GDotplotter

**A drawing dotplot software for showing genome homology**

**---------------------------------------------------------------------------------------------------------------------------------**

**Download**

Source code, binaries, Perl scripts and documentation for GDotplotter can be freely obtained from the website https://github.com/tianyuwuai/GDotplotter.

Source code: GDotplotter.Source.zip

Windows release: GDotplotter.Release.zip

Perl scripts for Linux, MacOS and Windows: GDotplotter.Perl.Script.zip

**Prerequisites**

For running GDotplotter’s Perl script successfully on any systems, it is needed to install the Perl and the GD module into your system.

For running GDotplotter’s graphical user interface on Windows, ActivePerl is required and also need add Perl to PATH environment variable.

**Usage**

1. blast2dotplot.pl

$ perl blast2dotplot.pl querychr sbjctchr querygff1 objctgff2 blastm8 pos\_or\_order queryinitial sbjctinitial e-value score hitnumber

1. blast2dotplot-cdsvschr.pl

$ perl blast2dotplot-cdsvschr.pl querychr sbjctchr querygff1 objctgff2 blastm8 queryinitial sbjctinitial e-value score hitnumber

1. mcscan2dotplot.pl

$ perl mcscan2dotplot.pl querychr sbjctchr querygff1 objctgff2 mcscan\_align pos\_or\_order queryinitial sbjctinitial score e-value length

1. adhore2dotplot.pl

$ perl adhore2dotplot.pl querychr sbjctchr querygff1 objctgff2 inputfile pos\_or\_order queryinitial sbjctinitial

1. colinearscan2dotplot.pl

$ perl colinearscan2dotplot.pl querychr sbjctchr querygff1 objctgff2 blockfile pos\_or\_order queryinitial sbjctinitial p-value length

1. colinearscan2dotplot-genevschr.pl

$ perl colinearscan2dotplot-genevschr.pl querychr sbjctchr querygff1 objctgff2 blockfile queryinitial sbjctinitial p-value length

1. comparedotplot.pl

$ perl comparedotplot.pl querychr sbjctchr querygff1 objctgff2 pos\_or\_order queryinitial sbjctinitial file1 ? file2 ?

**Inputs Files and formats**

1. GDotplotter allows users to provide 6 type files as the toolkit input file.
2. Blast M8 output file which nucleotide(protein) blast nucleotide(protein);
3. Blast M8 output file which CDS blast chromosome genome;

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Sb10G01042 | chr06 | 83.33 | 84 | 14 | 0 | 286 | 369 | 7926555 | 7926472 | 2.00E-06 | 56 |

1. MCScan .aligns file corresponding to pairwise synteny;
2. i-ADHoRe’s anchor points table which is written into a file called anchorpoints.txt;

e. ColinearScan block file that CDS blast chromosome sequence result M8 file as the ColinearScan input file;

f. ColinearScan block file that nucleotide(protein) blast nucleotide(protein) result M8 file as the ColinearScan input file.

2. GDotplotter also allows users to provide any two type files of a, c, d and f for comparing different collinear block output files which are got from different programs.

3. In addition, both species’ .gff files are also needed to offer each gene physical position or gene order on a chromosome in drawing a dotplot map. The .gff file contains the following tab-delimited format.

|  |  |  |  |
| --- | --- | --- | --- |
| Chr01 | Sb01G00001 | 1619 | 2809 |

**Parameters**

Parameterized GDotplotter is convenient for drawing specific dotplots. Peculiarly, there are some different parameters after users selecting one input file type.

|  |  |  |
| --- | --- | --- |
| querychr |  | Query species chromosome number. Join the specific chromosome number in "\_" |
| sbjctchr |  | Subject species chromosome number. Join the specific chromosome number in "\_" |
| querygff1 |  | Query species .gff file. |
| objctgff2 |  | Subject species .gff file. |
| inputfile |  | The path of input file. |
| pos\_or\_order |  | [pos|order] Drawing by the physical location of a gene or gene order along chromosomes. |
| queryinitial |  | Initial of query species for headline of x axis. |
| sbjctinitial |  | Initial of subject species for headline of y axis. |
| **Blast** |  |  |
| e-value |  | Filter BLAST file by e-value, save all gene pairs which e-value less than setting. |
| score |  | Filter BLAST file by score, save all gene pairs which score more than setting. |
| hitnumber |  | Filter BLAST file by utmost matching gene pairs. |
| **MCScan** |  |  |
| score |  | Filter MCScan file by score, save blocks which score more than setting. |
| e-value |  | Filter MCScan file by e-value, save blocks which e-value less than setting. |
| length |  | Saving blocks which length more than setting. |
| **ColinearScan** |  |  |
| p-value |  | Filter ColinearScan file by p-value, saving smaller. |
| length |  | Saving blocks which length more than setting. |

**Example**

There is a shell named “run.example.sh” to draw different dotplots by using some example data. You can just simply run it or check the details.

$ sh run.example.sh

**Changelog**

Mar 26, 2016 initial release.

**Contact**

Any question, problem, bugs are welcome and should be dumped to

Tianyu Lei: leitianyu.china@gmail.com