

Rapid, interactive visualization of tabular multi-omics data with OmicLoupe

NBIS omics integration course
Jakob Willforss, 9th October 2020

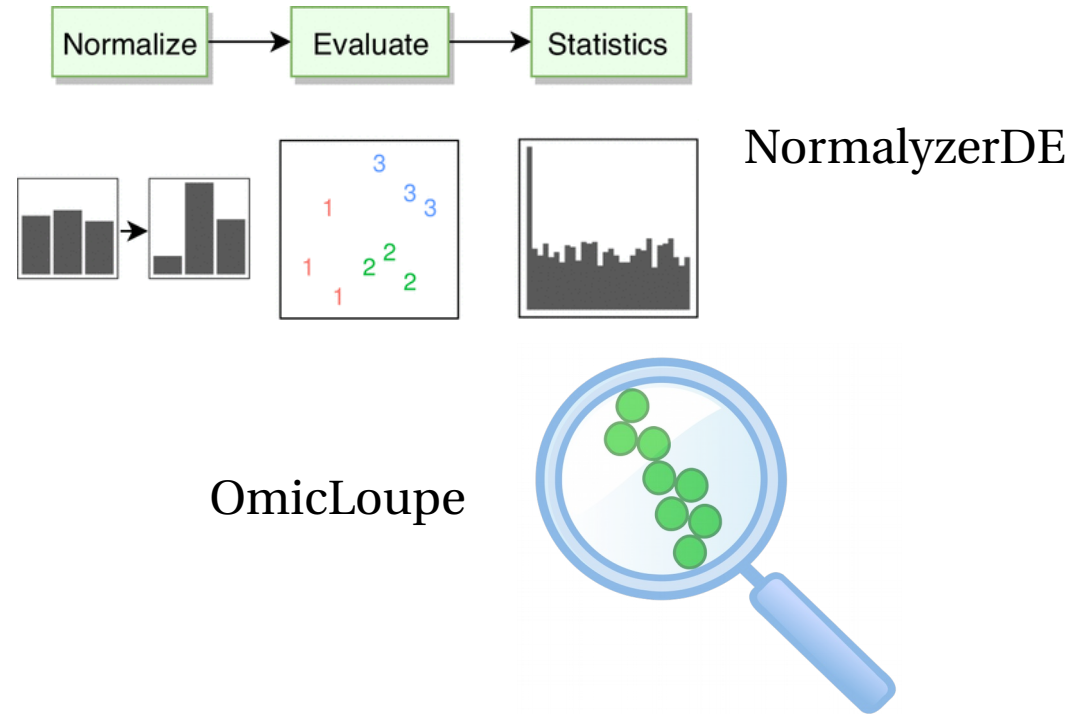


What I do

Proteomics for biomarker discovery



Improved methods for interpretation of omics



The plan for this hour

1. Lecture

2. Demonstration / hands-on

Focus: Integrative study proteomics/transcriptomics

Article | Published: 14 May 2020

Proteomics of SARS-CoV-2-infected host cells reveals therapy targets

Denisa Bojkova, Kevin Klann, Benjamin Koch, Marek Widera, David Krause, Sandra Ciesek, Jindrich Cinatl

✉ & Christian Münch ✉

Nature **583**, 469–472(2020) | [Cite this article](#)

RESEARCH ARTICLE

SARS-CoV-2 productively infects human gut enterocytes

✉ Mart M. Lamers^{1,*}, ✉ Joep Beumer^{2,*}, ✉ Jelte van der Vaart^{2,*}, Kèvin Knoops³, Jens Puschhof², Tim I. Breugem¹, ✉ Ra...

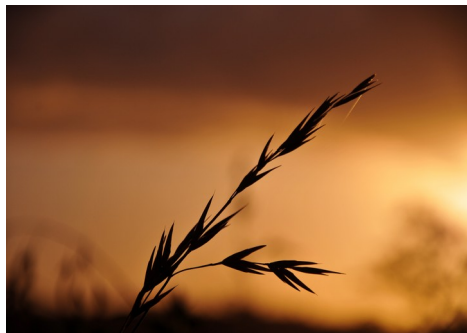
✚ See all authors and affiliations

Science 03 Jul 2020:
Vol. 369, Issue 6499, pp. 50-54
DOI: 10.1126/science.abc1669

My Ph.D. projects before OmicLoupe



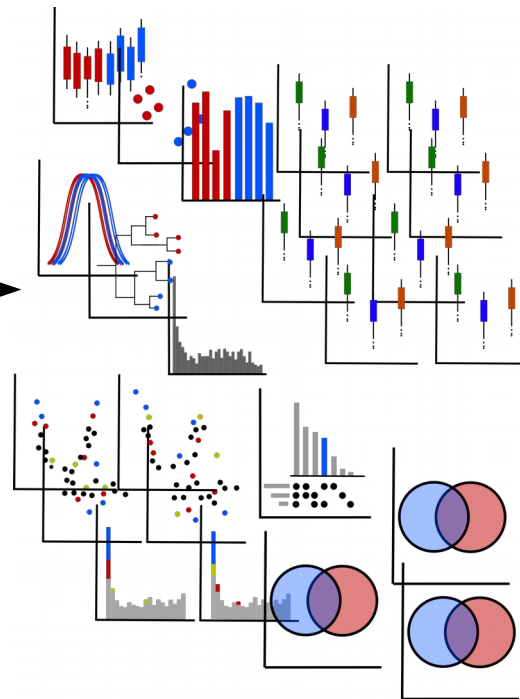
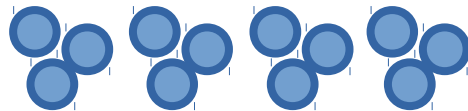
Seasons



