets | | |
| Browse MSigDB | Recent folders (double click to list content) | Name | Date Modified | |
| ······································ | /Users/aikchoontan/RESEARCH/MLN4924_NEDD8/MLN4924 /Users/aikchoontan/PROJECTS/CODES | HG_U133A.chip | Monday, February 2, 2009 7:32 PM Monday, February 2, 2009 7:32 PM | |
| | /Users/aikchoontan/Downloads/COAD_RNASEQ_LEVEL3/GSEA_TC | | Monday, February 2, 2009 7:32 PM | |
| Analysis history | /Users/aikchoontan/AFFY_RAW_DATA/AFFY_HG1_ST_EXPLANTS_U | Leukemia.gct | Monday, February 2, 2009 7:32 PM | |
| CSEA reports Processes: click 'status' field for results Name Status 1 Gsea ··· Success 5 2 Gsea ··· Success 5 | /Users/aikchoontan/AFFY_RAW_DATA/AFFY_HG1_ST_EXPLANTS_UI /Users/aikchoontan/PUBLICATIONS/CDK8_Joaquin/SAMR/CSEA_AM /Users/aikchoontan/RESEARCH/TCCA_COAD/RNASeq_pett/PKM/ /Users/aikchoontan/RESEARCH/Ford_TRAIL_Lina/ANALYSIS_05171 /Users/aikchoontan/TAK-733_CLASSIFIER_CRC /Users/aikchoontan/GSEA2-2.02 /Users/aikchoontan/GSEA2-2.02/KEGC_092010 /Users/aikchoontan/GSEA2-2.02/KESUTS /Users/aikchoontan/GSEA2-2.02/KESUTS /Users/aikchoontan/RESEARCH/THYROID_MET/ALLSIGV4_G1000.0 /Users/aikchoontan/RESEARCH/CCLE/SQUAMOUS_CELL_LUNG/RM/ | Leukemina_ALLvsAML_C2_G500.Gsea.1372801 Leukemina_ALLvsAML_C2_P500.Gsea.13728025 | Tuesday, July 2, 2013 4:00 PM Tuesday, July 2, 2013 4:02 PM | ormats r more options) |
| | F | ile Format: CSEA supported file type | | |
| | | | Cancel Choose | |
| Show results folder | GSEA_ANALYSIS/kegg.hsa.cdk8.gmt | | | |
| 5:18:59 PM 🛛 🕀 4315 [INFO] Already a synch | ed dataset-template NO extracting done | | 1 | 394M of 600M |

Files loaded into GSEA



Select *.gct in Run GSEA

| Steps in GSEA analysis | Home 🛱 Load data 🛪 - 🕄 Bun Gsea | 💌 🎽 Gsea 🗴 📕 Gsea 🗴 | | | |
|---|--------------------------------------|---------------------------|-------------------------|----------|--|
| PP | Gsea: Set parameters and run enrichm | ent tests | | | |
| Load data | Required fields | | | | |
| | Expression dataset | Leukemia collansed symbol | [10056x48 (ann: 10056 (| 18 chin | |
| Run GSEA | | | 10050X40 (unit: 10050,- | | |
| | Gene sets database | | | | |
| Leading edge analysis | Number of permutations | 500 | | | |
| | Phenotype labels | | | | |
| Gene set tools | Collapse dataset to gene symbols | false | | ÷ | |
| Chip2Chip mapping | Permutation type | gene_set | | \$ | |
| | Chip platform(s) | | | | |
| | | | | | |
| | Basic fields | | | Show | |
| | | | | | |
| Analysis history | | | | | |
| | | | | | |
| | Advanced fields | | | Show | |
| | | | | | |
| GSEA reports Processes: click 'status' field for | | | | | |
| results Statur | | | | | |
| 1 B Gsea Success 5 | | | | | |
| 2 Bi Gsea Success 5 | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |

Select *.gmt in GSEA

| 000 | GSEA v2.06 (0 | Gene set enrichment analysis Broad Institute) |
|--|---|---|
| File Options Downloads Tools | Help | |
| Steps in GSEA analysis | Home 🛛 🏠 Load data 🛛 🗙 Run Gsea | 🔺 📲 Gsea x 🛛 🖓 Gsea x |
| Load data | Gsea: Set parameters and run enrichme | ent tests |
| | Required fields | |
| 200 | Expression dataset | Leukemia collapsed symbols [10056x48 (ann: 10056,48,chip + |
| Run GSEA | | |
| | Gene sets database | |
| Leading edge analysis | Number of permutations | 500 |
| 00 | Phenotype labels | |
| Gene set tools | Collapse dataset to gene symbols | false |
| | Permutation type | |
| Chip2Chip mapping | Permutation type | gene_set |
| | Chip platform(s) | |
| Browse MSigDB | | |
| | Basic fields | Show |
| | | |
| Analysis history | | |
| | | |
| | Advanced fields | Select one or more gene sets(s) |
| | | Gene matrix (local gmx/gmt) Subsets Text entry |
| GSEA reports | | kegg.hsa.2010.9.gmt [214 gene sets] |
| Processes: click 'status' field for | | c2.v1.symbols.gmt [522 gene sets] |
| Name Status | | |
| 1 III Gsea ···· Success 5 2 III Gsea ···· Success 5 | | |
| | | |
| | | |
| | | |
| | | |
| | | |
| | | |
| | | |
| | | |
| | | (?) Help Cancel OK |
| | | |
| | | |
| | | |
| | | |
| | | |
| Show results folder | 🅐 🧳 Reset | ≫ Last 📋 Command Normal (cpu usage) 😜 🕨 🕨 Run |
| 5:22:44 PM | 3 files c2 v1 symbols ant Leukomia clc La | ukemia collansed symbols ort. Files loaded successfully: 3 / 3 There were NO reasonable and successfully: 3 / 3 There were NO |

Select *.cls in GSEA

| | Home 🛛 🖸 Load data 🛛 🐼 Run Gsea | 🗖 🖌 🚰 Gsea × 🛛 🚝 Gsea × | 4 ▷ ◄ |
|---|---------------------------------------|--|-------|
| 💟 Load data | Gsea: Set parameters and run enrichme | ent tests | |
| ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ | Required fields Expression dataset | Leukemia_collapsed_symbols [10056x48 (ann: 10056,48,chip 🛟 | |
| Run GSEA | Gene sets database | aikchoontan/CSEA2-2.02/example_datasets/c2.v1.symbols.gmt | |
| Leading edge analysis | Number of permutations | 500 | |
| - | Phenotype labels | | |
| ne set tools | Collapse dataset to gene symbols | false 🗘 | |
| Chip2Chip mapping | Permutation type | gene_set | |
| | Chip platform(s) | | |
| Browse MSigDB | Basic fields | Show | |
| Analysis history | | | |
| | Advanced fields | O O Select a phenotype | |
| - | | Select source file Leukemia.cls [48 samples(24,24)=>2 classes] | _ |
| | | | |
| EA reports cesses: click 'status' field for | | Select one phenotype) | |
| Careports cesses: click 'status' field for ults Name Status | | Select one phenotype) ALL_versus_AML AML_versus_ALL | - |
| EA REPORTS cesses: click 'status' field for ults Name Status Gsea Success 5 Gsea Success 5 | | Select one phenotype) ALL_versus_AML AML_versus_ALL | - |
| A reports cesses: click 'status' field for ults Name Status III Gsea Success 5 III Gsea Success 5 | | Select one phenotype) ALL_versus_AML AML_versus_ALL | • |
| EA reports cesses: click 'status' field for ults Name Status Gsea Success 5 Gsea Success 5 | | Select one phenotype) ALL_versus_AML AML_versus_ALL Options | - |
| A reports cesses: click 'status' field for ults Name Status III Gsea Success 5 III Gsea Success 5 | | Select one phenotype) ALL_versus_AML AML_versus_ALL Options Show phenotypes from all source files | - |
| EA reports cesses: click 'status' field for ults Name Status © Gsea ···· Success 5 © Gsea ···· Success 5 | | Select one phenotype) ALL_versus_AML AML_versus_ALL Options Show phenotypes from all source files Create an on-the-fly phenotype | - |
| LA reports iccesses: click 'status' field for uits Name Status I Gsea ^{····} Success 5 I Gsea ^{····} Success 5 | | Select one phenotype) ALL_versus_AML AML_versus_ALL Options Create an on-the-fly phenotype Use a gene as the phenotype | - |
| A reports cesses: click 'status' field for ults Iname Status Geea Success 5 B Gsea Success 5 | | Select one phenotype) ALL versus_AML AML_versus_ALL Options Create an on-the-fly phenotype Use a gene as the phenotype With the phenotype of the phenotype in the phenotype is a gene as the phenotype in the phenotype is a gene in the ph | - |
| A reports cesses: click 'status' field for ults Name Status © Gsea ···· Success 5 © Gsea ···· Success 5 | | Select one phenotype) ALL_versus_AML AML_versus_ALL Options Create an on-the-fly phenotype Use a gene as the phenotype ? Help | - |

Collapsed Data

| • • • | GSEA v2.06 (C | ene set enrichment analysis Broad Institute) | | |
|--|---|--|-------------------------------|-------|
| ile Options Downloads Tools | Help | | | |
| Steps in GSEA analysis | Home Load data × Run Gsea | 🗙 💾 Gsea 🗴 📲 🎁 Gsea 🗴 | | 4 0 - |
| Load data | Gsea : Set parameters and run enrichme | nt tests | | |
| | Required fields | | | |
| Run GSEA | Expression dataset | Leukemia_collapsed_symbols [10056x48 (ann: 10056,4 | 18,chip | |
| | Gene sets database | 'aikchoontan/GSEA2-2.02/example_datasets/c2.v1.sym | bols.gmt . | |
| Leading edge analysis | Number of permutations | 500 | | |
| | Phenotype labels | true (use 'chip' to collapse dataset to symbols before analy | ysis) | ľ |
| Gene set tools | Collapse dataset to gene symbols | Taise (use dataset 'as is' in the original format) | | |
| Chip2Chip mapping | Chin platform(a) | pnenotype | | |
| | Chip platform(s) | | | |
| Browse MSigDB | Basic fields | | Show | |
| Analysis history | | | | |
| | | | | |
| | Advanced fields | | Show | |
| GSEA reports | | | | |
| rocesses: click 'status' field for esults | | | | |
| Name Status | | | | |
| Gsea Success 5 | | | | |
| a Usea Success S | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | ⑦ | 🖇 Last 🗐 Command | Normal (cpu usage) | Run |
| Show results folder | | | | |
| 6:13 PM 🛛 🕀 1948 [INFO] Loading | 3 files c2.v1.symbols.gmt Leukemia.cls Le | ukemia_collapsed_symbols.gct Files loaded successfully: 3 | / 3 There were NO 📋 394M of 6 | юом; |

