Intervene Documentation

Release v0.6.4

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May 16, 2018

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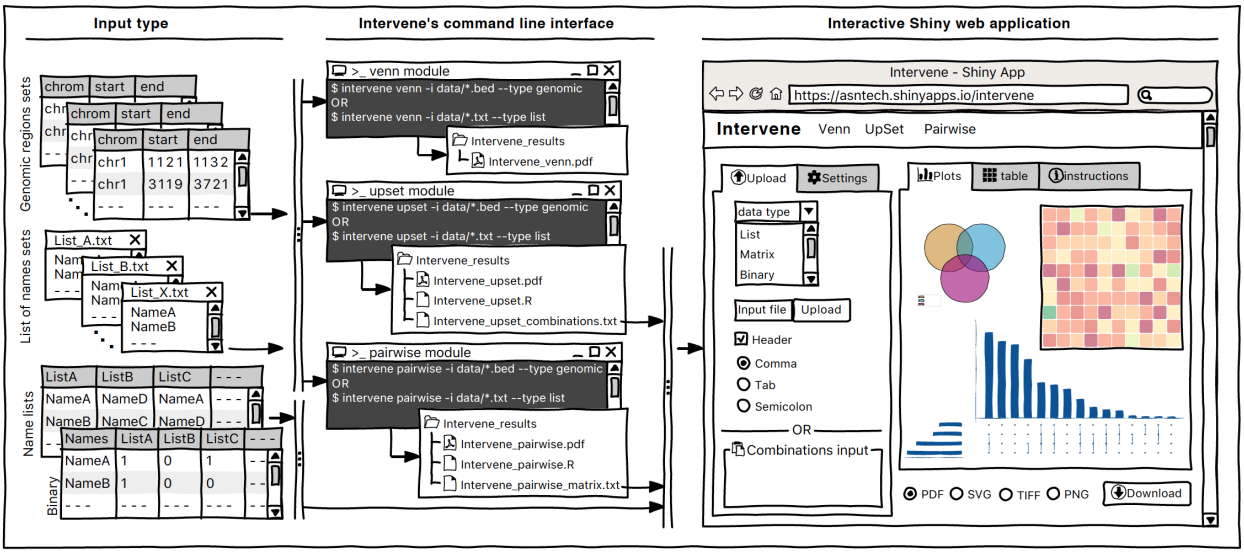
Welcome to Intervene - a tool for intersection and visualization of multiple genomic region sets



CHAPTER 1

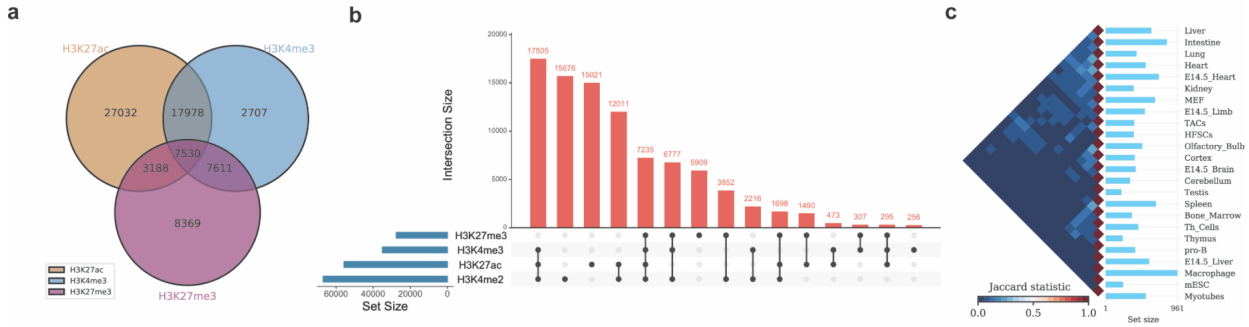
Introduction

Intervene is a tool for intersection and visualization of multiple genomic region and gene sets (or lists of items).

Intervene provides an easy and automated interface for effective intersection and visualization of genomic region sets or lists of items, thus facilitating their analysis and interpretations. Intervene contains three modules.

- *venn* to compute Venn diagrams of up-to 6 sets
- *upset* to compute UpSet plots of multiple sets
- *pairwise* to compute and visualize intersections of genomic sets as clustered heatmap.

Intervene gives user flexibility to choose figure colors, labels, size, quality, and type to make them as publication standard.



CHAPTER 2

Installation

Intervene is available on PyPi, through Bioconda, and source code available on GitHub and Bitbucket. Intervene takes care of the installation of all the required Python modules. If you already have a working installation of Python, the easiest way to install the required Python modules is by installing Intervene using `pip`.

If you're setting up Python for the first time, we recommend to install it using the Conda or Miniconda Python distribution. This comes with several helpful scientific and data processing libraries, and available for platforms including Windows, Mac OSX and Linux.

You can use one of the following ways to install Intervene.

2.1 Quick installation

2.1.1 Install uisng Conda

We highly recommend to install Intervene using Conda, this will take care of the dependencies. If you already have Conda or Miniconda installed, go ahead and use the below command.

```
conda install -c bioconda intervene
```

Note: This will install all the dependencies and you are ready to use **Intervene**.

2.1.2 Install using *pip*

You can install Intervene from PyPi using pip.

```
pip install intervene
```

Note: If you install using pip, make sure to install BEDTools and R packages listed below.

2.2 Prerequisites

Intervene requires the following Python modules and R packages:

- Python (=> 2.7): https://www.python.org/
- BEDTools (Latest version): https://github.com/arq5x/bedtools2
- pybedtools (>= 0.7.9): https://daler.github.io/pybedtools/
- Pandas (>= 0.16.0): http://pandas.pydata.org/
- Seaborn (>= 0.7.1): http://seaborn.pydata.org/
- R (>= 3.0): https://www.r-project.org/
- R packages including UpSetR, corrplot

2.2.1 Install BEDTools

Intervene is using pybedtools, which is a Python wrapper for the BEDTools. BEDTools should be installed before using Intervene. It is recomended to have the latest version of the tool. Please read the installation instructions at https://github.com/arq5x/bedtools2 to install BEDTools, and make sure it is accessible through your PATH variable.