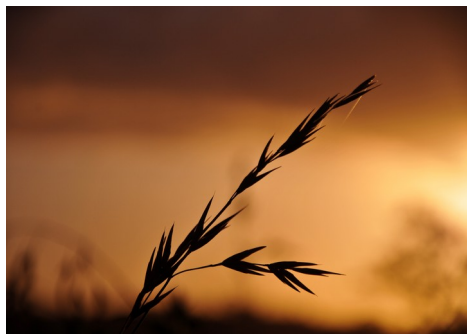
Timepoints



Seasons + validation

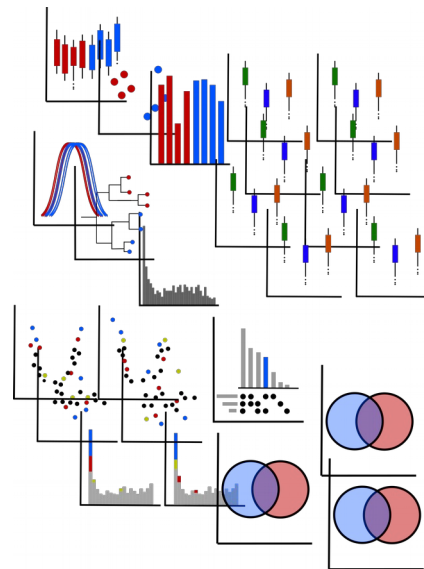


My Ph.D. projects before OmicLoupe



Works OK, but:

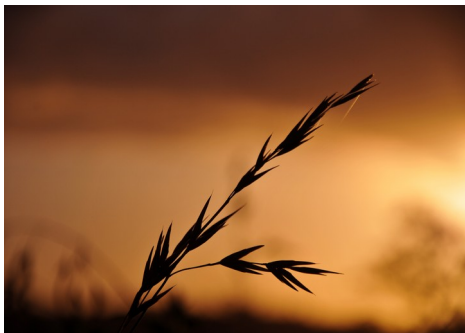
- Repeated work
- Slow to explore many settings
- Tricky to swiftly inspect details in figures
- Tricky to compare between figures



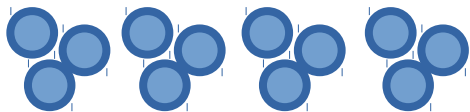
With OmicLoupe



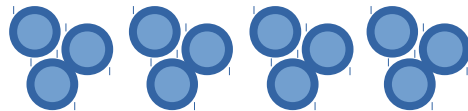
Seasons



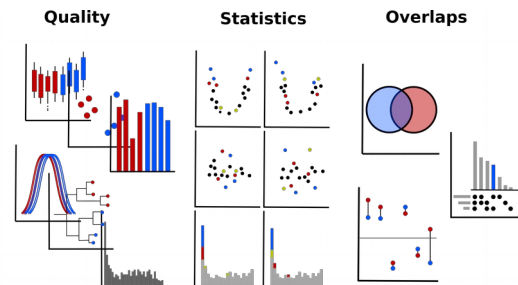
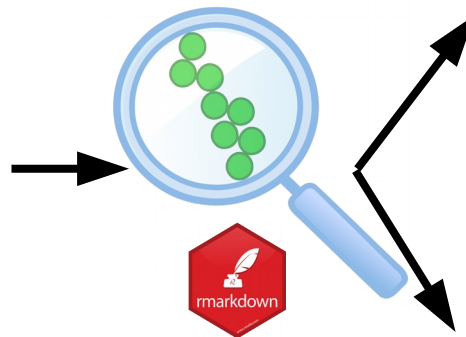
Timepoints



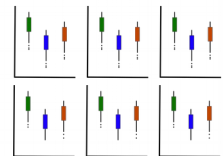
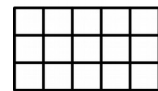
Seasons + validation



Interactively inspect



Download / Spotcheck



Save figure settings (JSON)

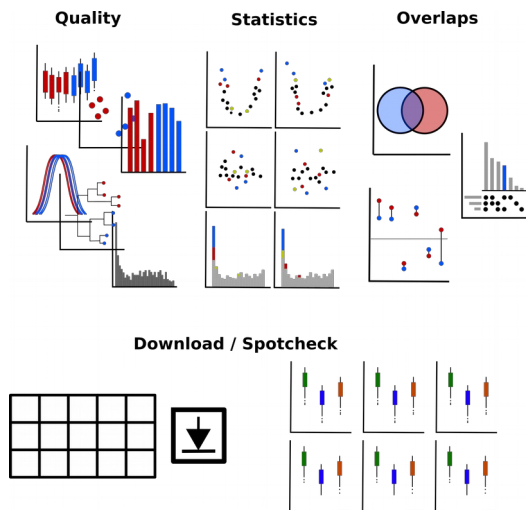
Design philosophy:

Minimal time & effort in →
Maximal output & insight out

Outliers, batch effects, technical trends, biological trends

What trends are present in each dataset?

What trends are shared across datasets?



What is OmicLoupe?

R Shiny + Plot.ly software for **rapid, interactive omics-exploration**

Tool for **understanding** your single-omics data

Tool for understanding **shared trends** across comparisons/datasets/omics

Reproducible, publication quality **visualizations**

Can be provided to **end-users** to further explore their data

Modular, can easily be extended (maybe with ideas from you!)

What does it do?