If Collapsed Data = True, Select *.chip

| 000 | GSEA v2.06 (Ge | ene set enrichment analysis Broad Institute) |
|------------------------------------|--|---|
| File Options Downloads Tools | Help | |
| Steps in GSEA analysis | Home Load data × Run Gsea | 🗙 👸 Gsea x 🛛 🎁 Gsea x |
| Load data | Gsea: Set parameters and run enrichmen | nt tests |
| | Required fields | |
| S Run GSEA | Expression dataset | Leukemia_collapsed_symbols [10056x48 (ann: 10056,48,chip |
| | Gene sets database | aikchoontan/GSEA2-2.02/example_datasets/c2.v1.symbols.gmt |
| Leading edge analysis | Number of permutations | 500 |
| | Phenotype labels | 1/GSEA2-2.02/example_datasets/Leukemia.cls#ALL_versus_AML |
| Gene set tools | Collapse dataset to gene symbols | true ; |
| Chip2Chip mapping | Permutation type | phenotype 🛟 |
| | Chip platform(s) | |
| Browse MSigDB | | |
| | Basic fields | Show |
| Analysis history | | |
| <u> </u> | | |
| | Advanced fields | elect one or more chip(s) |
| | | Chips (from website) Chips (local .chip) |
| GSEA reports | | gseaftp.broadinstitute.org://pub/gsea/annotations/GENE_SYMBOL.chip |
| results | | gseartp.broadinstitute.org://pub/gsea/annotations/Seq_Accession.chip |
| Name Status | | gseaftp.broadinstitute.org://pub/gsea/annotations/HG_Focus.chip |
| 2 B Gsea Success 5 | | search.broadinstitute.org://pub/gsea/annotations/HG_0135A.chip |
| | | gseaftp.broadinstitute.org://pub/gsea/annotations/HG_U133A_2.chip |
| | | gseaftp.broadinstitute.org://pub/gsea/annotations/HG_U133_Plus_2.cnip gseaftp.broadinstitute.org://pub/gsea/annotations/HG_U95Av2.chip |
| | | gseaftp.broadinstitute.org://pub/gsea/annotations/HG_U95B.chip |
| | | geaftp.broadinstitute.org://pub/gsea/annotations/HG_U95D.chip |
| | | gseaftp.broadinstitute.org://pub/gsea/annotations/Hu35KsubA.chip |
| | | gseaftp.broadinstitute.org://pub/gsea/annotations/Hu35Ksub8.chip |
| | | gseaftp.broadinstitute.org://pub/gsea/annotations/Hu35KsubC.chip |
| | | |
| | | (7) Help Cancel OK |
| | | |
| | | |
| | | |
| | | |
| | 2 Parat | & Last Command Normal (on usage) |
| Show results folder | V V Neset | |
| :27:12 PM 🕀 1948 [INFO] Loading . | 3 files c2.v1.symbols.gmt Leukemia.cls Leu | kemia_collapsed_symbols.gct Files loaded successfully: 3 / 3 There were NO 📋 399M of 600M |

Select Type of Permutations

| 00 | GSEA v2.06 (Ge | ene set enrichment analysis Broad Institute) | |
|-------------------------------------|--|--|---------------------|
| File Options Downloads Tools | Help | | |
| Steps in GSEA analysis | Home Load data × Run Gsea | 🗙 🛅 Gsea × 🛛 🗂 Gsea × | 4 4 - |
| Load data | Gsea: Set parameters and run enrichmen | nt tests | |
| | Required fields | | - |
| Run CSEA | Expression dataset | Leukemia_collapsed_symbols [10056x48 (ann: 10056,48,chip | |
| Kun GSEA | Gene sets database | aikchoontan/GSEA2-2.02/example_datasets/c2.v1.symbols.gmt | |
| Leading edge analysis | Number of permutations | 500 | |
| | Phenotype labels | 1/GSEA2-2.02/example_datasets/Leukemia.cls#ALL_versus_AML | |
| Gene set tools | Collapse dataset to gene symbols | false | |
| Chip2Chip mapping | Permutation type | ✓ phenotype | |
| | Chip platform(s) | gene_set | |
| | | | |
| | Basic fields | | Show |
| | | | |
| Analysis history | | | |
| | | | |
| | Advanced fields | | Show |
| | | | |
| Processes: click 'status' field for | | | |
| results | | | |
| 1 Gsea Status | | | |
| 2 🛛 Gsea 💛 Success 5 | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | 🕜 💛 Reset | 🖇 Last 📄 Command Normal (ep | ou usage) 🛟 🕨 🕨 Run |
| Show results folder | | | |
| 5:28:16 PM 📑 1948 [INFO] Loading | 3 files c2.v1.symbols.gmt Leukemia.cls Leu | kemia_collapsed_symbols.gct Files loaded successfully: 3 / 3 There wer | e NO 📋 403M of 600M |

Select Number of Permutations

| 00 | GSEA v2.06 (C | Gene set enrichment analysis Broad Institute) | |
|-------------------------------------|---|--|-------|
| File Options Downloads Tools | Help | | |
| Steps in GSEA analysis | Home 💟 Load data 🛛 🔛 Run Gsea | 🗙 🛛 👸 Gsea 🗙 🖓 👸 Gsea 🗴 | 4 ▷ ▼ |
| Load data | Gsea : Set parameters and run enrichme | ent tests | |
| | Required fields | | |
| 879 | Expression dataset | Leukemia_collapsed_symbols [10056x48 (ann: 10056,48,chip 🛟 | |
| C • 2 Run GSEA | Gene sets database | aikchoontan/CSEA2-2.02/example_datasets/c2.v1_symbols_gmt | |
| | dene sets database | | |
| Leading edge analysis | Number of permutations | 500 | |
| | Phenotype labels | | |
| Gene set tools | Collapse dataset to gene symbols | 10 | |
| | Permutation type | 1000 | |
| Chip2Chip mapping | . Simulation type | | |
| | Chip platform(s) | | |
| Browse MSigDB | | | |
| | Basic fields | Sho | w) |
| | | | |
| Analysis history | | | |
| | | | |
| | Advanced fields | Sho | W |
| | | | |
| GSEA reports | | | |
| Processes: click 'status' field for | | | |
| results Name Status | | | |
| 1 GSea Success 5 | | | |
| 2 🖬 Gsea 👘 Success 5 | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | | | |
| | ⑦ 💛 Reset | 🖇 Last 📄 Command 🛛 Normal (cpu usage | Run |
| Show results folder | | | |
| | | | |

Select Analysis Name

| 00 | GSEA v2.06 (G | ene set enrichment analysis Broad Institute) | |
|-------------------------------------|--|---|---------------------|
| File Options Downloads Tools | Help | | |
| Steps in GSEA analysis | Home Load data × Run Gsea | 🗙 🛛 👸 Gsea x | 4 Þ 🕶 |
| Load data | Gsea: Set parameters and run enrichme | nt tests | |
| | Required fields | | |
| Run GSEA | Expression dataset | Leukemia_collapsed_symbols [10056x48 (ann: 10056,48,chip | |
| | Number of permutations | 500 | |
| Leading edge analysis | Phenotype labels | I/GSEA2-2.02/example_datasets/Leukemia.cls#ALL_versus_AML (…) | |
| Gene set tools | Collapse dataset to gene symbols | false | |
| Chip2Chip mapping | Permutation type | phenotype 🗘 | |
| | Chip platform(s) | | |
| Browse MSigDB | | | |
| | Basic fields | | Hide |
| Analysis history | Analysis name | Leukemia_GSEA_P500_C2 | ← |
| | Enrichment statistic | weighted | |
| | Metric for ranking genes | Signal2Noise | |
| CCEA reports | Gene list sorting mode | real | |
| Processes: click 'status' field for | Gene list ordering mode | descending | |
| results Name Status | Max size: exclude larger sets | 500 | |
| 2 Bi Gsea Success 5 | Min size: exclude smaller sets | 10 | |
| | Save results in this folder | | |
| | Advanced fields | | Show |
| | | | |
| Show results folder | ⑦ 🗳 Reset | S Last 🔁 Command Normal (cr | u usage) 🛟 🕨 🕨 Run |
| 5-29-07 PM 🔲 1948 [INFO] Loading | 3 files_c2.v1.symbols.gmt Leukemia.cls.Leu | Ikemia collapsed symbols.gct Files loaded successfully: 3 / 3 There wer | e NO 1 408M of 600M |

Select Enrichment Statistic

| 00 | GSEA v2.06 (C | ene set enrichment analysis Bro | ad Institute) | | |
|---|---|-----------------------------------|---------------------------|----------------------|--------------|
| File Options Downloads Tools | Help | - " | | | |
| Steps in GSEA analysis | Home Load data × Run Gsea | × Gsea × Gsea × | | | 4 1 7 |
| Load data | Gsea : Set parameters and run enrichme | nt tests | | | |
| | Required fields | | | | |
| A Run CSEA | Expression dataset | Leukemia_collapsed_symbols | 10056x48 (ann: 10056,4 | 48,chip 🛟 | |
| Kull USEA | Gene sets database | aikchoontan/GSEA2-2.02/exan | nple_datasets/c2.v1.sym | nbols.gmt | |
| Leading edge analysis | Number of permutations | 500 | | | |
| <u></u> | Phenotype labels | 1/GSEA2-2.02/example_dataset | s/Leukemia.cls#ALL_ver | rsus_AML ··· | |
| Gene set tools | Collapse dataset to gene symbols | false | | \$ | |
| Chip2Chip mapping | Permutation type | phenotype | | \$ | |
| | Chip platform(s) | | | | |
| W Browse MSigDB | | | | | |
| 17 | Basic fields | | | Hide | |
| | Analysis name | Loukomia CSEA DE00 C2 | | | |
| | Enrichment statistic | classic ✓ weighted | | | |
| | Matric for ranking gapos | weighted_p2 | | | |
| | metre for fairking genes | weighted_p1.5 | | | |
| | Gene list sorting mode | real | | | |
| Processes: click 'status' field for | Gene list ordering mode | descending | | ÷ | |
| results Name Status | Max size: exclude larger sets | 500 | | | |
| 1 □ Gsea […] Success 5 2 □ Gsea […] Success 5 | Min size: exclude smaller sets | 10 | | | |
| | Save results in this folder | | | | |
| | | | | | |
| | Advanced fields | | | Show | |
| | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |
| | | | | | |
| | | 0 | | | |
| Show results folder | ⑦ | 🖇 Last | 📄 Command | Normal (cpu usage) 📫 | Run |
| 5:29:48 PM | . 3 files. c2.v1.svmbols.gmt Leukemia.cls.Le | ukemia collapsed symbols oct File | es loaded successfully: 3 | 3 / 3 There were NO | 395M of 600M |