2.2.2 Install required R packages

Intervene rquires three R packages, UpSetR , corrplot for visualization and Cairo to generate high-quality vector and bitmap figures. To install these, open R/RStudio and use the following command.

```
install.packages(c("UpSetR", "corrplot","Cairo"))
```

2.3 Install Intervene from source

You can install a development version by using `git` from our bitbucket repository at https://bitbucket.org/CBGR/intervene or Github.

2.3.1 Install development version from *Bitbucket*

If you have *git* installed, use this:

```
git clone https://bitbucket.org/CBGR/intervene.git
cd intervene
python setup.py sdist install
```

2.3.2 Install development version from *GitHub*

If you have *git* installed, use this:

```
git clone https://github.com/asntech/intervene.git
cd intervene
python setup.py sdist install
```

CHAPTER 3

How to use Intervene

Once you have installed Intervene, you can type:

```
intervene --help
```

This will show the main help, which lists the three subcommands/modules: `venn`, `upset`, and `pairwise`.

```
usage: intervene <subcommand> [options]

positional arguments <subcommand>:
  {venn,upset,pairwise}
                        List of subcommands
    venn                Venn diagram of intersection of genomic regions or list sets␣
↪(upto 6-way).
    upset               UpSet diagram of intersection of genomic regions or list sets.
    pairwise            Pairwise intersection and heatmap of N genomic region sets in
↪<BED/GTF/GFF> format.

optional arguments:
  -h, --help            show this help message and exit
  -v, --version         show program's version number and exit
```

To view the help for the individual subcommands, please type:

To view `venn` module help, type

```
intervene venn --help
```

To view `upset` module help, type

```
intervene upset --help
```

To view `pairwise` module help, type

```
intervene pairwise --help
```

3.1 Run Intervene on test data

To run Intervene using example data, use the following commands. To access the test data make sure you have `sudo` or `root` access.

To run `venn` module with test data, type

```
intervene venn --test
```

To run `upset` module with test data, type

```
intervene upset --test
```

To run `pairwise` module with test data, type

```
intervene pairwise --test
```

If you have installed Intervene locally from the source code, you may have problem to find test data. You can download the test data here https://github.com/asntech/intervene/tree/master/intervene/example_data and point to it using `-i` instead of `--test`.

```
./intervene/intervene venn -i intervene/example_data/ENCODE_hESC/*.bed
./intervene/intervene upset -i intervene/example_data/ENCODE_hESC/*.bed
./intervene/intervene pairwise -i intervene/example_data/dbSUPER_mm9/*.bed
```

These subcommands will save the results in the current working directory with a folder named `Intervene_results`. If you wish to save the results in a specific folder, you can type:

```
intervene <module_name> --test --output ~/path/to/your/results/folder
```

CHAPTER 4

Intervene modules

Intervene provides three types of plots to visualize intersections of genomic regions and list sets. These are pairwise heatmap of N genomic region sets, classic Venn diagrams of genomic regions and list sets of up to 6-way and UpSet plots.

Note: By default the intersection genomic regions is computed using default parameters of *BedTools*. Intervene version > v0.6.0 now allows users to provide all the arguments available in BedTools' commands by using **–bedtools-options**.

4.1 Venn diagram module

Once you have installed Intervene, you can type:

Usage:

```
intervene venn [options]
```

Note: Please scroll down to see a detailed summary of available **options**.

Help:

```
intervene venn --help
```

Example:

```
intervene venn -i path/to/BED/files/*.bed
```

This will save the results in the current working directory with a folder named `Intervene_results`. If you wish to save the results in a specific folder, you can type:

```
intervene venn -i path/to/BED/files/*.bed --output ~/results/path
```

Summary of options

Option	Description
-h, –help	To show the help message and exit
-i, –input	Input genomic regions in (BED/GTF/GFF) format or lists of genes/SNPs IDs. For files in a directory use *.<extension>. e.g. *.bed
–type	{genomic,list}. Type of input sets. Genomic regions or lists of genes/SNPs. Default is `genomic`
–names	Comma-separated list of names as labels for input files. If it is not set file names will be used as labels. For example: –names=A,B,C,D,E,F
–filenames	Use file names as labels instead. Default is `False`
–bedtools-options	List any of the arguments available for bedtool's intersect command. Type bedtools intersect –help to view all the options. For example: –bedtools-options f=0.8,r,etc
–colors	Comma-separated list of matplotlib-valid colors for fill. E.g., –colors=r,b,k
–bordercolors	Comma-separated list of matplotlib-valid colors for borders. E.g., –bordercolors=r,b,k
-o, –output	Output folder path where results will be stored. Default is current working directory.
–save-overlaps	Save overlapping regions/names for all the combinations as bed/txt files. Default is `False`
–overlap-thresh	Minimum threshold to save the overlapping regions/names as bed/txt. Default is `1`
–figtype	{pdf,svg,ps,tiff,png} Figure type for the plot. e.g. –figtype svg. Default is `pdf`
–figsize	Figure size as width and height.e.g. –figsize 12 12.
–fontsize	Font size for the plot labels. Default is `14`
–dpi	Dots-per-inch (DPI) for the output. Default is: `300`
–fill	{number,percentage} Report number or percentage of overlaps (Only if –type=list). Default is `number`
–test	This will run the program on test data.

4.2 UpSet plot module

Once you have installed Intervene, you can type:

Usage:

```
intervene upset [options]
```

Note: Please scroll down to see a detailed summary of available **options**.