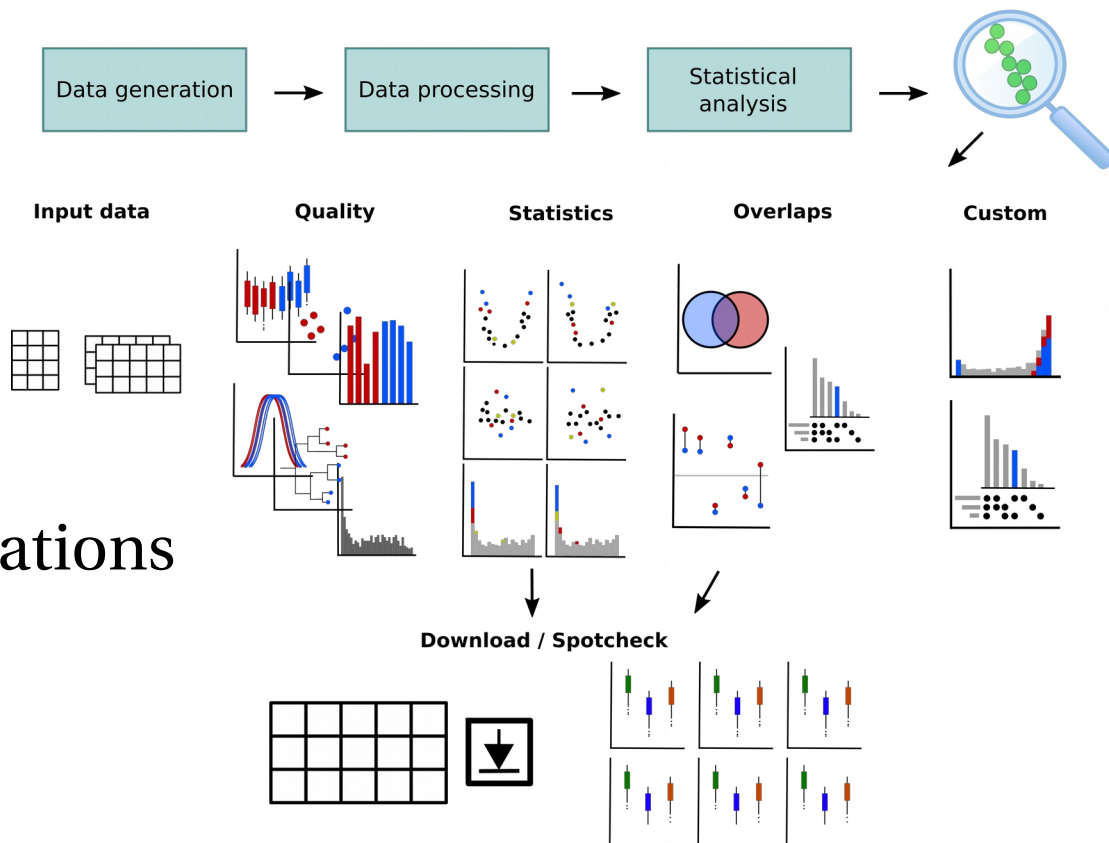
Sample-level visualizations

Interactive Qstatistical visualizations

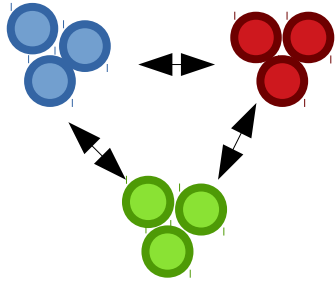
Overlap analysis

Single-feature inspections

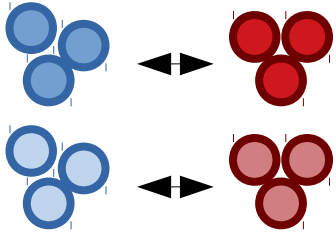
Further custom visualizations



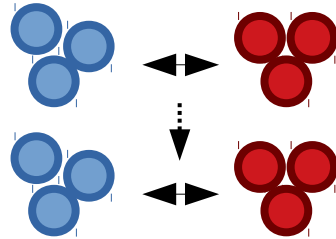
Comparing trends - Use cases



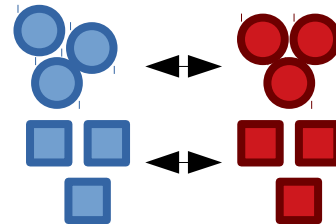
One omic – Multiple comparisons



One dataset – Multiple methods



One study – Multiple repeated samplings



Multiomics



Today's focus

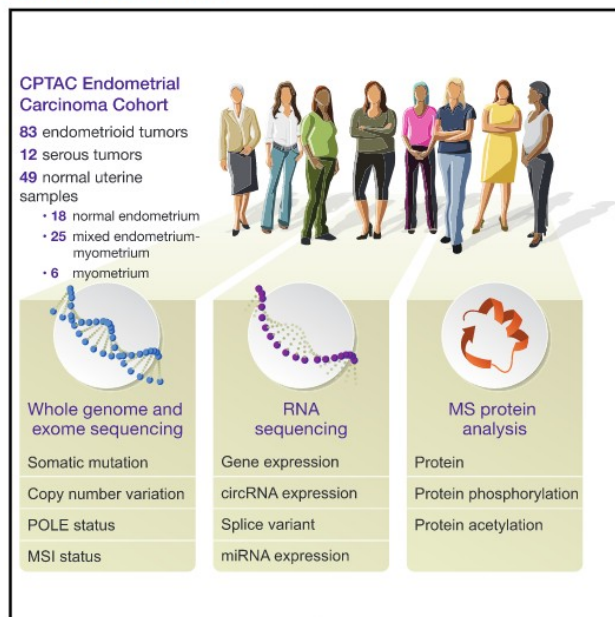
Visualizing a multi-omics study with OmicLoupe

Cell

Resource

Proteogenomic Characterization of Endometrial Carcinoma

Graphical Abstract



Authors

Yongchao Dou, Emily A. Kawaler, Daniel Cui Zhou, ..., Tao Liu, David Fenyő, the Clinical Proteomic Tumor Analysis Consortium

Correspondence

karin.rodland@pnpl.gov (K.D.R.), lding@wustl.edu (L.D.), bing.zhang@bcm.edu (B.Z.), tao.liu@pnpl.gov (T.L.), david@fenyolab.org (D.F.)