Select Metric for Ranking

| 00 | GSEA v2.06 (0 | ene set enrichment analysis Broad Institute) | | |
|---------------------------------------|---|--|----------------------------------|----------------------|
| File Options Downloads Tools | Help | | | |
| Steps in GSEA analysis | Home Load data × Run Gsea | 🗙 🛗 Gsea 🛛 🛗 Gsea 🗴 | | 4 > |
| Load data | Gsea: Set parameters and run enrichme | nt tests | | |
| | Required fields | | | |
| Pun GSEA | Expression dataset | Leukemia_collapsed_symbols [10056x48 (ann: 1005 | 6,48,chip 🗧 | |
| Kun GSEA | Gene sets database | aikchoontan/GSEA2-2.02/example_datasets/c2.v1.s | ymbols.gmt (···) | |
| | Number of permutations | 500 | | |
| Leading edge analysis | | | | |
| | Phenotype labels | 1/GSEA2-2.02/example_datasets/Leukemia.cls#ALL_v | versus_AML | |
| Gene set tools | Collapse dataset to gene symbols | false | \$ | |
| Chip2Chip mapping | Permutation type | phenotype | * | |
| | Chip platform(s) | | | |
| | | | | |
| Browse MSigDB | Pasic fields | | Hida | |
| | basic netus | | | |
| Analysis history | Analysis name | Leukemia_GSEA_P500_C2 | | |
| | Enrichment statistic | weighted | \$ | |
| | Metric for ranking genes | Signal2Noise | • | |
| | Gene list sorting mode | ✓ Signal2Noise | | |
| GSEA reports | | Cosine | | |
| Processes: click 'status' field for | Gene list ordering mode | Euclidean | | |
| Name Status | Max size: exclude larger sets | Pearson | U | |
| 1 Gsea Success 5 | Min size: exclude smaller sets | Ratio_of_Classes | <u>*</u> | |
| | Save results in this folder | DIT_OI_Classes | | |
| | | | | |
| | Advanced Galde | | (Shaw | |
| | Advanced fields | | Snow | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | (?) Contract Reset | 🖇 Last 📄 Command | Normal (cpu usage) | Run |
| Show results folder | C v veste | | (che availe) | |
| 5:30:39 PM 🛛 🕀 1948 [INFO] Loading . | 3 files c2.v1.symbols.gmt Leukemia.cls Le | ukemia_collapsed_symbols.gct Files loaded successfully | r: 3 / 3 There were NO 📋 399M of | <mark>60</mark> фм;/ |

Gene Sorting Mode

| | GSEA v2.06 (0 | Gene set enrichment analysis Bro | ad Institute) | |
|------------------------------------|---------------------------------------|----------------------------------|---------------------------------|------------------|
| ile Options Downloads Tools | Help | | | |
| Steps in GSEA analysis | | | | 4 Þ v |
| Load data | Gsea, set parameters and run enrichme | ent tests | | |
| | Required fields | | | |
| Run GSEA | Expression dataset | Leukemia_collapsed_symbols [| 10056x48 (ann: 10056,48,chip 🗧 | |
| | Gene sets database | aikchoontan/GSEA2-2.02/exam | pple_datasets/c2.v1.symbols.gmt | |
| I sading adap analysis | Number of permutations | 500 | • | |
| g g | Phenotype labels | 1/GSEA2-2.02/example_dataset | s/Leukemia.cls#ALL_versus_AML | |
| Gene set tools | Collapse dataset to gene symbols | false | • | |
| Chip2Chip mapping | Permutation type | phenotype | • | |
| | Chip platform(s) | | | |
| | | | | |
| | Basic fields | | (Hide) | |
| | Analysis name | Leukemia GSFA P500_C2 | | |
| Analysis history | Enrichmont statistic | weighted | | |
| | Matric for ranking ganos | Signal2Noise | | |
| | Cons list serting mode | real | | |
| SEA reports | Gene list sorting mode | | | |
| rocesses: click 'status' field for | Gene list ordering mode | descending | | |
| Name Status | Max size: exclude larger sets | 500 | • • | |
| Gsea Success 5 | Min size: exclude smaller sets | 10 | | |
| | Save results in this folder | | | |
| | | | | |
| | Advanced fields | | Show | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | ? Keset | 🖇 Last | 🗄 Command Normal (cpu usage) 🛟 | ▶ Run |
| Show results folder | | | | |

Set Gene Set Sizes

| Ontions Downloads Tools | GSEA v2.06 (| Gene set enrichment analysis –– Broad Institute) | | |
|---|---|--|--------------------|-------|
| eps in GSEA analysis | Home 🔯 Load data 🗴 🐺 Run Gsea | 🖂 📲 Gsea 🗴 📲 🚰 Gsea 🗴 | | 4 6 👻 |
| Load data | Gsea: Set parameters and run enrichme | ent tests | | |
| Run GSEA | Expression dataset | Leukemia_collapsed_symbols [10056x48 (ann: 100 | 056,48,chip | |
| 3 | Gene sets database Number of permutations | aikchoontan/CSEA2-2.02/example_datasets/c2.v1 | L.symbols.gmt | |
| Leading edge analysis | Phenotype labels | 1/GSEA2-2.02/example_datasets/Leukemia.cls#AL | L_versus_AML . | |
| ne set tools | Collapse dataset to gene symbols Permutation type | false | • | |
| | Chip platform(s) | | | |
| Browse MSigDB | Basic fields | | Hide | |
| Analysis history | Analysis name | Leukemia_GSEA_P500_C2 | | |
| | Enrichment statistic Metric for ranking genes | weighted Signal2Noise | • | |
| A reports | Gene list sorting mode | real | • | |
| esses: click 'status' field for Its Name Status | Max size: exclude larger sets | 500 | — | |
| Gsea Success 5 Gsea Success 5 | Min size: exclude smaller sets Save results in this folder | 10 | | |
| | Advanced fields | | Show | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | (?) 🖉 Reset | 🖇 Last 📄 Command | Normal (cpu-usage) | Run |

Save GSEA Results in Specific Folder

| 000 | GSEA | v2.06 (Gene set enrichment analysis Broad | d Institute) | |
|--|-----------------------------------|---|-------------------------------------|---------------------|
| File Options Downloads Tools | Help | | | |
| Steps in GSEA analysis | Home D Load data × Ru | n Gsea 🗙 🛗 Gsea 🗴 🛗 Gsea 🗴 | | 4 Þ 🕶 |
| Load data | Gsea: Set parameters and run e | nrichment tests | | |
| | Required fields | | | |
| 5003 | Expression dataset | Leukemia_collapsed_symbols [1 | 0056x48 (ann: 10056,48,chip 🛟 | |
| E S Run GSEA | Construction descriptions | | | |
| | Gene sets database | 🤗 🔿 🔿 Open | | |
| Leading edge analysis | Number of permutations | Recent: 🔲 RMA | 🗧 🛇 🗙 🧭 😭 | |
| | Phenotype labels | DeGregori Uruguay | | |
| Cone set tools | Collapse dataset to gene symi | DrugDevelopment | | |
| | | | | |
| Chip2Chip mapping | Permutation type | ► GLASGOW | | |
| | Chip platform(s) | ▶ | | |
| | | NatureInsight_Genomics_Medi OSI906 | cine_2004 | |
| | Rasic fields | PracticalBioinformatics | | Hide |
| | basic fields | | | (Inde |
| | Analysis name | ▼ ■ LECTURES | | |
| | Enrichment statistic | ► CLASS01 | Ť | |
| | Metric for ranking genes | ► CLASS02 | | |
| | | CLASS04 | - 1 | |
| | Gene list sorting mode | | ~ | |
| Processes: click 'status' field for | Gene list ordering mode | ► 🔲 UCD | ▲ ▼ | |
| results | Max size: exclude larger sets | | | |
| Name Status 1 Gsea Success 5 | Min size: exclude smaller sets | | Cancel Select | |
| 2 🛛 Gsea 💛 Success 5 | win size. exclude smaller sets | | | |
| | Save results in this folder | | | |
| | | | | • |
| | Advanced fields | | | Show |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | | | |
| | | A | | |
| Show results folder | 🕐 🤣 Reset | 🏷 Last | E] Command | ou usage) 😜 🕨 🕨 Run |
| 5:34:11 PM III 1948 [INFO] Loading | 3 files c2 v1 symbols amt Leukemi | a cls Leukemia collapsed symbols act. Files | loaded successfully: 3 / 3 There we | e NO a 409M of 60dM |

Advance Options

| | GSEA v2.06 (Ge | ne set enrichment analysis Broad Institute) | |
|--|---|--|-----------------------------|
| File Options Downloads Tools | Help | | |
| Steps in GSEA analysis | Home Load data × Ki Run Gsea | Gisea × Gisea × | ↓ ↓ |
| Load data | Phenotype labels | 1/GSEA2-2.02/example_datasets/Leukemia.cls#ALL_versus_A | |
| 6v3 | Collapse dataset to gene symbols | false | • |
| C • 2 Run GSEA | Permutation type | phenotype | • |
| Leading edge analysis | Chip platform(s) | | |
| Gene set tools | Basic fields | | Hide |
| Chip2Chip mapping | Analysis name | Leukemia_GSEA_P500_C2 | |
| | Enrichment statistic | weighted | • |
| Browse MSigDB | Metric for ranking genes | Signal2Noise | • |
| 17 | Gene list sorting mode | real | • |
| Analysis history | Gene list ordering mode | descending | \$ |
| | Max size: exclude larger sets | 500 | |
| | Min size: exclude smaller sets | 10 | |
| | Save results in this folder | :hoontan/TEACHING/PracticalBioinformatics/LECTURES/CLASS | 504 |
| SEA reports rocesses: click 'status' field for esults | Advanced fields | | Hide |
| Name Status Image: Sea image: Success 5 image: Su | Collapsing mode for probe sets => 1 gene | Max_probe | • |
| | Normalization mode | meandiv | • |
| | Randomization mode | no_balance | • |
| | Omit features with no symbol match | true | • |
| | Make detailed gene set report | true | ÷ |
| | Median for class metrics | false | • |
| | Number of markers | 100 | • |
| | Plot graphs for the top sets of each phenotype | 20 | • |
| | Seed for permutation | timestamp | |
| | Save random ranked lists | false | • |
| | Make a zipped file with all reports | false | |
| | ? Contract Contrac | 🖇 Last 🗐 Command 🛛 🕅 | ormal (cpu usage) 🛟 🕨 🕨 Run |
| Show results folder | | | |