Help: You can also see list of options by typing this on the terminal.

```
intervene upset --help
```

Example:

```
intervene upset -i path/to/BED/files/*.bed
```

This will save the results in the current working directory with a folder named `Intervene_results`. If you wish to save the results in a specific folder, you can type:

```
intervene upset -i path/to/BED/files/*.bed --output ~/results/path
```

Summary of options

Option	Description
-h, –help	show this help message and exit
-i, –input	Input genomic regions in <BED/GTF/GFF/VCF> format or list files. For files in a directory use *.<ext>. e.g. *.bed
–type	Type of input sets. Genomic regions or lists of genes sets {genomic,list}. Default is `genomic`
–names	Comma-separated list of names as labels for input files. If it is not set file names will be used as labels. For example: –names=A,B,C,D,E,F
–filenames	Use file names as labels instead. Default is `True`
–bedtools-options	List any of the arguments available for bedtool's intersect command. Type bedtools intersect –help to view all the options. For example: –bedtools-options f=0.8,r,etc
-o, –output	Output folder path where plots will store. Default is current working directory.
–save-overlaps	Save overlapping regions/names for all the combinations as bed/txt files. Default is `False`
–overlap-thresh	Minimum threshold to save the overlapping regions/names as bed/txt. Default is `1`
–order	The order of intersections of sets {freq,degree}. e.g. –order degree. Default is `freq`
–ninter	Number of top intersections to plot. Default is `30`
–showzero	Show empty overlap combinations. Default is `False`
–showsize	Show intersection sizes above bars. Default is `True`
–mbcolor	Color of the main bar plot. Default is `gray23`
–sbcolor	Color of set size bar plot. Default is `#56B4E9`
–mblabel	The y-axis label of the intersection size bars. Default is `No of Intersections`
–sxlabel	The x-axis label of the set size bars. Default is `Set size`
–figtype	Figure type for the plot. e.g. –figtype svg {pdf,svg,ps,tiff,png} Default is `pdf`
–figsize	Figure size for the output plot (width,height).
–dpi	Dots-per-inch (DPI) for the output. Default is `300`
–scriptonly	Set to generate Rscript only, if R/UpSetR package is not installed. Default is `False`
–showshiny	Print the combinations of intersections to input to Shiny App. Default is `False`

4.3 Pairwise intersection module

Once you have installed Intervene, you can type:

Usage:

```
intervene pairwise [options]
```

Note: Please scroll down to see a detailed summary of available **options**.

Help:

```
intervene pairwise --help
```

Example:

```
intervene pairwise -i path/to/BED/files/*.bed --type genomic --compute jaccard --
↪htype tribar
```

This will save the results in the current working directory with a folder named `Intervene_results`. If you wish to save the results in a specific folder, you can type:

```
intervene pairwise -i path/to/BED/files/*.bed --type genomic --compute jaccard --
↪htype tribar --output ~/results/path
```

Summary of options

Option	Description
-h, –help	show this help message and exit
-i, –input	Input genomic regions in (BED/GTF/GFF) format. For files in a directory use *.<extension>. e.g. *.bed
–type	{genomic,list}. Type of input sets. Genomic regions or lists of genes/SNPs. Default is `genomic`
–compute	Compute count/fraction of overlaps or statistical relationships. {`count`, `frac`, `jaccard`, `fisher`, `reldist`}
	–compute=count - calculates the number of overlaps.
	–compute=frac - calculates the fraction of overlap.
	–compute=jaccard - calculate the Jaccard statistic. Read more details here
	–compute=reldist - calculate the distribution of relative distances. Read more details here
	–compute=fisher - calculate Fisher's statistic. Read more details here
	Note: For jaccard and reldist regions should be pre-shorted or set –sort''
–bedtools-options	List any of the arguments available for bedtool's subcommands: interset, jaccard, fisher. Type *bedtools <subcommand> –help* to view all the options. For example: –bedtools-options f=0.8,r,etc.
	Note: –compute options count and frac uses BedTools' intersect command.
–corr	Compute the correlation. By default set to False
–corrtype	Select the type of correlation from `pearson`, `kendall` or `spearman`.
	–corrtype=pearson: computes the Pearson correlation. (Default)
	–corrtype=kendall: computes the Kendall correlation.
	–corrtype=spearman: computes the Spearman correlation.
	Note: This only works if –corr is set.
–htype	{tribar,color,pie,circle,square,ellipse,number,shade}. Heatmap plot type. Default is `tribar`.
	Read the below note for `tribar` option.
–triangle	Show lower/upper triangle of the matrix as heatmap. Default is `lower`
–diagonal	Show the diagonal values in the heatmap. Default is `False`.
–names	Comma-separated list of names as labels for input files. If it is not set file names will be used as labels. For example: –names=A,B,C,D,E,F
–filenames	Use file names as labels instead. Default is `False`.
–sort	Set this only if your files are not sorted. Default is `False`.
–genome	Required argument if –compute=fisher. Needs to be a string assembly name such as `mm10` or `hg38`
-o, –output	Output folder path where results will be stored. Default is current working directory.
–barlabel	x-axis label of boxplot if –htype=tribar. Default is `Set size`
–barcolor	Boxplot color (hex vlaue or name, e.g. blue). Default is `#53cfff`.
–fontsize	Label font size. Default is `8`.
–title	Heatmap main title. Default is `Pairwise intersection`
–space	White space between barplt and heatmap, if –htype=tribar. Default is `1.3`.
–figtype	{pdf,svg,ps,tiff,png} Figure type for the plot. e.g. –figtype svg. Default is `pdf`
–figsize	Figure size for the output plot (width,height). e.g. –figsize 8 8

Continued on next page

Table 1 – continued from previous page

Option	Description
–dpi	Dots-per-inch (DPI) for the output. Default is: `300`.
–scriptonly	Set to generate Rscript only, if R/Corrplot package is not installed. Default is `False`
–test	This will run the program on test data.