In Brief

Proteogenomic analyses of prospectively collected endometrial carcinomas provide insights into the role of underlying molecular pathways and the immune landscape that drive disease.

Quality control (some examples)

PCA

Density

Boxplot

(Had to remove the figures as they will be used in a publication, sorry)

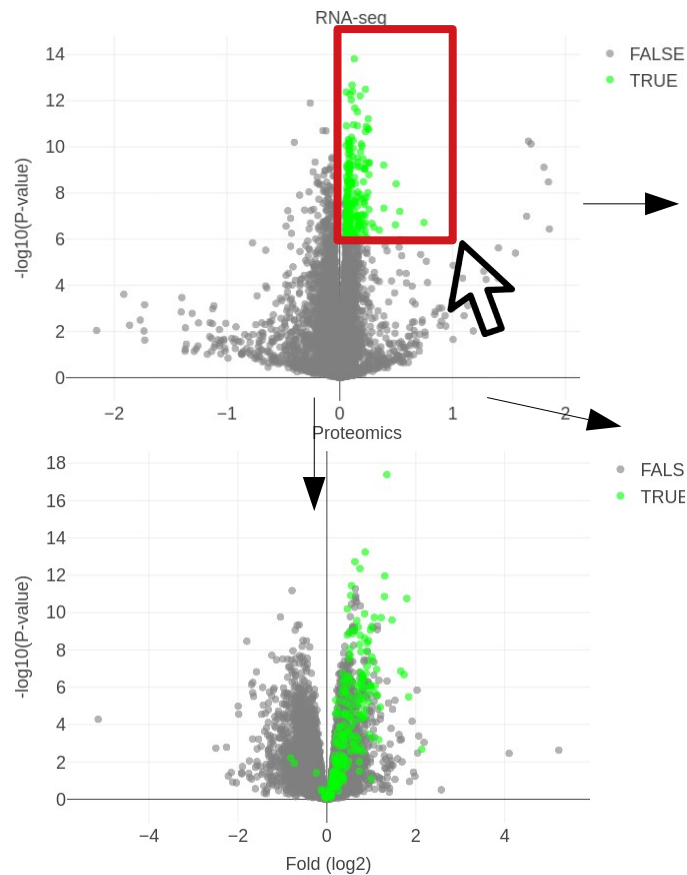
Statistical comparisons

Volcano

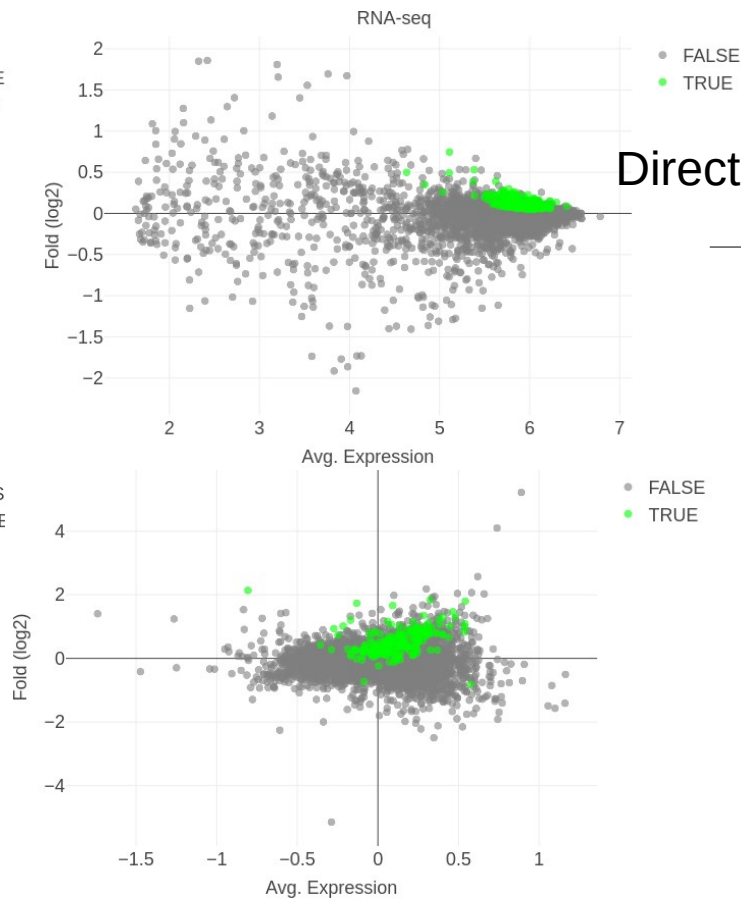
MA

P-value histogram

Volcano



MA



Directly inspect

Show entries

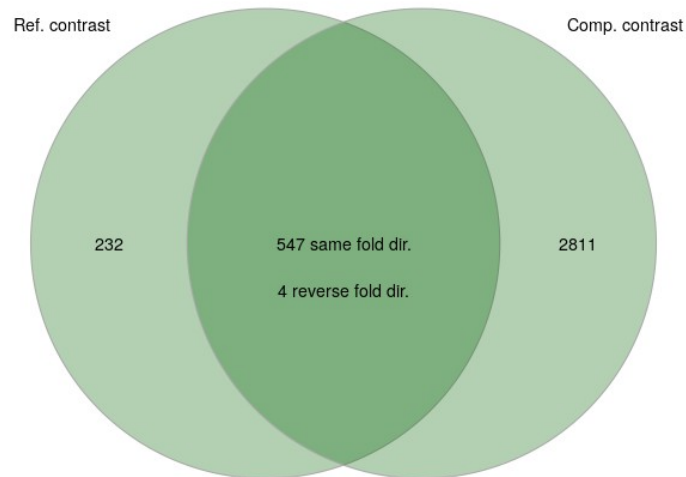
| | pass_thres | comb_id | d1.idx | d1.cnv_high_low.PValue |
|----|------------|---------|----------|------------------------|
| 1 | None | C15 | AARS2 | 0.014 |
| 2 | None | C37 | ABCF3 | 0 |
| 3 | None | C217 | ADPRM | 0.609 |
| 4 | None | C330 | ALDH1B1 | 0.442 |
| 5 | None | C428 | ANKRD22 | 0.358 |
| 6 | None | C490 | AP2S1 | 0.519 |
| 7 | None | C569 | ARF3 | 0.808 |
| 8 | None | C594 | ARHGAP25 | 0.003 |
| 9 | None | C720 | ASH2L | 0.014 |
| 10 | Second | C732 | ASS1 | 0.021 |

Showing 1 to 10 of 207 entries

Highlight in figure, see distribution across plots (volcano, MA, p-value histogram)

High versus low severity tumours (cnvhigh vs cnvlow) In proteomics and transcriptomics

Venn diagram



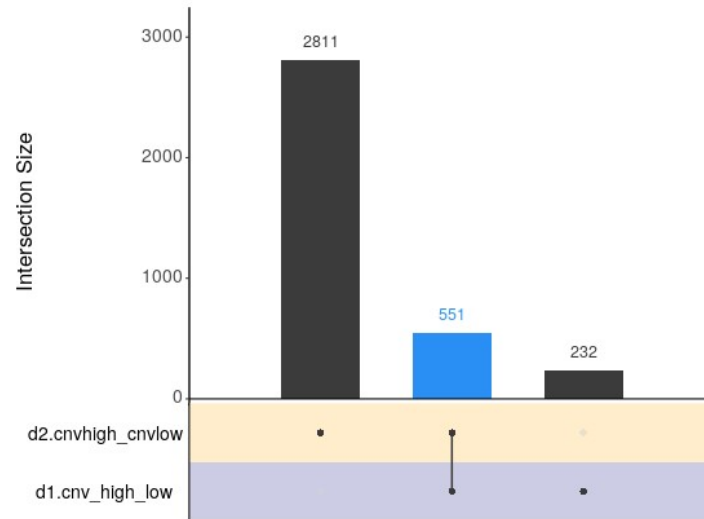
Download & inspect overlaps

Show 10 entries

| | pass_thres | comb_id | d1.idx | d1.cnv_high_low.PValue |
|----|------------|---------|----------|------------------------|