Plot number of Markers

| | GSEA v2.06 (Ge | ne set enrichment analysis Broad Institute) | |
|--|---|--|----------------------|
| tens in CSEA analysis | Help | | 4 5 - |
| | Number of permutations | 500 | |
| Load data | Phenotype labels | 1/GSEA2-2.02/example_datasets/Leukemia.cls#ALL_versus_AML | |
| 27 | Collapse dataset to gene symbols | false | |
| Run GSEA | Permutation type | phenotype | |
| Leading edge analysis | Chip platform(s) | | • |
| ne set tools | Basic fields | | Hide |
| Chip2Chip mapping | Analysis name | Leukemia_GSEA_P500_C2 | |
| | Enrichment statistic | weighted | |
| Browse MSigDB | Metric for ranking genes | Signal2Noise | |
| | Gene list sorting mode | real | |
| L | Gene list ordering mode | descending | |
| Analysis history | Max size: exclude larger sets | 500 | |
| | Min size: exclude smaller sets | 10 | |
| | Save results in this folder | :hoontan/TEACHING/PracticalBioinformatics/LECTURES/CLASS04 | |
| A reports | | | |
| ults | Advanced fields | | Hide |
| Status III Gsea Success 5 III Gsea Success 5 | Collapsing mode for probe sets => 1 gene | Max_probe | |
| | Normalization mode | meandiv | |
| | Randomization mode | no_balance | |
| | Omit features with no symbol match | true | |
| | Make detailed gene set report | true | |
| | Median for class metrics | false | |
| | Number of markers | 100 | |
| | Plot graphs for the top sets of each phenotype | 20 | |
| | Seed for permutation | timestamp | |
| | Save random ranked lists | false | |
| | Make a zipped file with all reports | false | |
| Show results folder | ? Contract Contrac | Section Last Dommand Normal (| cpu usage) 🛟 🕨 🕨 Run |
| | | | |

Plot Graphs for the Top Gene Sets

| 00 | GSEA v2.06 (Ger | ne set enrichment analysis Broad Institute) | |
|--|---------------------------------------|--|-----------------------|
| File Options Downloads Tools Hel | | | |
| Steps in GSEA analysis Ho | me W2 Load data × Run Gsea > | Gisea × Gisea × | • • • |
| Load data | Number of permutations | 300 | |
| F | Phenotype labels | 1/GSEA2-2.02/example_datasets/Leukemia.cls#ALL_versus_AML | |
| C • J Run GSEA | Collapse dataset to gene symbols | (false : | |
| English and a second se | Permutation type | phenotype | |
| | Chip platform(s) | | |
| Leading edge analysis | | | _ |
| | Pasis fields | | Hida |
| Gene set tools | basic fields | | |
| Chip2Chip mapping | Analysis name | Leukemia_GSEA_P500_C2 | <u> </u> |
| E | Enrichment statistic | weighted | |
| Browse MSigDB | Metric for ranking genes | Signal2Noise : | |
| | Gene list sorting mode | real | |
| | Gene list ordering mode | descending | |
| Analysis history | May size avolude larger sets | 500 | - - |
| | max size. exclude larger sets | | |
| ' | Min size: exclude smaller sets | 10 | |
| S | Save results in this folder | :hoontan/TEACHING/PracticalBioinformatics/LECTURES/CLASS04 | |
| GSEA reports Processes: click 'status' field for | | | |
| results | Advanced fields | | Hide |
| Name Status 1 I Gsea Success 5 | Collapsing mode for probe sets => 1 | Max probe | a 🚺 |
| 2 🖾 Gsea 💛 Success 5 | gene . | | |
| | Normalization mode | meandiv | |
| 5 | Randomization mode | no_balance : | |
| | Omit features with no symbol match | true | |
| , | Make detailed gene set report | true | |
| | Median for class metrics | false | |
| | Number of markers | 100 | • |
| | Plot graphs for the top sets of each | 100 | |
| 1 | phenotype | 100 | |
| S | Seed for permutation | timestamp | |
| s | Save random ranked lists | false | |
| , | Make a zipped file with all reports | false | |
| | | | × |
| Show recults folder | ? | Section Last Command Normal | (cpu usage) 💠 🕨 🕨 Run |
| | las - 2 - 1 | and a share of a substance of the landed success (11, 2, 12, 20) | |

Execute GSEA

| 00 | GSEA v2.06 (Ge | ne set enrichment analysis Broad Institute) | |
|---|---|--|------------------|
| File Options Downloads Tools | Help | | |
| Steps in GSEA analysis | Home 🛛 🛄 Load data 🛛 🔛 🔛 Run Gsea | x Gsea x Gsea x | ▼ 4 Þ |
| Load data | Number of permutations Phenotype labels | 500 //GSEA2-2.02/example_datasets/Leukemia.cls#ALL_versus_AML ··· | |
| Run GSEA | Collapse dataset to gene symbols | false | |
| Ceading edge analysis | Chip platform(s) | phenotype | |
| Gene set tools | Basic fields | | Hide |
| Chip2Chip mapping | Analysis name | Leukemia_GSEA_P500_C2 | |
| | Enrichment statistic | weighted | |
| 💓 Browse MSigDB | Metric for ranking genes | Signal2Noise | |
| | Gene list sorting mode | real | |
| Analysis history | Gene list ordering mode | descending | |
| | Max size: exclude larger sets | 500 | |
| | Min size: exclude smaller sets | 10 | |
| | Save results in this folder | :hoontan/TEACHING/PracticalBioinformatics/LECTURES/CLASS04 | |
| GSEA reports Processes: click 'status' field for results Name Status | Advanced fields | | Hide |
| I III Gsea Success 5 2 III Gsea Success 5 | Collapsing mode for probe sets => 1 gene | Max_probe | |
| 3 🖾 Gsea Running | Normalization mode | meandiv | |
| | Randomization mode | no_balance | |
| | Omit features with no symbol match | true | |
| | Make detailed gene set report | true | |
| | Median for class metrics | | |
| | Number of markers Plot graphs for the top sets of each | | |
| | phenotype Soud for normalization | | |
| | Save random ranked lists | talse | |
| | Make a zipped file with all reports | false : | <u>.</u> |
| Chau recults folder | ⑦ 🖑 Reset | 🖇 Last 🗄 Com | u usage) 🗘 🕨 kun |
| Show results folder | | | |

Running Status (message)

| | | | _ |
|------------------------|--|----------|--------|
| Application messages | 5 | | |
| TLETALION. 441/300 101 | Leukenna_conapseu_symbols.Leukenna.cls#ALL_velsus_AML | | |
| Iteration: 446/500 for | r Leukemia_collapsed_symbols.Leukemia.cls#ALL_versus_AML | | - |
| Iteration: 451/500 for | r Leukemia_collapsed_symbols.Leukemia.cls#ALL_versus_AML | | |
| Iteration: 456/500 for | r Leukemia_collapsed_symbols.Leukemia.cls#ALL_versus_AML | | - |
| Iteration: 461/500 for | Leukemia_collapsed_symbols.Leukemia.cls#ALL_versus_AML | | |
| Iteration: 466/500 for | r Leukemia_collapsed_symbols.Leukemia.cls#ALL_versus_AML | | - |
| Iteration: 471/500 for | r Leukemia collapsed symbols.Leukemia.cls#ALL versus AML | | - |
| Iteration: 476/500 for | r Leukemia_collapsed_symbols.Leukemia.cls#ALL_versus_AML | | - |
| Iteration: 481/500 for | r Leukemia collapsed symbols.Leukemia.cls#ALL versus AML | | - |
| Iteration: 486/500 for | r Leukemia collapsed symbols.Leukemia.cls#ALL versus AML | | |
| Iteration: 491/500 for | r Leukemia, collapsed, symbols, Leukemia, cls#ALL, versus, AML | | _ |
| Iteration: 496/500 for | r Leukemia collapsed symbols. Leukemia.cls#ALL versus AMI | | |
| Finished permutations | s creating reports | | |
| INFO – Already a sync | hed dataset-template NO extracting done | | |
| Creating marker selec | tion reports | | |
| Creating EDR reports | | T | - |
| creating r Div reports | | | |
| | | 4 1 | |
| | | 1 | Cor |
| | Clear All Output | Copy | a) Cor |
| | | | |
| | wa sumahad dataset template | | |
| + 7015 [INFO] Alread | y a synched dataset-template NO extracting done | | |
| | | | |

Parameters as Command Line

0 0

Command Line for: xtools.gsea.Gsea

java -Xmx512m xtools.gsea.Gsea -res /Users/aikchoontan/GSEA2-2.02/example_datasets/Leukemia_collapsed_symbols.gct -cls /Users/aikchoontan/GSEA2-2.02/example_datasets/Leuken

| | phenotype | or the top sets or each | 100 | ▼ | |
|---------------------|---------------|-------------------------|-----------|----------------------------|-------|
| | Seed for perr | nutation | timestamp | • | |
| | Save random | ranked lists | false | * | |
| | Make a zippe | d file with all reports | false | \$ | |
| Show results folder | 0 | 💛 Reset | 👙 Last | Command Normal (cpu usage) | 🕨 Run |
| Show results folder | | | | \uparrow | |

4 1

Copy

Cancel

Run Completed

| | GSEA reports | | | | | | |
|---------------|-------------------------------------|--------|---------------|--|--|--|--|
| | Processes: click 'status' field for | | | | | | |
| | results | | | | | | |
| | | Name | Status | | | | |
| | 1 | 🛚 Gsea | ··· Success 5 | | | | |
| | 2 | 🛚 Gsea | ··· Success 5 | | | | |
| \rightarrow | 3 | 🛚 Gsea | ··· Success 5 | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | | | | | | | |
| | Show results folder | | | | | | |

Outputs GSEA

GSEA Report for Dataset Leukemia_collapsed_symbols

Enrichment in phenotype: ALL (24 samples)

- · 219 / 394 gene sets are upregulated in phenotype ALL
- 0 gene sets are significant at FDR < 25%
- 3 gene sets are significantly enriched at nominal pvalue < 1%
- 17 gene sets are significantly enriched at nominal pvalue < 5%
- <u>Snapshot</u> of enrichment results
- · Detailed enrichment results in html format
- · Detailed enrichment results in excel format (tab delimited text)
- Guide to interpret results

Enrichment in phenotype: AML (24 samples)

- 175 / 394 gene sets are upregulated in phenotype AML
- 0 gene sets are significantly enriched at FDR < 25%
- 2 gene sets are significantly enriched at nominal pvalue < 1%
- 19 gene sets are significantly enriched at nominal pvalue < 5%
- <u>Snapshot</u> of enrichment results
- Detailed <u>enrichment results in html</u> format
- · Detailed enrichment results in excel format (tab delimited text)
- <u>Guide to</u> interpret results

Dataset details

- The dataset has 10056 features (genes)
- · No probe set => gene symbol collapsing was requested, so all 10056 features were used