Note: The option `--htype=tribar` will generate a horizontal bar plot with an adjacent heatmap rotated 45 degrees to show the lower triangle of the matrix comparing all sets of bars. If you want to view upper triangle, please `--triangle upper`. It's only recomended to use `tribar` if `compute` is set to `jaccard` or `fisher`.

CHAPTER 5

Example gallery

Here we provide some examples of how Intervene can be used to generate different types of set intersection plots.

5.1 Venn module examples

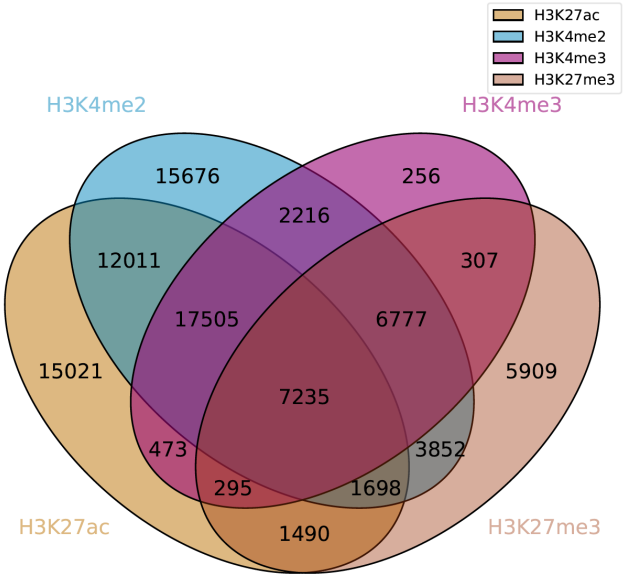
In this example, a 3-way Venn diagram of ChIP-seq peaks of histone modifications (H3K27ac, H3Kme3 and H3K27me3) in hESC from ENCODE data (Dunham et al., 2012).

```
intervene venn -i ~/ENCODE/data/H3K27ac.bed ~/ENCODE/data/H3Kme3.bed ~/ENCODE/data/
↪H3K27me3.bed --filenames
```

By adding one more BED file to `-i` argument, Intervene will generate a 4-way Venn diagram of overlap of ChIP-seq peaks.

```
intervene venn -i ~/ENCODE/data/H3K27ac.bed ~/ENCODE/data/H3Kme3.bed ~/ENCODE/data/
↪H3K27me3.bed  ~/ENCODE/data/H3Kme2.bed --filenames
```

Read more about the `venn` diagrams module here:




```
intervene venn --help
```

5.2 UpSet module examples

In this example, a UpSet plot of ChIP-seq peaks of four histone modifications (H3K27ac, H3Kme3 H3Kme2, and H3K27me3) in hESC from ENCODE data (Dunham et al., 2012).

```
intervene upset -i ~/ENCODE/data/H3K27ac.bed ~/ENCODE/data/H3Kme3.bed ~/ENCODE/data/
↪H3K27me3.bed ~/ENCODE/data/H3Kme2.bed --filenames
```

Read more about the `upset` module:

```
intervene upset --help
```

5.3 Pairwise module examples

In this example, we performed a pairwise intersections of super-enhancers in 24 mouse cell and tissue types from dbSUPER (Khan and Zhang, 2016) and showed the fraction of overlap in heatmap.

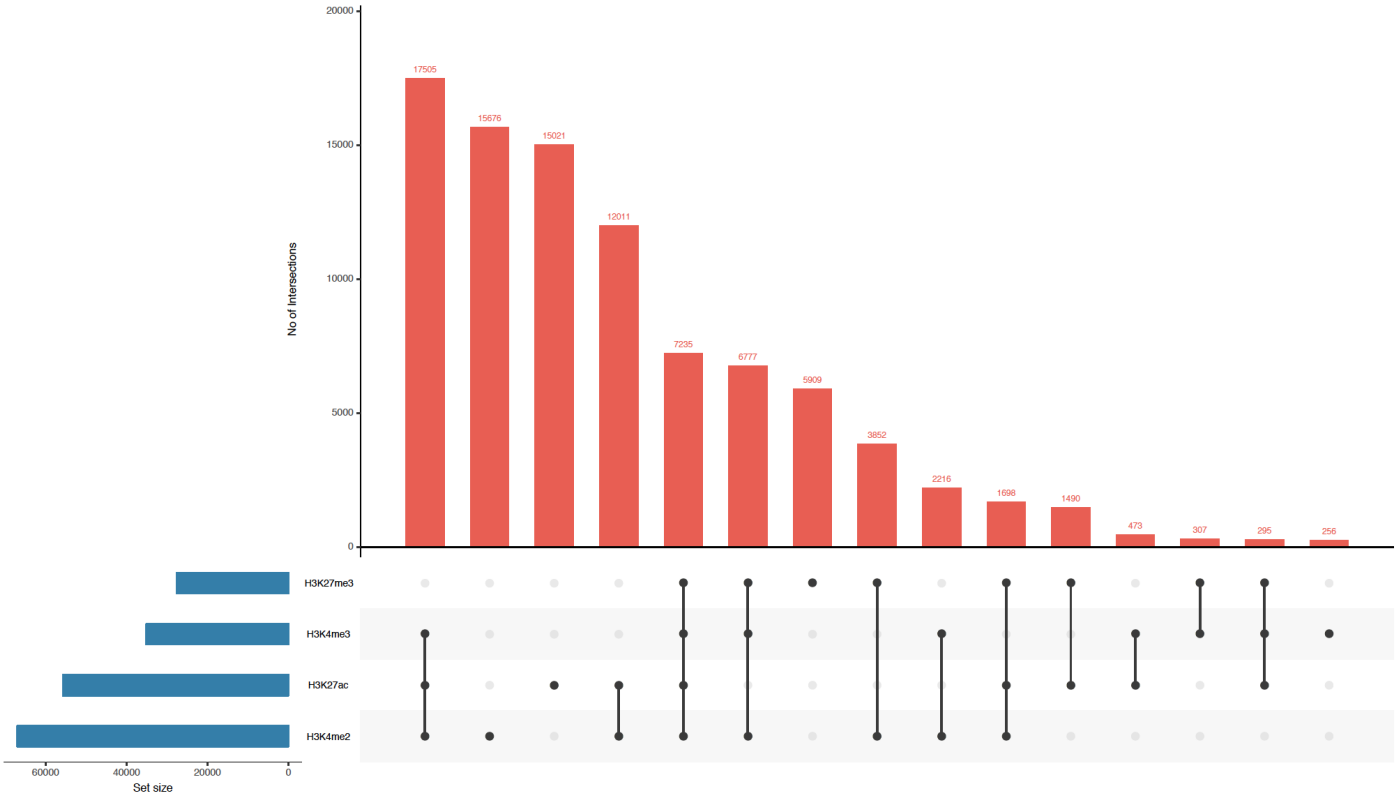
```
intervene pairwise -i ~/dbSUPER/mm9/*.bed --filenames --compute frac --htype pie
```