| 1 | None | C15 | AARS2 | 0.014 |
| 2 | None | C37 | ABCF3 | 0 |
| 3 | None | C217 | ADPRM | 0.609 |
| 4 | None | C330 | ALDH1B1 | 0.442 |
| 5 | None | C428 | ANKRD22 | 0.358 |
| 6 | None | C490 | AP251 | 0.519 |
| 7 | None | C569 | ARF3 | 0.808 |
| 8 | None | C594 | ARHGAP25 | 0.003 |
| 9 | None | C720 | ASH2L | 0.014 |
| 10 | Second | C732 | ASS1 | 0.021 |

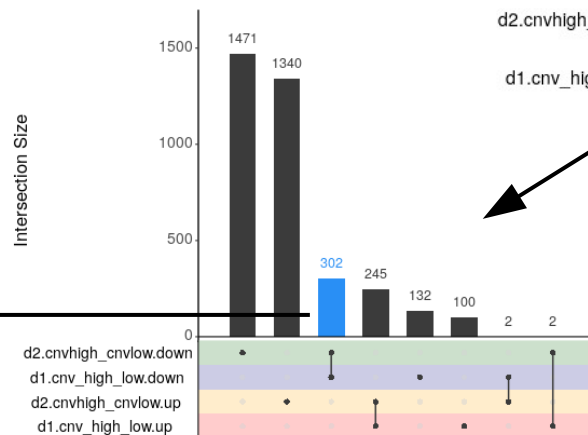
Showing 1 to 10 of 207 entries

Upset

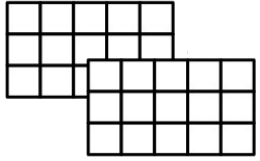


Split on fold direction
Suddenly more informative!

d1 = proteomics, d2 = RNA-seq



The workflow



Expression table(s):

RNA-seq, proteomics, metabolomics, microarray ...



Statistics

NormalyzerDE:

<https://github.com/ComputationalProteomics/NormalyzerDE>

Limma, DESeq2 ... (any other statistical tool)



OmicLoupe explorations

Sample input

Data matrix/matrices

(expression data and feature annotations)

Design matrix/matrices

(sample names and conditions)

Statistical values for each contrast

P-values, FDR, log2 fold and average expression

If multiple data matrices: **One column with shared IDs**

Sample input: Design- and data matrix

One column matching data matrix samples
Columns with sample-conditions

| | A | B |
|---|---------------------|-------|
| 1 | sample | group |
| 2 | Igillet_i160308_001 | A |
| 3 | Igillet_i160308_003 | A |
| 4 | Igillet_i160308_010 | A |
| 5 | Igillet_i160308_002 | B |
| 6 | Igillet_i160308_004 | B |
| 7 | Igillet_i160308_011 | B |
| 8 | | |