Gene set details

- · Gene set size filters (min=10, max=500) resulted in filtering out 128 / 522 gene sets
- · The remaining 394 gene sets were used in the analysis
- · List of gene sets used and their sizes (restricted to features in the specified dataset)

Gene markers for the ALL versus AML comparison

- · The dataset has 10056 features (genes)
- # of markers for phenotype ALL: 5460 (54.3%) with correlation area 60.5%
- # of markers for phenotype AML: 4596 (45.7%) with correlation area 39.5%
- Detailed <u>rank ordered gene list</u> for all features in the dataset
- · Heat map and gene list correlation profile for all features in the dataset
- <u>Buttefly plot</u> of significant genes

Global statistics and plots

- Plot of <u>p-values vs. NES</u>
- Global ES histogram

Other

· Parameters used for this analysis

Snapshot of enrichment results



Enrichment Results in ALL

Table: Gene sets enriched in phenotype ALL (24 samples) [plain text format]

| | GS follow link to MSigDB | GS DETAILS | SIZE | ES | NES | NOM p-val | FDR q-val | FWER p-val | RANK AT MAX | LEADING EDGE |
|----|---|------------|------|------|------|-----------|-----------|------------|-------------|---------------------------------|
| 1 | SETPATHWAY | Details | 11 | 0.78 | 1.83 | 0.000 | 0.755 | 0.348 | 1489 | tags=55%, list=15%, signal=64% |
| 2 | SIG_BCR_SIGNALING_PATHWAY | Details | 44 | 0.53 | 1.82 | 0.016 | 0.400 | 0.356 | 2233 | tags=50%, list=22%, signal=64% |
| 3 | GLUT_UP | Details | 269 | 0.44 | 1.77 | 0.016 | 0.454 | 0.502 | 2596 | tags=43%, list=26%, signal=57% |
| 4 | CARM-ERPATHWAY | Details | 26 | 0.61 | 1.76 | 0.030 | 0.386 | 0.538 | 1548 | tags=50%, list=15%, signal=59% |
| 5 | BCRPATHWAY | Details | 34 | 0.53 | 1.73 | 0.004 | 0.395 | 0.614 | 830 | tags=26%, list=8%, signal=29% |
| 6 | DNAFRAGMENTPATHWAY | Details | 10 | 0.70 | 1.70 | 0.015 | 0.437 | 0.668 | 1923 | tags=60%, list=19%, signal=74% |
| 7 | SIG_PIP3_SIGNALING_IN_B_LYMPHOCYTES | Details | 32 | 0.51 | 1.69 | 0.031 | 0.405 | 0.680 | 2026 | tags=50%, list=20%, signal=62% |
| 8 | FETAL_LIVER_HS_ENRICHED_TF_JP | Details | 68 | 0.43 | 1.68 | 0.016 | 0.381 | 0.692 | 2711 | tags=47%, list=27%, signal=64% |
| 9 | MRNA_SPLICING | Details | 47 | 0.61 | 1.66 | 0.059 | 0.400 | 0.728 | 3190 | tags=79%, list=32%, signal=115% |
| 10 | CXCR4PATHWAY | Details | 23 | 0.52 | 1.66 | 0.012 | 0.360 | 0.728 | 2192 | tags=43%, list=22%, signal=55% |
| 11 | ST_PHOSPHOINOSITIDE_3_KINASE_PATHWAY | Details | 32 | 0.46 | 1.63 | 0.029 | 0.399 | 0.772 | 2026 | tags=41%, list=20%, signal=51% |
| 12 | HTERT_UP | Details | 108 | 0.42 | 1.61 | 0.019 | 0.426 | 0.808 | 2249 | tags=40%, list=22%, signal=51% |
| 13 | CR_REPAIR | Details | 39 | 0.56 | 1.60 | 0.058 | 0.417 | 0.816 | 3683 | tags=77%, list=37%, signal=121% |
| 14 | PROTEASOME_DEGRADATION | Details | 31 | 0.60 | 1.59 | 0.083 | 0.424 | 0.834 | 1699 | tags=45%, list=17%, signal=54% |
| 15 | ACHPATHWAY | Details | 14 | 0.51 | 1.58 | 0.048 | 0.421 | 0.844 | 1357 | tags=43%, list=13%, signal=49% |
| 16 | CALCINEURINPATHWAY | Details | 18 | 0.54 | 1.58 | 0.027 | 0.398 | 0.848 | 2307 | tags=39%, list=23%, signal=50% |
| 17 | RAP_UP | Details | 169 | 0.40 | 1.56 | 0.048 | 0.447 | 0.874 | 1364 | tags=29%, list=14%, signal=33% |
| 18 | ST_B_CELL_ANTIGEN_RECEPTOR | Details | 38 | 0.44 | 1.55 | 0.045 | 0.431 | 0.878 | 2233 | tags=39%, list=22%, signal=51% |
| 19 | MRNA_PROCESSING | Details | 40 | 0.58 | 1.54 | 0.097 | 0.444 | 0.890 | 2070 | tags=63%, list=21%, signal=78% |
| 20 | SIG_CHEMOTAXIS | Details | 40 | 0.44 | 1.54 | 0.008 | 0.426 | 0.890 | 873 | tags=25%, list=9%, signal=27% |
| 21 | CELL_CYCLE | Details | 72 | 0.46 | 1.53 | 0.087 | 0.412 | 0.892 | 3214 | tags=61%, list=32%, signal=89% |
| 22 | MAP00970_AMINOACYL_TRNA_BIOSYNTHESIS | Details | 16 | 0.61 | 1.53 | 0.086 | 0.398 | 0.892 | 2730 | tags=75%, list=27%, signal=103% |
| 23 | UCALPAINPATHWAY | Details | 16 | 0.49 | 1.53 | 0.051 | 0.389 | 0.898 | 614 | tags=19%, list=6%, signal=20% |
| 24 | ST_DICTYOSTELIUM_DISCOIDEUM_CAMP_CHEMOTAXIS_PATHWAY | Details | 30 | 0.42 | 1.51 | 0.038 | 0.422 | 0.910 | 2094 | tags=37%, list=21%, signal=46% |
| 25 | GPCRPATHWAY | Details | 33 | 0.43 | 1.47 | 0.060 | 0.506 | 0.934 | 2356 | tags=33%, list=23%, signal=43% |
| 26 | PAR1PATHWAY | Details | 20 | 0.47 | 1.47 | 0.070 | 0.505 | 0.938 | 1053 | tags=25%, list=10%, signal=28% |
| 27 | ATRBRCAPATHWAY | Details | 19 | 0.52 | 1.46 | 0.060 | 0.505 | 0.942 | 2951 | tags=53%, list=29%, signal=74% |
| 28 | TRNA_SYNTHETASES | Details | 17 | 0.58 | 1.46 | 0.131 | 0.503 | 0.948 | 2730 | tags=71%, list=27%, signal=97% |
| 29 | MAP00562_INOSITOL_PHOSPHATE_METABOLISM | Details | 18 | 0.46 | 1.45 | 0.067 | 0.494 | 0.948 | 463 | tags=28%, list=5%, signal=29% |
| 30 | MAP00240_PYRIMIDINE_METABOLISM | Details | 41 | 0.49 | 1.45 | 0.121 | 0.494 | 0.950 | 1929 | tags=44%, list=19%, signal=54% |
| 31 | TELPATHWAY | Details | 18 | 0.50 | 1.41 | 0.082 | 0.587 | 0.962 | 1821 | tags=33%, list=18%, signal=41% |
| 32 | MAP00230_PURINE_METABOLISM | Details | 80 | 0.40 | 1.41 | 0.143 | 0.576 | 0.966 | 3333 | tags=52%, list=33%, signal=78% |
| 33 | PITX2PATHWAY | Details | 16 | 0.47 | 1.40 | 0.089 | 0.573 | 0.968 | 1318 | tags=38%, list=13%, signal=43% |
| 34 | INSULIN_2F_UP | Details | 169 | 0.37 | 1.38 | 0.153 | 0.635 | 0.974 | 2697 | tags=38%, list=27%, signal=51% |
| 35 | DNA_DAMAGE_SIGNALLING | Details | 89 | 0.36 | 1.37 | 0.124 | 0.628 | 0.976 | 1971 | tags=31%, list=20%, signal=39% |
| 36 | PROTEASOMEPATHWAY | Details | 21 | 0.59 | 1.37 | 0.210 | 0.632 | 0.980 | 2917 | tags=71%, list=29%, signal=100% |
| 37 | HCMVPATHWAY | Details | 16 | 0.46 | 1.36 | 0.137 | 0.623 | 0.980 | 347 | tags=19%, list=3%, signal=19% |
| 38 | MEF2DPATHWAY | Details | 19 | 0.43 | 1.36 | 0.107 | 0.620 | 0.984 | 777 | tags=21%, list=8%, signal=23% |
| 39 | SA_B_CELL_RECEPTOR_COMPLEXES | Details | 23 | 0.39 | 1.35 | 0.125 | 0.616 | 0.984 | 2084 | tags=30%, list=21%, signal=38% |
| 40 | IL7PATHWAY | Details | 16 | 0.50 | 1.35 | 0.146 | 0.607 | 0.984 | 2212 | tags=50%, list=22%, signal=64% |

Results on SETPATHWAY (Summary)

| Table: GSEA Results Summary | | | | |
|-----------------------------------|--|--|--|--|
| Dataset | Leukemia_collapsed_symbols.Leukemia.cls#ALL_versus_AML | | | |
| Phenotype | Leukemia.cls#ALL_versus_AML | | | |
| Upregulated in class | ALL | | | |
| GeneSet | SETPATHWAY | | | |
| Enrichment Score (ES) | 0.7762963 | | | |
| Normalized Enrichment Score (NES) | 1.8301569 | | | |
| Nominal p-value | 0.0 | | | |
| FDR q-value | 0.7549038 | | | |
| FWER p-Value | 0.348 | | | |

Results on SETPATHWAY (Enrichment Plot)



Fig 1: Enrichment plot: SETPATHWAY Profile of the Running ES Score & Positions of GeneSet Members on the Rank Ordered List

Results on SETPATHWAY (Genes)

Table: GSEA details [plain text format]

| | PROBE | DESCRIPTION (from dataset) | GENE SYMBOL | GENE_TITLE | RANK IN GENE LIST | RANK METRIC SCORE | RUNNING ES | CORE ENRICHMENT |
|----|-------------|-------------------------------|-------------|------------|-------------------|-------------------|------------|-----------------|
| 1 | ANP32A | na | | | 301 | 0.958 | 0.1730 | Yes |
| 2 | <u>SET</u> | na | | | 612 | 0.807 | 0.3131 | Yes |
| 3 | DFFB | na | | | 666 | 0.791 | 0.4755 | Yes |
| 4 | CREBBP | na | | | 1069 | 0.659 | 0.5752 | Yes |
| 5 | APEX1 | na | | | 1460 | 0.576 | 0.6584 | Yes |
| 6 | HMGB2 | na | | | 1489 | 0.570 | 0.7763 | Yes |
| 7 | NME1 | na | | | 5550 | -0.009 | 0.3740 | No |
| 8 | DFFA | na | | | 5685 | -0.027 | 0.3665 | No |
| 9 | <u>GZMA</u> | na | | | 6060 | -0.073 | 0.3446 | No |
| 10 | PRF1 | na | | | 6447 | -0.114 | 0.3304 | No |
| 11 | GZMB | na | | | 6618 | -0.135 | 0.3422 | No |