By setting the `--htype` to `color` will produce this plot.

```
intervene pairwise -i ~/dbSUPER/mm9/*.bed --filenames --compute frac --htype color
```

By setting the `--htype` to `tribar` will produce a triangular heatmap and with a bar-plot of set sizes.

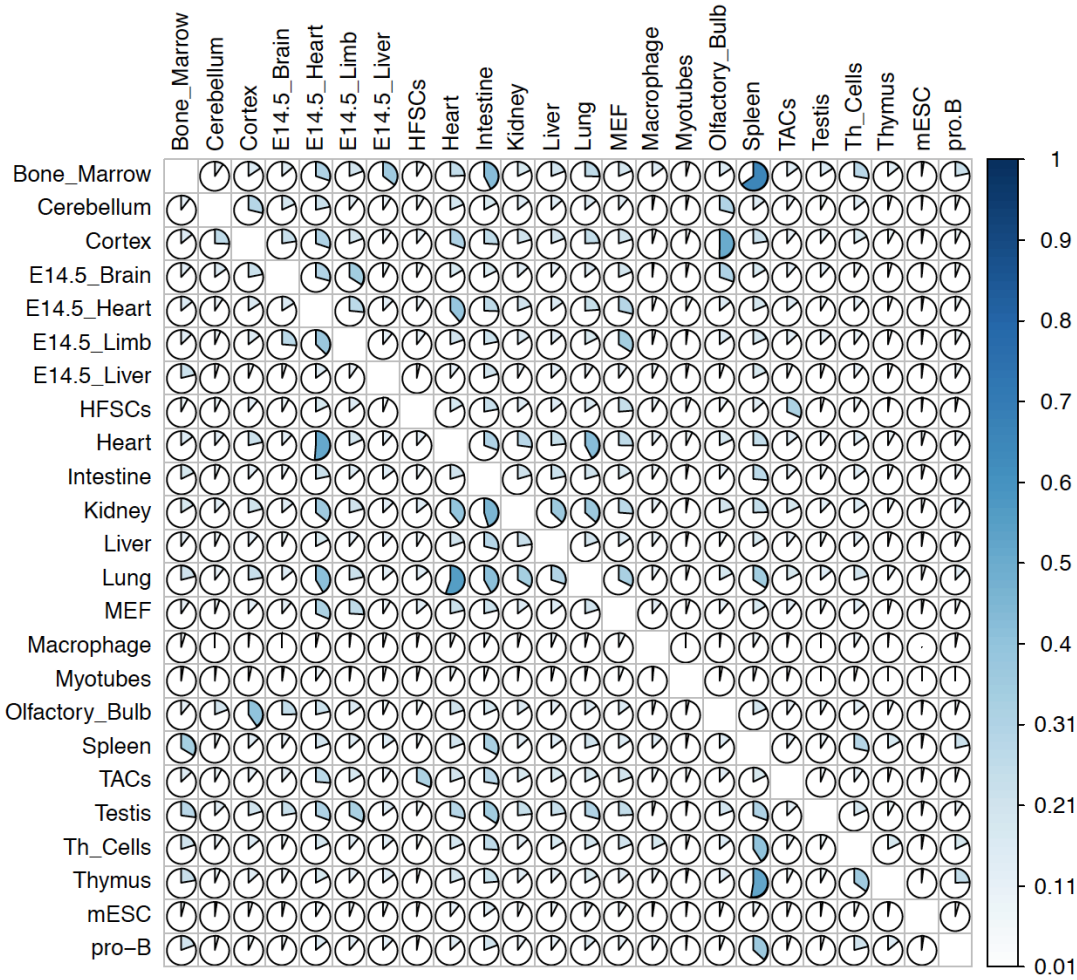
```
intervene pairwise -i ~/dbSUPER/mm9/*.bed --filenames --compute frac --htype tribar
```