Design matrix

| Annotation | | | | Statistical contrast(s) | | | | Sample values | | | | | | |
|------------|---------------|-----------|---------|-------------------------|-------------|---------------|--------------|----------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|
| | A | B | C | D | E | F | G | H | I | J | K | L | M | N |
| 1 | protein_clean | class | Protein | pep_count | comp.logFC | comp.AveExpr | comp.P.Value | comp.adj.P.Val | Igillet_i160308_001 | Igillet_i160308_003 | Igillet_i160308_010 | Igillet_i160308_002 | Igillet_i160308_004 | Igillet_i160308_011 |
| 2 | sp A5YKK6 C | human | sp A5Y | 3 | 0.073784318 | 11.3225318223 | 0.6786698897 | 0.90829599045 | 11.3053574142909 | 11.3448550103576 | 11.2067065648476 | 11.5676815760961 | 11.3386650815976 | 11.1719252863554 |
| 3 | sp A6NDG6 P | human | sp A6N | 2 | 0.006031125 | 11.8171520319 | 0.9768654934 | 0.99225626494 | 11.8928902180519 | 11.8594667265317 | 11.6900524644403 | 11.5955302341385 | 12.2099263677684 | 11.6550461806867 |
| 4 | sp A6NHR9 S | human | sp A6N | 3 | 0.956455969 | 10.1125441201 | 0.000635318 | 0.00292589446 | 9.72739285571531 | 9.80319264154475 | 9.65929969991161 | NA | 10.692847883279 | 10.6799875201249 |
| 5 | sp A6NL28 T | human | sp A6N | 3 | 0.345339762 | 12.8661147738 | 0.2327309507 | 0.54158389469 | 13.1678034694425 | 12.6076458632851 | 12.3048853451425 | 12.9169448583949 | 13.502020002742 | 12.6973891036369 |
| 6 | sp A8MWD9 P | human | sp A8M | 3 | 0.151960587 | 15.1225403267 | 0.4168190744 | 0.74842864064 | 15.0785821219339 | 15.0567513793221 | 15.004346598198 | 15.2741940213053 | 15.3958206314456 | 14.9255472078366 |
| 7 | sp C8Z543 A | yeast | sp C8Z | 15 | NA | 12.0375169527 | NA | NA | 11.4590027424857 | 12.0572472258314 | 12.5963008897086 | NA | NA | NA |
| 8 | sp C8Z9Z9 A | yeast | sp C8Z | 3 | NA | 11.1074554499 | NA | NA | 10.7191307214481 | 11.8940039341242 | 10.7092316941399 | NA | NA | NA |
| 9 | sp C8ZDR4 H | yeast | sp C8Z | 3 | NA | 11.3154450479 | NA | NA | 11.1341650919135 | 11.8987098865356 | 10.9134601653582 | NA | NA | NA |
| 10 | sp C8ZFZ7 B | yeast | sp C8Z | 6 | NA | 12.546299468 | NA | NA | 12.6808536344715 | 12.4437430369664 | 12.5143017325099 | NA | NA | NA |
| 11 | sp C8ZG13 P | yeast | sp C8Z | 2 | NA | 11.005518271 | NA | NA | 11.1268408938074 | 10.9133287296018 | 10.9763851894952 | NA | NA | NA |
| 12 | sp O00116 A | human | sp O00 | 7 | 0.387193082 | 12.0875631472 | 0.080954491 | 0.25186991899 | 12.145471397551 | 11.9120655377126 | 11.6243628834736 | 12.4594595073696 | 12.3452771616492 | 12.0387423955942 |
| 13 | sp O00139 K | human | sp O00 | 2 | 0.009327052 | 10.9318839361 | 0.9665470883 | 0.99140348478 | 11.0812888908325 | 10.7680239980367 | 10.935146457096 | 10.7210844881852 | NA | 11.1538758462433 |
| 14 | sp O00148 D | human | sp O00 | 9 | 0.273229384 | 13.0972781038 | 0.1311679728 | 0.36223799977 | 13.0405681366035 | 12.8399973670675 | 13.0014247325095 | 13.2333602773008 | 13.3602269183308 | 13.1080911911772 |
| 15 | sp O00148 D | human | sp O00 | 12 | 0.093832475 | 15.9851177832 | 0.5975302322 | 0.8622727463 | 16.0842424333428 | 15.9020245999128 | 15.8283376033529 | 16.2139081723778 | 15.9557395819064 | 15.9264543084892 |
| 16 | sp O00148 D | ambiguous | sp O00 | 2 | 0.754974214 | 14.8001969308 | 0.0324117393 | 0.11512081996 | 14.3229700574638 | 14.138330851045 | 15.0333208270964 | 15.5114134323332 | NA | 14.9949494862226 |
| 17 | sp O00151 P | human | sp O00 | 2 | 0.575279174 | 10.393404225 | 0.0773638338 | 0.24287252586 | 10.1431774462571 | 9.87562265895916 | 10.298493808076 | 11.1054870281953 | 9.9529521767828 | 10.9846922315613 |
| 18 | sp O00154 B | human | sp O00 | 5 | 0.078752393 | 12.220518744 | 0.7080232516 | 0.92004199982 | 12.0819792418602 | 12.1861080477041 | 12.2753403528755 | 12.4390542786356 | 11.8578922526316 | 12.4827382903155 |
| 19 | sp O00159 M | human | sp O00 | 11 | 0.170384172 | 12.1034443887 | 0.3604086284 | 0.6959318992 | 11.961578981285 | 12.1242195565334 | 11.9689583696402 | 12.2560119707843 | 12.3666746037258 | 11.943222850094 |

Data matrix

Sample input: Statistical contrast(s)