Results on SETPATHWAY (Heatmap)



Fig 2: SETPATHWAY Blue-Pink O' Gram in the Space of the Analyzed GeneSet

Results on SETPATHWAY (Random ES Distribution)





Results on Enriched in the AML Phenotype



Fig 1: Enrichment plot: MAP00380_TRYPTOPHAN_METABOLISM Profile of the Running ES Score & Positions of GeneSet Members on the Rank Ordered List

Heatmap of the Top 100 Genes

GSEA Report for Dataset Leukemia collapsed symbols SampleName TCL17 DNTT CD24 CD79B CRIM1 Enrichment in phenotype: ALL (24 samples) MME BLNK TOP2E 219 / 394 gene sets are upregulated in phenotype ALL PPP30 0 gene sets are significant at FDR < 25% FOXOLA 3 gene sets are significantly enriched at nominal pvalue < 1% KIAA1093 17 gene sets are significantly enriched at nominal pvalue < 5% MYST3 SMARCA4 TCF3 · Snapshot of enrichment results · Detailed enrichment results in html format · Detailed enrichment results in excel format (tab delimited text) SNX2 KIAA101 UPF2 Guide to interpret results DYRK3 KIAA103 Enrichment in phenotype: AML (24 samples) **ZHX2** IFI16 175 / 394 gene sets are upregulated in phenotype AML NFYA 0 gene sets are significantly enriched at FDR < 25% MTMR 1 · 2 gene sets are significantly enriched at nominal pvalue < 1% AUTS 19 gene sets are significantly enriched at nominal pvalue < 5% KTAA0582 Snapshot of enrichment results GDI2 ZNF423 Detailed enrichment results in html format ZC3HAV · Detailed enrichment results in excel format (tab delimited text) CACNB3 ZCCHC11 Guide to interpret results SPTBN1 POU2AF1 41625 a **Dataset details** GLBX SPTAN SSBP2 The dataset has 10056 features (genes) THUMPD ARTH No probe set => gene symbol collapsing was requested, so all 10056 features were used CHES ETE3S C7orf2 KTN1 /// TXNDC Gene set details TAGLN GTB1 · Gene set size filters (min=10, max=500) resulted in filtering out 128 / 522 gene sets TFDP2 FLNA The remaining 394 gene sets were used in the analysis CHRFAM7A /// CHRNA List of gene sets used and their sizes (restricted to features in the specified dataset) TYROBI Gene markers for the ALL versus AML comparison GAA SRrp35 ZC3HDC ATP1B The dataset has 10056 features (genes) # of markers for phenotype ALL: 5460 (54.3%) with correlation area 60.5% SIAT4C # of markers for phenotype AML: 4596 (45.7%) with correlation area 39.5% PTPN · Detailed rank ordered gene list for all features in the dataset CEDDIN Heat map and gene list correlation profile for all features in the dataset · Buttefly plot of significant genes ALPPL. L-MOD 1 PCBD **Global statistics and plots** PRKCSH KCNH? Plot of p-values vs. NES Global ES histogram 39448 r at Other APLP2 HOXAS · Parameters used for this analysis RNASE2 FZR1 1894 f at RTN2 SLCO3AI LTC45 xtools.gsea.Gsea [Tue, Sep 24, '13 5 PM 36] Report: Leukemia_GSEA_P500_C2.Gsea.1380065792604.rpt by user: aikchoontan Website: www.br

KTAA11

Gene Ranking



Results also available as Excel Files



In Results Folder, look for index.html

| Name 🔺 | Date Modified | Size | Kind |
|--------------------------|----------------|--|-----------------------|
| IL7PATHWAY.html | Today, 5:37 PM | 8 KB | HTML ument |
| L7PATHWAY.xls | Today, 5:37 PM | 4 KB | Microrkbook |
| IL10PATHWAY_1613.png | Today, 5:38 PM | 16 KB | Portabimage |
| IL10PATHWAY.html | Today, 5:38 PM | 8 KB | HTML ument |
| L10PATHWAY.xls | Today, 5:38 PM | 4 KB | Microrkbook |
| 🗟 index.html | Today, 5:38 PM | 4 KB | HTML ument |
| INFLAMPATHWAY_1388.p.g | Today, 5:37 PM | 20 KB | Portabimage |
| INFLAMPATHWAY.html | Today, 5:37 PM | 8 KB | HTML ument |
| NFLAMPATHWAY.xls | Today, 5:37 PM | 4 KB | Microrkbook |
| INS_1577.png | Today, 5:38 PM | 25 KB | Portabimage |
| INS.html | Today, 5:38 PM | GSEA Report for Dataset Leuken | nia collapsed symbols |
| 🛅 INS.xls | Today, 5:38 PM | | |
| INSULIN_2F_DOWN_1550.png | Today, 5:38 PM | Enrichment in phenotype: ALL (24 sample | 5) |
| INSULIN_2F_DOWN.html | Today, 5:38 PM | 219 / 394 gene sets are upregulated in phenotype A 0 gene sets are significant at FDR < 25% 3 gene sets are significantly enriched at pominal pro | LL |
| NSULIN_2F_DOWN.xls | Today, 5:38 PM | 17 gene sets are significantly enriched at nominal pro <u>Snapshot</u> of enrichment results Detailed enrichment results in html format | value < 5% |
| | | Detailed enrichment results in excel format (tab deline) Guide to interpret results | nited text) |

Enrichment in phenotype: AML (24 samples)

- 175 / 394 gene sets are upregulated in phenotype AML
- Ogene sets are significantly enriched at FDR < 25%
 2 gene sets are significantly enriched at nominal pvalue < 1%
 19 gene sets are significantly enriched at nominal pvalue < 5%

- Bragshot of envictment results
 Construction of envictment results
 Detailed enrichment results in html format
 Detailed enrichment results in excel format (tab delimited text)
 Guide to interpret results

Dataset details

 The dataset has 10056 features (genes) No probe set => gene symbol collapsing was requested, so all 10056 features were used

Gene set details

- · Gene set size filters (min=10, max=500) resulted in filtering out 128 / 522 gene sets
- The remaining 394 gene sets were used in the analysis
 List of gene sets used and their sizes (restricted to features in the specified dataset)

Gene markers for the ALL versus AML comparison

- The dataset has 10056 features (genes)
- # of markers for phenotype ALL: 5460 (54.3%) with correlation area 60.5%
 # of markers for phenotype ALL: 5450 (45.7%) with correlation area 39.5%
- · Detailed rank ordered gene list for all features in the dataset

xtools asea. Gsea. Tue. Sep 24. 13.5 PM 361 Report: Leukemia. GSEA. P500. C2. Gsea. 1380065792604.rot. by user: aikchoontan Website: www.broadinstitute.org/GSEA. Questions & Suggestions: Email

- Heat map and gene list correlation profile for all features in the dataset
 Buttefly plot of significant genes

Global statistics and plots

 Plot of <u>p-values vs. NES</u> Global ES histogram

Other

· Parameters used for this analysis

In Results Folder, look for gsea_report_for*.xls

| | Name | | Date Modified | Size | Kind | |
|---|--------------------------------|-----------|----------------|-------|--------------|--|
| | GO_0005739.html | | Today, 5:37 PM | 33 KB | HTML ument | |
| | GO_0005739.xls | | Today, 5:37 PM | 12 KB | Microrkbook | |
| | GPCRPATHWAY_1109.png | | Today, 5:37 PM | 29 KB | Portabimage | |
| | GPCRPATHWAY.html | | Today, 5:37 PM | 12 KB | HTML ument | |
| | GPCRPATHWAY.xls | | Today, 5:37 PM | 4 KB | Microrkbook | |
| | GPCRS_CLASS_A_RHODOPSIN-LIKE | _1466.png | Today, 5:38 PM | 78 KB | Portabimage | |
| | GPCRS_CLASS_A_RHODOPSIN-LIKE | .html | Today, 5:38 PM | 29 KB | HTMLument | |
| | GPCRS_CLASS_A_RHODOPSIN-LIKE | .xls | Today, 5:38 PM | 8 KB | Microrkbook | |
| | GPCRS_CLASS_B_SECRETIN-LIKE_1 | 370.png | Today, 5:37 PM | 20 KB | Portabimage | |
| | GPCRS_CLASS_B_SECRETIN-LIKE.ht | ml | Today, 5:37 PM | 8 KB | HTML ument | |
| | GPCRS_CLASS_B_SECRETIN-LIKE.xl | s | Today, 5:37 PM | 4 KB | Microrkbook | |
| | gsea_report_for_ALL_1380065792 | 604.html | Today, 5:38 PM | 53 KB | HTML ument | |
| | gsea_report_for_ALL_1380065792 | 604.xls | Today, 5:38 PM | 29 KB | Microrkbook | |
| ~ | gsea_report_for_AML_138006579 | 2604.html | Today, 5:38 PM | 45 KB | HTML ument | |
| | gsea_report_for_AML_1380065793 | 2604.xls | Today, 5:38 PM | 25 KB | Microrkbook | |
| 7 | gset_rnd_es_dist_1038.png | | Today, 5:37 PM | 33 KB | Portabimage | |
| | gset_rnd_es_dist_1041.png | | Today, 5:37 PM | 29 KB | Portabimage | |
| | gset_rnd_es_dist_1044.png | | Today, 5:37 PM | 29 KB | Portabimage | |
| | gset_rnd_es_dist_1047.png | | Today, 5:37 PM | 33 KB | Portabimage | |
| | gset_rnd_es_dist_1050.png | | Today, 5:37 PM | 33 KB | Portabimage | |
| | gset_rnd_es_dist_1053.png | | Today, 5:37 PM | 33 KB | Portabimage | |
| | gset_rnd_es_dist_1056.png | | Today, 5:37 PM | 29 KB | Portabimage | |
| | gset_rnd_es_dist_1059.png | | Today, 5:37 PM | 29 KB | Portabimage | |
| | gset_rnd_es_dist_1062.png | | Today, 5:37 PM | 33 KB | Portabimage | |
| | gset_rnd_es_dist_1065.png | | Today, 5:37 PM | 33 KB | Portabimage | |
| | gset_rnd_es_dist_1068.png | | Today, 5:37 PM | 29 KB | Portabimage | |
| | gset_rnd_es_dist_1071.png | | Today, 5:37 PM | 29 KB | Portabimage | |
| | gset_rnd_es_dist_1074.png | | Today, 5:37 PM | 33 KB | Portabimage | |
| | gset_rnd_es_dist_1077.png | | Today, 5:37 PM | 33 KB | Portabimage | |
| | gset_rnd_es_dist_1080.png | | Today, 5:37 PM | 29 KB | Portabimage | |
| | gset_rnd_es_dist_1083.png | | Today, 5:37 PM | 33 KB | Portabimage | |
| | gset_rnd_es_dist_1086.png | | Today, 5:37 PM | 29 KB | Portabimage | |
| | gset_rnd_es_dist_1089.png | | Today, 5:37 PM | 29 KB | Portabimage | |
| | gset_rnd_es_dist_1092.png | | Today, 5:37 PM | 33 KB | Portabimage | |
| | gset_rnd_es_dist_1095.png | | Today, 5:37 PM | 29 KB | Portabimage | |
| | gset_rnd_es_dist_1098.png | | Today, 5:37 PM | 29 KB | Portabimage | |
| | gset_rnd_es_dist_1101.png | | Today, 5:37 PM | 29 KB | Portabimage | |
| | gset_rnd_es_dist_1104.png | | Today, 5:37 PM | 29 KB | Portabimage | |
| | gset_rnd_es_dist_1107.png | | Today, 5:37 PM | 33 KB | Portabimage | |
| | gset_rnd_es_dist_1110.png | | Today, 5:37 PM | 29 KB | Portabimage | |
| | gset_rnd_es_dist_1113.png | | Today, 5:37 PM | 29 KB | Portabimage | |
| | gset_rnd_es_dist_1116.png | | Today, 5:37 PM | 33 KB | Portabimage | |
| | gset_rnd_es_dist_1119.png | | Today, 5:37 PM | 29 KB | Portabimage | |
| | gset_rnd_es_dist_1122.png | | Today, 5:37 PM | 33 KB | Portabimage | |
| | gset_rnd_es_dist_1125.png | | Today, 5:37 PM | 33 KB | Portabimage | |
| | aset rnd es dist 1128.png | | Today, 5:37 PM | 33 KB | Portab image | |