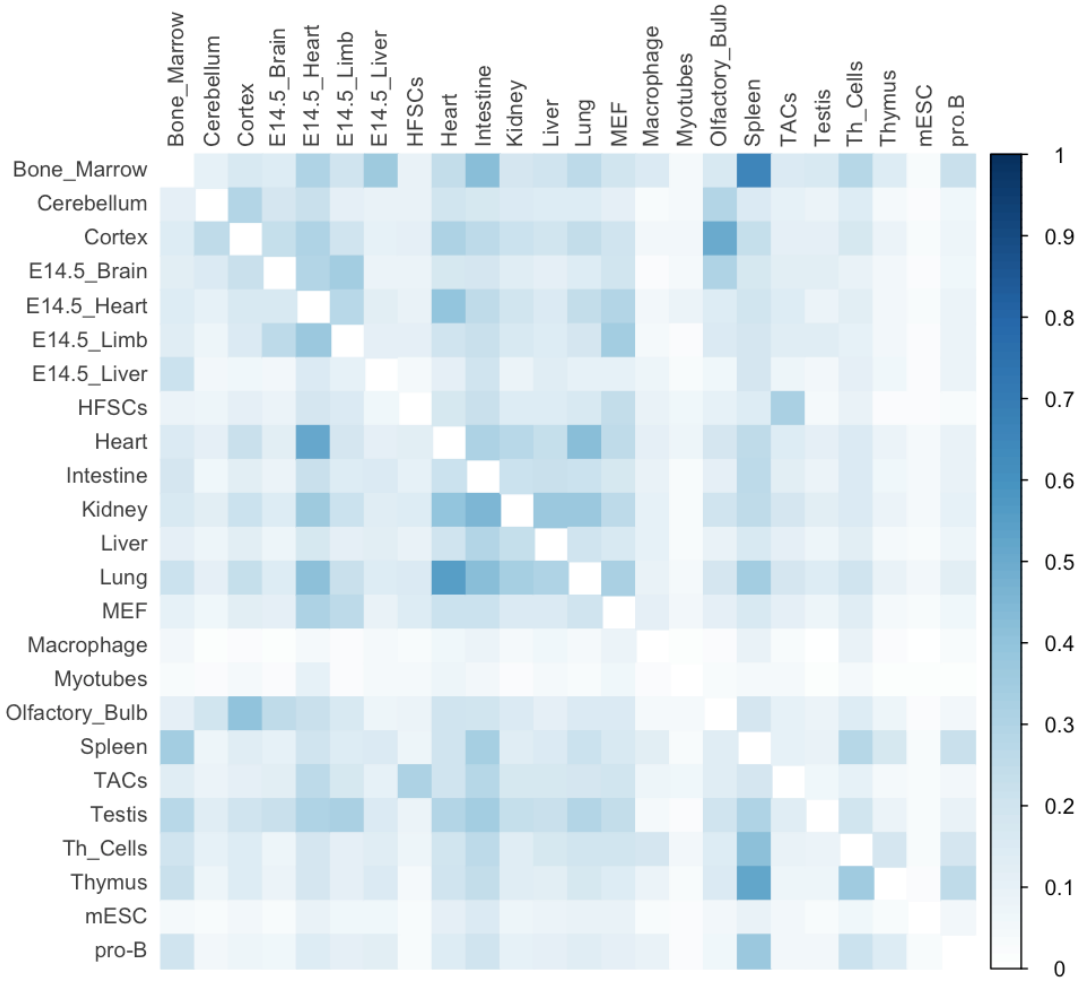


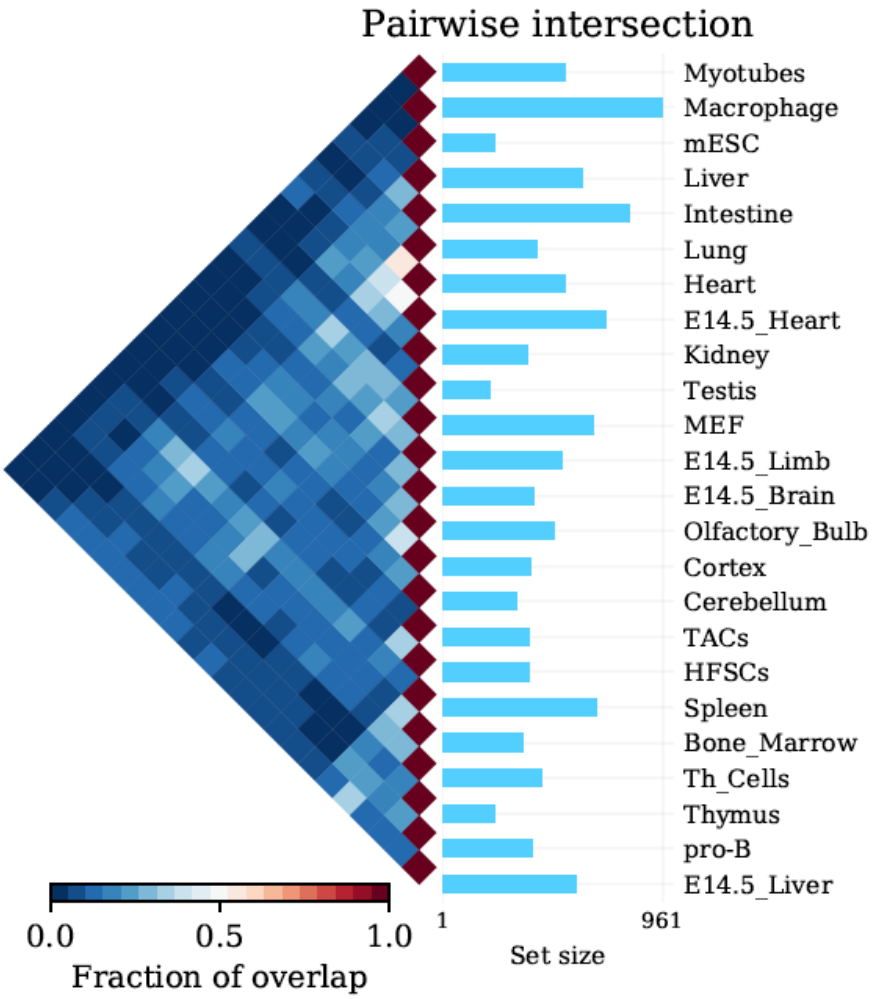
Note: Please make sure that the `tribar` will only show lower triangle of the matrix as heatmap and diagoals are set to zero. It recommended to use this if `--compute is set to ``jaccard`, `fisher` or `reldist`.