Current comparison

Format: [contrast name].[stat-values]

| | Annotation | | | | Statistical contrast(s) | | | | Sample values | | | | |
|----|---------------|-------|---------|-----------|-------------------------|---------------|--------------|----------------|---------------------|---------------------|---------------------|---------------------|---------------------|
| | A | B | C | D | E | F | G | H | I | J | K | L | |
| 1 | protein_clean | class | Protein | pep_count | comp.logFC | comp.AveExpr | comp.P.Value | comp.adj.P.Val | Igillet_i160308_001 | Igillet_i160308_003 | Igillet_i160308_010 | Igillet_i160308_002 | Igillet_i160308_004 |
| 2 | sp A5YKK6 C | human | sp A5Y | 3 | 0.073784318 | 11.3225318223 | 0.6786698897 | 0.90829599045 | 11.3053574142909 | 11.3448550103576 | 11.2067065648476 | 11.5676815760961 | 11.3053574142909 |
| 3 | sp A6NDG6 P | human | sp A6N | 2 | 0.006031125 | 11.8171520319 | 0.9768654934 | 0.99225626494 | 11.8928902180519 | 11.8594667265317 | 11.6900524644403 | 11.5955302341385 | 12.2067065648476 |
| 4 | sp A6NHR9 S | human | sp A6N | 3 | 0.956455969 | 10.1125441201 | 0.000635318 | 0.00292589446 | 9.72739285571531 | 9.80319264154475 | 9.65929969991161 | NA | 10.1125441201 |
| 5 | sp A6NL28 T | human | sp A6N | 3 | 0.345339762 | 12.8661147738 | 0.2327309507 | 0.54158389469 | 13.1678034694425 | 12.6076458632851 | 12.3048853451425 | 12.9169448583949 | 13.1678034694425 |
| 6 | sp A8MWD9 P | human | sp A8M | 3 | 0.151960587 | 15.1225403267 | 0.4168190744 | 0.74842864064 | 15.0785821219339 | 15.0567513793221 | 15.004346598198 | 15.2741940213053 | 15.3053574142909 |
| 7 | sp C8Z543 A | yeast | sp C8Z | 15 | NA | 12.0375169527 | NA | NA | 11.4590027424857 | 12.0572472258314 | 12.5963008897086 | NA | NA |
| 8 | sp C8Z9Z9 A | yeast | sp C8Z | 3 | NA | 11.1074554499 | NA | NA | 10.7191307214481 | 11.8940039341242 | 10.7092316941399 | NA | NA |
| 9 | sp C8ZDR4 H | yeast | sp C8Z | 3 | NA | 11.3154450479 | NA | NA | 11.1341650919135 | 11.8987098865356 | 10.9134601653582 | NA | NA |
| 10 | sp C8ZFZ7 B | yeast | sp C8Z | 6 | NA | 12.546299468 | NA | NA | 12.6808536344715 | 12.4437430369664 | 12.5143017325099 | NA | NA |
| 11 | sp C8ZG13 P | yeast | sp C8Z | 2 | NA | 11.005518271 | NA | NA | 11.1268408938074 | 10.9133287296018 | 10.9763851894952 | NA | NA |
| 12 | sp O00116 A | human | sp O00 | 7 | 0.387193082 | 12.0875631472 | 0.080954491 | 0.25186991899 | 12.145471397551 | 11.9120655377126 | 11.6243628834736 | 12.4594595073696 | 12.3053574142909 |
| 13 | sp O00139 K | human | sp O00 | 2 | 0.009327052 | 10.9318839361 | 0.9665470883 | 0.99140348478 | 11.0812888908325 | 10.7680239980367 | 10.935146457096 | 10.7210844881852 | NA |
| 14 | sp O00140 P | human | sp O00 | 2 | 0.009327052 | 10.9318839361 | 0.9665470883 | 0.99140348478 | 11.0812888908325 | 10.7680239980367 | 10.935146457096 | 10.7210844881852 | NA |

If using multiple tables

Proteomics

| | A | B | C | D | E | F | G |
|---|-------------|-----------|----------------------|------------------|-------------------------------|---------------------------------------|--------------------------------|
| 1 | gene_symbol | accession | species_names | featureAvg | infected_2h-control_2h_PValue | infected_2h-control_2h_log2FoldChange | infected_2h-control_2h_AdjPVal |
| 2 | AFP | P02771 | Homo sapiens OX=9606 | 11.031331403655 | 0.30969902158687 | -0.307359232716664 | 0.99980939482126 |
| 3 | FABP1 | P07148 | Homo sapiens OX=9606 | 10.954591559394 | 0.587573151279121 | -0.209476148787799 | 0.99980939482126 |
| 4 | VIL1 | P09327 | Homo sapiens OX=9606 | 10.698272236802 | 0.416645112976052 | -0.191097088944636 | 0.99980939482126 |
| 5 | KRT18 | P05783 | Homo sapiens OX=9606 | 11.2095110506113 | 0.633331356317085 | -0.132690067072895 | 0.99980939482126 |
| 5 | | Q9P2E9 | Homo sapiens OX=9606 | 10.4230791312684 | 0.459488934884819 | -0.167897844503694 | 0.99980939482126 |
| 7 | ANXA4 | P09525 | Homo sapiens OX=9606 | 10.6499881385456 | 0.82781011607852 | -0.050223942845536 | 0.99980939482126 |
| 8 | KRT8 | P05787 | Homo sapiens OX=9606 | 10.619917799405 | 0.844472953537969 | -0.060373667476336 | 0.99980939482126 |
| 9 | MUC13 | Q9H3R2 | Homo sapiens OX=9606 | 9.37852849994093 | 0.831812491341271 | 0.078448770880204 | 0.99980939482126 |
| 0 | CDH17 | Q12864 | Homo sapiens OX=9606 | 9.86333520601928 | 0.518411935369265 | -0.142734075113003 | 0.99980939482126 |
| 1 | LGALS3 | P17931 | Homo sapiens OX=9606 | 10.2031600815392 | 0.489722341053065 | -0.135236521146233 | 0.99980939482126 |
| 2 | SERPINA1 | P01009 | Homo sapiens OX=9606 | 10.0902246911767 | 0.55887555105166 | -0.136333152852051 | 0.99980939482126 |
| 3 | IDH1 | O75874 | Homo sapiens OX=9606 | 9.87676816158489 | 0.184527739086192 | -0.358249535050817 | 0.99980939482126 |
| 4 | | | | | | | |