| 00 | CSEA v2.06 (Gene set enrichment analysis Broad Institute) |
|---|---|
| File Options Downloads Tool | ls Help |
| Steps in GSEA analysis | Home 1112 Load data × 1123 Run Gsea × 1186 Gsea × |
| Load data | Select a GSEA result from the application cache |
| Run GSEA | [OR] Locate a GSEA result folder from the file system |
| Leading edge analysis | 0.0 |
| Gene set tools | Waiting for input> |
| Chip2Chip mapping | |
| W Browse MSigDB | |
| Analysis history | |
| CSEA reports Processes: click 'status' field for | |
| Name Status | |
| 1 B Gsea Success 5 | |
| 2 🖬 Gsea ···· Success 5 3 📾 Gsea ···· Success 5 | |
| | |
| | |
| | |
| | |
| | |
| | |
| | |
| | |
| | |
| | |
| | |
| | |
| | |
| | |
| Show results folder | |
| 5:56:05 PM | a synched dataset-template NO extracting done |

| 0 0 | Select an option |
|----------------------|---|
| | |
| HNC_AZ_KEGG_GS00.0 | Jsea.1241018383520.rpt [wed, Apr 29, '09] |
| KEGG_GSUU.Gsea.150 | 2B C1000 Ccap 1220460020007 rpt [Tup Eab 28 '12] |
| KEGG_KIMA_GEINES_23_ | 2K_G1000.GSed.1550409929997.fpt [Tue, Feb 26, 12] |
| KEGG_TINBC_ENMD207 | 76 WITH RT20 C1000 Crep 1320468035752 rpt [Tue Feb 28 |
| KEGG_TNBC_ENMD207 | 76 WITHOUT 134 Csep 1330467411613 rpt [Tue Feb 28, '12] |
| KEGG_TNBC_ENMD207 | 76 WITHOUT MDAMR134 C1000 Csea 1330468263758 rot [Tu |
| KRASmPIK3CAm BioCA | RTA C500 Csea 1333989931733 rpt [Mon_Apr 9_'12] |
| KRASmPIK3CAm KEGG | G500 Gsea.1333989792028 rpt [Mon. Apr 9, '12] |
| Leukemia GSEA P500 | C2.Gsea.1380065792604.rpt [Tue, Sep 24, '13] |
| Leukemina ALLvsAML (| C2 G500.Gsea.1372801898748.rpt [Tue, Jul 2, '13] |
| Leukemina_ALLvsAML_C | C2_P500.Gsea.1372802522099.rpt [Tue, Jul 2, '13] |
| LexR_AMBION_G500.G | sea.1349227665580.rpt [Tue, Oct 2, '12] |
| LexR_KEGG_G500.Gse | a.1349227492973.rpt [Tue, Oct 2, '12] |
| LexR_PREvsPOST2_AME | BION_G500.Gsea.1372950060698.rpt [Thu, Jul 4, '13] |
| LexR_PREvsPOST2_KEG | G_G500.Gsea.1372950012625.rpt [Thu, Jul 4, '13] |
| LexRTRAIL_vs_pcDNAT | RAIL_AMBION_G500.Gsea.1372952594743.rpt [Thu, Jul 4, '13] |
| LexRTRAIL_vs_pcDNAT | RAIL_KEGG_G500.Gsea.1372952606534.rpt [Thu, Jul 4, '13] |
| (| |
| | (Cancel) (OV) |
| () Help | Cancel |
| | |

| 0 0 | | | GSEA v2.06 | (Gene set enrichm | ent analysis Bi | road Institute) | | | |
|-----------------------|---------------------|--------------------|--------------------------|-------------------|--------------------|-------------------------|-----------------|-------------------|--------------------------|
| File Options D | ownloads Tools | s Help | | | | | | | |
| Steps in GSEA anal | ysis | Home 💯 Loa | ad data 🛛 🛪 🛛 🔛 Run Gse | a × 🛛 👸 Gsea × | 🛛 👸 Gsea 🛛 🖌 | 🔝 Leading edge an | alysis × | | 4 🕨 👻 |
| Load data | | Select a GSEA | result from the applica | tion cache | ics | /LECTURES/CLASS04/ | Leukemia_GSEA_F | 2500_C2.Gsea.1380 | 0065792604 |
| Run GSEA | | [OR] Locate a | a GSEA result folder fro | m the file system | | | | | |
| | | | | | C | | Load GSEA Re | sults | |
| Leading edge a | analysis | | | positiv | e phonotype: pa | nos pagativa phonot | | | |
| Gene set tools | | Filter Gene Sets | | positiv | e prienotype: na j | pos negative prierio | ype: AML | | |
| | | Q | | 394 out of 3 | 94 gene sets | | | | |
| Chip2Chip ma | pping | Gene Set | Size ES | NES | NOM p | -val EDR g-val | FWER p-va | Rank at Max | Leading Edge |
| | | SETPATHWAY | 11 | 0.776 | 1.83 | 0 | 0.755 | 0.348 | 1.489 tags=55%, list= |
| | | SIG BCR SIGNALL. | . 44 | 0.527 | 1.824 | 0.016 | 0.399 | 0.356 | 2.233 tags=50% list= |
| | P | GLUT UP | 269 | 0.44 | 1.769 | 0.016 | 0.454 | 0.502 | 2.596 tags=43%, list= |
| Di owse wisigu | ъ | CARM-ERPATH | 26 | 0.61 | 1.755 | 0.03 | 0.384 | 0.536 | 1.548 tags=50%, list= |
| | | BCRPATHWAY | 34 | 0.533 | 1.728 | 0.004 | 0.395 | 0.614 | 830 tags=26%, list= |
| | | DNAFRAGMENT | 10 | 0.703 | 1.696 | 0.015 | 0.437 | 0.668 | 1.923 tags=60% list= |
| _ | | SIG PIP3 SIGNAL | 32 | 0.508 | 1.687 | 0.031 | 0.405 | 0.68 | 2.026 tags = 50%, list = |
| Analysis histor | у | FETAL LIVER HS | 68 | 0.435 | 1.678 | 0.016 | 0.381 | 0.692 | 2.711 tags=47% list= |
| | | MRNA SPLICING | 47 | 0.613 | 1.657 | 0.059 | 0.4 | 0.728 | 3.190 tags=79% list= |
| | | CXCR4PATHWAY | 23 | 0.521 | 1.657 | 0.012 | 0.36 | 0.728 | 2.192 tags=43% list= |
| | | ST_PHOSPHOINO | 32 | 0.464 | 1.63 | 0.029 | 0.398 | 0.772 | 2.026 tags=41% list= |
| | | HTERT UP | 108 | 0.421 | 1.611 | 0.019 | 0.426 | 0.808 | 2.249 tags=40%, list= |
| | | CR REPAIR | 39 | 0.565 | 1.603 | 0.058 | 0.418 | 0.816 | 3.683 tags=77% list= |
| | | PROTEASOME D | 31 | 0.602 | 1.591 | 0.083 | 0.424 | 0.834 | 1.699 tags = 45% list= |
| GSEA reports | | ACHPATHWAY | 14 | 0.512 | 1.582 | 0.048 | 0.421 | 0.844 | 1.357 tags=43% list= |
| Processes: click 'sta | tus' field for | CALCINEURINPA | 18 | 0.536 | 1.58 | 0.027 | 0.398 | 0.848 | 2,307 tags=39% list= |
| results | | RAP UP | 169 | 0.396 | 1.555 | 0.048 | 0.447 | 0.874 | 1.364 tags=29% list= |
| Name | Status | ST B CELL ANTL | 38 | 0.438 | 1.552 | 0.045 | 0.43 | 0.878 | 2,233 tags=39% list= |
| 1 🗳 Gsea | ···· Success 5 | MRNA PROCESSI | 40 | 0.584 | 1.538 | 0.097 | 0.444 | 0.89 | 2.070 tags=63% list= |
| 2 🛛 🖾 Gsea | ···· Success 5 | SIG CHEMOTAXIS | 40 | 0.444 | 1 536 | 0.008 | 0.426 | 0.89 | 873 tags=25% list= |
| 3 🗳 Gsea | ···· Success 5 | | 72 | 0.464 | 1.534 | 0.087 | 0.411 | 0.892 | 3.214 tags=61% list= |
| | | MAP00970 AML | 16 | 0.612 | 1.532 | 0.086 | 0.397 | 0.892 | 2.730 tags=75% list= |
| | | UCALPAINPATH | 16 | 0.487 | 1.529 | 0.051 | 0.389 | 0.898 | 614 tags=19%, list= |
| | | ST DICTYOSTELL. | 30 | 0.42 | 1.511 | 0.038 | 0.421 | 0.91 | 2.094 tags=37%, list= |
| | | GPCRPATHWAY | 33 | 0.428 | 1.473 | 0.06 | 0.506 | 0.934 | 2.356 tags=33%, list= |
| | | PAR1PATHWAY | 20 | 0.47 | 1.467 | 0.07 | 0.505 | 0.938 | 1,053 tags=25%, list= |
| | | ATRBRCAPATHW | 19 | 0.523 | 1.461 | 0.06 | 0.505 | 0.942 | 2.951 tags=53%, list= |
| | | TRNA SYNTHET | 17 | 0.583 | 1.456 | 0.131 | 0.503 | 0.948 | 2,730 tags=71%, list= |
| | | MAP00562 INO | 18 | 0.462 | 1.453 | 0.067 | 0.494 | 0.948 | 463 tags=28%, list= |
| | | MAP00240_PYRI | 41 | 0.491 | 1.446 | 0.121 | 0.494 | 0.95 | 1,929 tags=44%, list= |
| | | TELPATHWAY | 18 | 0.495 | 1.409 | 0.082 | 0.587 | 0.962 | 1,821 tags=33%, list= |
| | | MAP00230_PURI | 80 | 0.399 | 1.406 | 0.143 | 0.576 | 0.966 | 3,333 tags=52%, list= |
| | | PITX2PATHWAY | 16 | 0.47 | 1.402 | 0.089 | 0.573 | 0.968 | 1,318 tags=38%, list= |
| | | INSULIN_2F_UP | 169 | 0.374 | 1.376 | 0.153 | 0.635 | 0.974 | 2,697 tags=38%, list= |
| | | DNA_DAMAGE_S | 89 | 0.356 | 1.373 | 0.124 | 0.627 | 0.976 | 1,971 tags=31%, list= |
| | | PROTEASOMEPA | 21 | 0.592 | 1.366 | 0.21 | 0.632 | 0.98 | 2,917 tags=71%, list= |
| | | HCMVPATHWAY | 16 | 0.461 | 1.363 | 0.137 | 0.622 | 0.98 | 347 tags=19%, list= |
| | | MEF2DPATHWAY | 19 | 0.425 | 1.358 | 0.107 | 0.62 | 0.984 | 777 tags=21%, list= |
| | | SA_B_CELL_RECE | 23 | 0.395 | 1.354 | 0.125 | 0.616 | 0.984 | 2,084 tags=30%, list= |
| | | IL7PATHWAY | 16 | 0.502 | 1.353 | 0.146 | 0.607 | 0.984 | 2,212 tags=50%, list= |
| | | RARRXRPATHWAY | 15 | 0.489 | 1.346 | 0.163 | 0.615 | 0.99 | 1,975 tags=53%, list= 🔻 |
| | | () He | lp | | Fo | or 0 selected gene sets | s: 🕨 Run lead | ing edge analysis | Build HTML Report |
| Show resu | lts folder | | | | | | | | |
| 5:57:43 PM 🗐 99 | 95 [INFO] Begun ir | nporting: RankedLi | st from: /Users/aikchoor | itan/TEACHING/Pra | acticalBioinformat | ics/LECTURES/CLASS | 04/Leukemia GSE | A P50 1 | 674M of 1399M |