Read more about the `pairwise` module here:

```
intervene pairwise --help
```


Bone_Marrow
Cerebellum
Cortex
E14.5_Brain
E14.5_Heart
E14.5_Limb
E14.5_Liver
HFSCs
Heart
Intestine
Kidney
Liver
Lung
MEF
Macrophage
Myotubes
Olfactory_Bulb
Spleen
TACs
Testis
Th_Cells
Thymus
mESC
pro.B
1
0.9
0.8
0.7
0.6
0.5
0.4
0.31
0.21
0.11
0.01


Bone_Marrow
Cerebellum
Cortex
E14.5_Brain
E14.5_Heart
E14.5_Limb
E14.5_Liver
HFSCs
Heart
Intestine
Kidney
Liver
Lung
MEF
Macrophage
Myotubes
Olfactory_Bulb
Spleen
TACs
Testis
Th_Cells
Thymus
mESC
pro-B
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0


Pairwise intersection
Myotubes
Macrophage
mESC
Liver
Intestine
Lung
Heart
E14.5_Heart
Kidney
Testis
MEF
E14.5_Limb
E14.5_Brain
Olfactory_Bulb
Cortex
Cerebellum
TACs
HFSCs
Spleen
Bone_Marrow
Th_Cells
Thymus
pro-B
E14.5_Liver
1
961
Set size
0.0
0.5
1.0
Fraction of overlap

CHAPTER 6

Interactive Shiny App

6.1 Introduction

Intervene Shiny App provides an interactive interface for intersection and effective visualization of gene or genomic region sets. Currently, Shiny app does not acccept genomic regions as input, but the text files generated by Interve's command line interface can be easily uploaded to further explore and customize the plots in an interactive way. Intervene has three modules: venn to generate Venn diagrams of up-to 6 sets, upset to generate UpSet plots of more than 3 sets and pairwise to compute and visualize pariwise intersections as clustered heatmap.

6.2 Venn module

Intervene's venn module provides up-to 6-way classical, Chow-Ruskey and Edwards' Euler/Venn diagrams to visualize the intersections of genomic regions or lists.

6.2.1 Usage instructions

To use this venn module, you can upload a correctly formatted csv/text file, with lists of names. Each column represents a set, and each row represents an element (names/gene/SNPs).

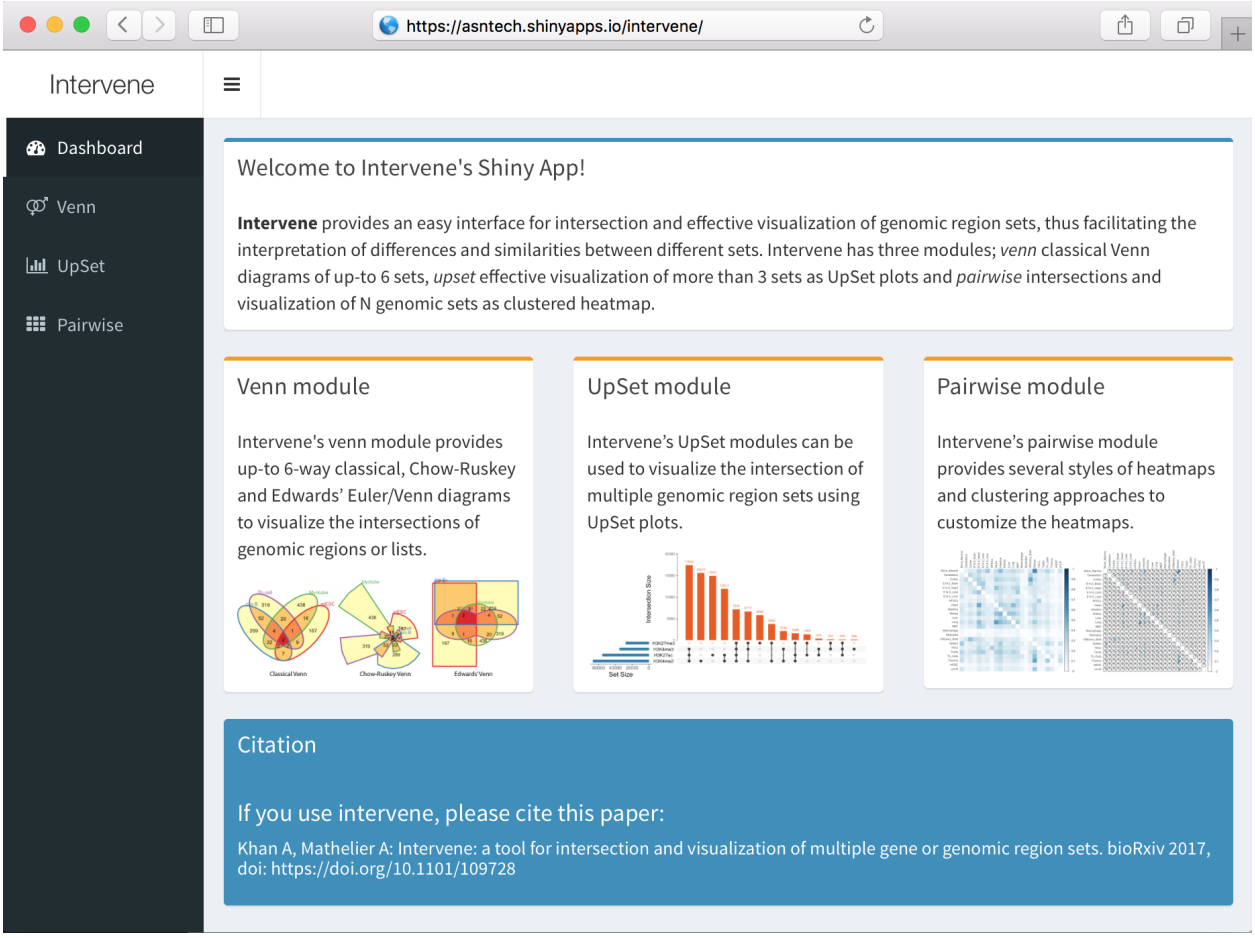
Before uploading the file, choose the correct separator, wheather the names in each column are seperated by a ' , ' choose comma, by a ' ; ' choose semicolon, or by tabs choose tab.