One column need to be in common

| | A | B | C | D | E | F |
|---|----------|--------------------|----------------------|--------------------|----------------------|------------------------|
| 1 | idx | diff_med_24h.logFC | diff_med_24h.AveExpr | diff_med_24h.t | diff_med_24h.P.Value | diff_med_24h.adj.P.Val |
| 2 | AAAS | 0.028183162940322 | 5.72297816146273 | 0.100490173895532 | 0.921125366636798 | 0.9917695300499 |
| 3 | AACS | 0.534149879708331 | 4.45269791483771 | 1.64919191277447 | 0.117377841874363 | 0.4509357956044 |
| 4 | AARS | 0.199342676608586 | 4.98757470941001 | 0.481363034947611 | 0.636367796688444 | 0.9279204702562 |
| 5 | AASDHPPT | -0.247161129015488 | 4.83935965937663 | -0.695725656217854 | 0.495959151345674 | 0.8313211270439 |
| 6 | ABCC1 | -1.23553413477472 | 2.70011516424125 | -1.65099903822641 | 0.117004717006166 | 0.4501955251607 |
| 7 | ABCD1 | 0.152322007640473 | 0.857479682917489 | 0.168071491533119 | 0.86850117891888 | 0.9917695300499 |
| 8 | ABCD3 | -0.281670225429062 | 6.41489681550556 | -1.32645373367621 | 0.202153780378643 | 0.5642399595980 |
| 9 | ABCE1 | 0.623063181229627 | 5.35006411905552 | 2.15407647213151 | 0.045802950961147 | 0.296402241764 |
| 0 | ABCF1 | 0.015813080864439 | 4.88613299788463 | 0.047478118279708 | 0.962682923075981 | 0.9917695300499 |
| 1 | ABCF2 | -0.130226640970301 | 2.65072144542587 | -0.333054000344062 | 0.742470579042446 | 0.9917695300499 |

RNA-seq

Proteomics of SARS-CoV-2-infected host cells reveals therapy targets

Denisa Bojkova, Kevin Klann, Benjamin Koch, Marek Widera, David Krause, Sandra Ciesek, Jindrich Cinatl

& Christian Münch

Nature 583, 469–472(2020) | Cite this article

RESEARCH ARTICLE

SARS-CoV-2 productively infects human gut enterocytes

Mart M. Lamers^{1,*}, Joep Beumer^{2,*}, Jelte van der Vaart^{2,*}, Kèvin Knoops³, Jens Puschhof², Tim I. Breugem¹, Ra...

+ See all authors and affiliations

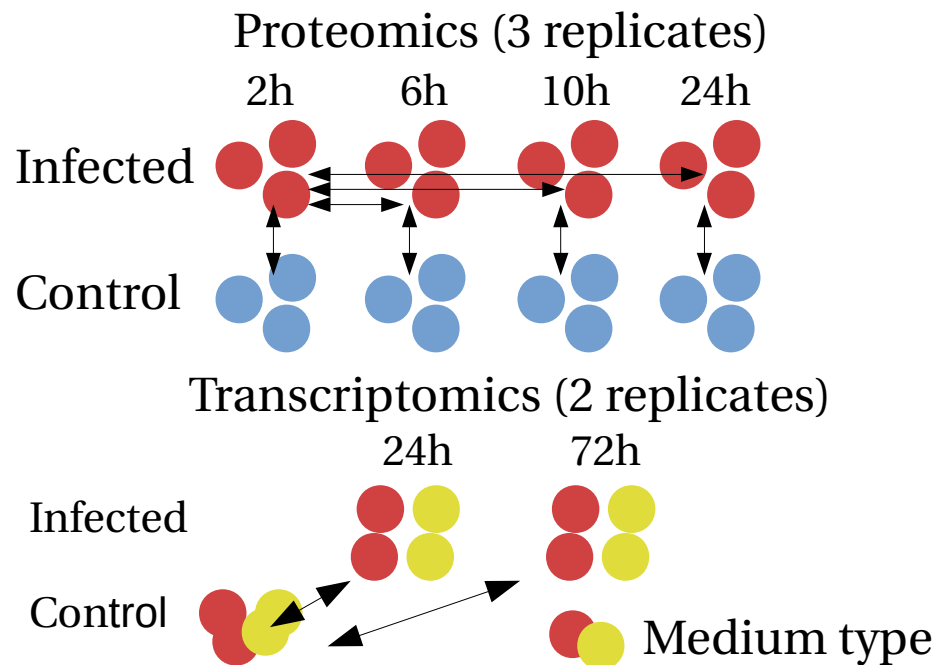
Science 03 Jul 2020:
Vol. 369, Issue 6499, pp. 50-54
DOI: 10.1126/science.abc1669

GITHUB:
DEMO SERVER:
TUTORIAL LINK:

github.com/ComputationalProteomics/OmicLoupe
<http://130.239.81.217:3838/omicloupe>
quantitativeproteomics.org/analysiscourse/omicloupe

```
> devtools::install_github("ComputationalProteomics/OmicLoupe")  
> OmicLoupe::runApp()
```

Subsequently, click/copy the link “<http://127.0.0.1:XXXX>” and run in the web browser



Thank you for listening!!

Feel free to contact me for further queries!

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