| Load data | | Salact a CEEA | regult from the | lication cacho | | | SSO4/Loukomia C | SEA BEOD C2 C | 1280065702604 | |
|------------------|----------------|------------------|---|--------------------------------------|-----------------|-------------------|-----------------|------------------|-------------------------|--|
| Run GSEA | | Select a GSEA | result from the app | dication cache | 1 | CS/LECTURES/CLA | SS04/Leukemia_G | SEA_P500_C2.Gsea | .1380065792604 | |
| | | [OR] Locate | a GSEA resultReport | <mark>directory</mark> he file syste | m | | | | | |
| | | | | | (| Load GSEA Results | | | | |
| | | | | | | | | | | |
| | | | positive phenotype: pa posnegative phenotype: AMI | | | | | | | |
| one set tools | | Filter Gene Sets | | | | | | | | |
| | | Q | | 394 out o | f 394 gene sets | | | | | |
| Chip2Chip ma | pping | Cone Set | Size F | s NES | NO | to-val | n-val EWER | Poval Pank: | t Max Leading Edge | |
| | | SETPATHWAY | 11 | 0.776 | 1.83 | 0 | 0.755 | 0.348 | 1,489 tags=55%, list= | |
| | | CR_HORMONAL | 11 | -0.677 | -1.659 | 0.004 | 1 | 0.748 | 1,600 tags=55%, list= | |
| 📄 Browse MSig | DB | BCRPATHWAY | 34 | 0.533 | 1.728 | 0.004 | 0.395 | 0.614 | 830 tags=26%, list= | |
| 17 | | SIG_CHEMOTAXIS | 40 | 0.444 | 1.536 | 0.008 | 0.426 | 0.89 | 8/3 tags=25%, list= | |
| | | CXCR4PATHWAY | 23 | 0.521 | 1.657 | 0.012 | 0.36 | 0.728 | 2.192 tags=43%, list= | |
| - | | CYTOKINEPATH | . 20 | -0.59 | -1.623 | 0.015 | 1 | 0.806 | 2,616 tags=55%, list= | |
| Analysis history | | DCPATHWAY | 19 | -0.62 | -1.614 | 0.015 | 0.956 | 0.816 | 2,292 tags=63%, list= | |
| | | DNAFRAGMENT | . 10 | 0.703 | 1.696 | 0.015 | 0.437 | 0.668 | 1,923 tags=60%, list= | |
| | | SIG_BCR_SIGNALI. | 44 | 0.527 | 1.824 | 0.016 | 0.399 | 0.356 | 2,233 tags=50%, list= | |
| | | FETAL LIVER HS | 68 | 0.435 | 1.678 | 0.016 | 0.381 | 0.692 | 2,390 tags=43%, ist= | |
| | | HTERT_UP | 108 | 0.421 | 1.611 | 0.019 | 0.426 | 0.808 | 2,249 tags=40%, list= | |
| reports | | BREAST_CANCE | . 93 | -0.377 | -1.491 | 0.022 | 0.467 | 0.942 | 1,463 tags=30%, list= | |
| sosi slick 'st | tus! field for | STEMPATHWAY | 15 | -0.572 | -1.54 | 0.023 | 0.496 | 0.908 | 1,607 tags=40%, list= | |
| sses: click st | atus neid for | CELL_ADHESION. | 29 | -0.492 | -1.588 | 0.026 | 0.663 | 0.848 | 1,119 tags=41%, list= | |
| me | Status | ST PHOSPHOINO | . 10 | 0.464 | 1.63 | 0.027 | 0.398 | 0.772 | 2.026 tags=41%, list= | |
| 🛚 Gsea | ··· Success 5 | MATRIX_METALL. | 22 | -0.533 | -1.582 | 0.03 | 0.606 | 0.852 | 928 tags=32%, list= | |
| 🛚 Gsea | ··· Success 5 | CARM-ERPATH | 26 | 0.61 | 1.755 | 0.03 | 0.384 | 0.536 | 1,548 tags=50%, list= | |
| 🖬 Gsea | ··· Success 5 | SIG_PIP3_SIGNAL. | 32 | 0.508 | 1.687 | 0.031 | 0.405 | 0.68 | 2,026 tags=50%, list= | |
| | | MONOCYTEPAT | . 11 | -0.682 | -1.603 | 0.031 | 0.841 | 0.838 | 829 tags= 55%, list= | |
| | | ST_DICTYOSTELL | | 0.42 | 1.511 | 0.034 | 0.421 | 0.91 | 2.094 tags= 37%, list= | |
| | | BCL2FAMILY AN. | . 23 | -0.599 | -1.595 | 0.039 | 0.737 | 0.844 | 2,244 tags=57%, list= | |
| | | ACE2PATHWAY | 11 | -0.637 | -1.563 | 0.042 | 0.554 | 0.876 | 2,585 tags=55%, list= | |
| | | EICOSANOID_SY | . 15 | -0.546 | -1.499 | 0.042 | 0.5 | 0.934 | 1,432 tags=47%, list= | |
| | | INFLAMPATHWAY | 27 | -0.551 | -1.495 | 0.044 | 0.483 | 0.938 | 2,616 tags=56%, list= | |
| | | SI_B_CELL_ANTI. | 38 | 0.438 | 1.552 | 0.045 | 0.43 | 0.878 | 2,233 tags=39%, list= | |
| | | CR CAM | 22 | -0.307 | -1.332 | 0.046 | 0.499 | 0.894 | 2 588 tags= 30%, list= | |
| | | RAP UP | 169 | 0.396 | 1.555 | 0.048 | 0.447 | 0.874 | 1.364 tags=29%, list= | |
| | | ELECTRON_TRA | . 62 | -0.393 | -1.432 | 0.048 | 0.483 | 0.972 | 1,802 tags=32%, list= | |
| | | ACHPATHWAY | 14 | 0.512 | 1.582 | 0.048 | 0.421 | 0.844 | 1,357 tags=43%, list= | |
| | | MAP00603_GLO | 10 | -0.649 | -1.531 | 0.049 | 0.491 | 0.908 | 3,180 tags=80%, list= | |
| | | MAPU0361_GA | 26 | -0.501 | -1.5 | 0.049 | 0.525 | 0.934 | 1,802 tags=38%, list= | |
| | | FREEPATHWAY | . 16 | -0.614 | -1 522 | 0.051 | 0.569 | 0.898 | 790 tags= 1970, IIST= | |
| | | BLYMPHOCYTEP. | . 10 | -0.669 | -1.553 | 0.056 | 0.536 | 0.892 | 1,943 tags=60%, list= | |
| | | CR_REPAIR | 39 | 0.565 | 1.603 | 0.058 | 0.418 | 0.816 | 3,683 tags=77%, list= 🔺 | |
| | | MRNA SPLICING | 47 | 0.613 | 1.657 | 0.059 | 0.4 | 0.728 | 3.190 tags=79%, list= | |

Interpreting Leading Edge Results



Workshop

Download Examples from

http://tanlab.ucdenver.edu/labHomepage/tea ching/CANB7640/WORKSHOP/CLASS04/

Assignment #4

Download Data Sets from

http://tanlab.ucdenver.edu/labHomepage/teaching/CANB7640/WORKSHOP/CLASS04/

- Refer to GSEA UserGuide in preparing your files
 - <u>http://software.broadinstitute.org/gsea/doc/GSEA</u>
 <u>UserGuideFrame.html</u>
 - <u>http://software.broadinstitute.org/gsea/doc/GSEA</u>
 <u>UserGuide.pdf</u>