Header names (first row) will be used as set names.

Intervene uses the Vennerable R package to generate different Venn diagrams.

6.3 UpSet module

Intervene's UpSet modules can be used to visualize the intersection of multiple genomic region sets using UpSet plots.


https://asntech.shinyapps.io/intervene/
Intervene
Dashboard
Venn
UpSet
Pairwise
Welcome to Intervene's Shiny App!
Intervene provides an easy interface for intersection and effective visualization of genomic region sets, thus facilitating the interpretation of differences and similarities between different sets. Intervene has three modules; venn classical Venn diagrams of up-to 6 sets, upset effective visualization of more than 3 sets as UpSet plots and pairwise intersections and visualization of N genomic sets as clustered heatmap.
Venn module
Intervene's venn module provides up-to 6-way classical, Chow-Ruskey and Edwards' Euler/Venn diagrams to visualize the intersections of genomic regions or lists.
UpSet module
Intervene's UpSet modules can be used to visualize the intersection of multiple genomic region sets using UpSet plots.
Pairwise module
Intervene's pairwise module provides several styles of heatmaps and clustering approaches to customize the heatmaps.
Citation
If you use intervene, please cite this paper:
Khan A, Mathelier A: Intervene: a tool for intersection and visualization of multiple gene or genomic region sets. bioRxiv 2017, doi: https://doi.org/10.1101/109728

6.3.1 Usage instructions

To use this module you can upload a correctly formatted .csv or text file, encoded in binary. Before uploading the file, choose the correct separator, wheather the names in each column are seperated by a ' , ' choose comma, by a ' ; ' choose semicolon, or by tabs choose tab. Header names (first row) will be used as set names.

UpSet module takes three types of inputs.

List type data

List data is a correctly formatted csv/text file, with lists of names. Each column represents a set, and each row represents an element (names/gene/SNPs). Header names (first row) will be used as set names.

Binary type data

In the binary input file each column represents a set, and each row represents an element. If a names is in the set then it is represented as a 1, else it is represented as a 0.

Combination/expression type data

Combination/expression type data is the possible combinations of set intersections. User can copy/past the combinations of intersection from the Intervene commnad line interface. For example;

H3K4me2&H3K4me3=2216, H3K4me2&H3K4me3&H3K27me3=6777, H3K27me3=5909, H3K4me3&H3K27me3=307, H3K4me3=256, H3K4me2&H3K27me3=3852, H3K4me2=15676, H3K27ac&H3K4me2&H3K4me3&H3K27me3=7235, H3K27ac&H3K4me2&H3K4me3=17505, H3K27ac&H3K4me2=12011, H3K27ac&H3K4me2&H3K27me3=1698, H3K27ac&H3K4me3=473, H3K27ac&H3K4me3&H3K27me3=295, H3K27ac&H3K27me3=1490, H3K27ac=15021

Intervene uses the UpSetR R package for visualization.

6.4 Pairwise module

Intervene's pairwise module provides several styles of heatmaps and clustering approaches to customize the heatmaps.

6.4.1 Usage instructions

To use pairwise module, you can upload a pairwise matrix file in .csv/txt format. Each column and row represents pairwise fraction of overlap/count etc between different names/genomic region sets.

Before uploading the file, choose the correct separator, wheather the matrix file is seperated by a ' , ' choose comma, by a ' ; ' choose semicolon, or by tabs choose tab.

Pairwise module takes input of two types:

List type data

List data is a correctly formatted csv/text file, with lists of names. Each column represents a set, and each row represents an element (names/gene/SNPs). Header names (first row) will be used as set names.

Pairwise matrix data

A pairwise matrix type data is a matrix of size NxN (all pairwise combinations) with values as number/fraction of overlap between two corresponding sets. For genomic region sets user can use the commpnad line interface of Intervene and upload the generated matrix here as matrix type.

For example here is the demo data generated by Intervene's command line interfacce for super-enhancers(SEs) of different cell/tissue-types from dbSUPER.

Intervene uses the Corrplot and plotly R packages to plot heatmap

6.5 Availability

The Intervene Shiny App is freely available at:

> https://intervene.shinyapps.io/intervene/ > https://asntech.shinyapps.io/intervene

CHAPTER 7

Support

If you have questions, or found any bug in the program, please write to us at `aziz.khan[at]ncmm.uio.no` and `anthony.mathelier[at]ncmm.uio.no`.

You can also report the issues to our GiHub repo

CHAPTER 8

Citation

If you use plots or any results obtained from the Intervene tool, please cite:

- Khan A, Mathelier A. Intervene: a tool for intersection and visualization of multiple gene or genomic region sets. BMC Bioinformatics. 2017;18:287. doi: 10.1186/s12859-017-1708-7.

CHAPTER 9

Changelog

9.1 Version 0.6.1

Released date: December 16, 2017

In this release, we have fixed various bugs and introduced new features:

- Users now can provide all the *BedTools* options by setting *–bedtools-options* argument in *venn*, *upset* and *pairwise* module. Thanks to Issue #3
- Now users can save all the overlapping genomic regions as BED and name lists as text file as by setting *–save-overlaps*. Thanks to those who suggested this feature.
- We added *–bordercolors* to change the Venn border colors.

9.2 Version 0.6.0

Released date: December 11, 2017

- Fixed the pairwise module's *–names* argument. Thanks to @adomingues for reporting the bug.

9.3 Version 0.5.9

Released date: December 08, 2017

- Fixed the bug with two lists, issue #1 reported by @dayanne-castro
- Fixed upset module memory issue for large number of sets