

OmicCircos in R

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OmicCircos

This session describes OmicCircos parameter setting and tuning to construct circular plots with desired biological features. Example data from human, mouse, and bacteria genome will be used to demonstrate functions for the color selection, annotation, labeling, zoom, and integration of traditional plotting. Programming experience in R studio is required.

Features:

- Data format
- Installation
- Basic plot setting
- Advance parameter tuning
- Integration of R statistics and plotting

circos.ca

CIRCOS

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Winner: Circle

the circle is more symmetric than square – eye is less burdened

circle's data payload is higher

- consider the ratio of the **axis length** to the **data area**
 - for a square: $2a/4a^2 = 1/2a$ (a = sum of x/y axes lengths)
 - for a circle: $2\pi a/\pi a^2 = 2/a$ (**4 times larger**)

concentric tracks are more efficient

- (+) more efficient use of figure area – longer axis allows for greater spatial detail
- (-) $\Delta r \Delta \phi$ is not constant in area ($\Delta x \Delta y$ is) – shape is distorted

mkweb.bcgsc.ca/circos

Bioconductor
OPEN SOURCE SOFTWARE FOR BIOINFORMATICS

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OmicCircos

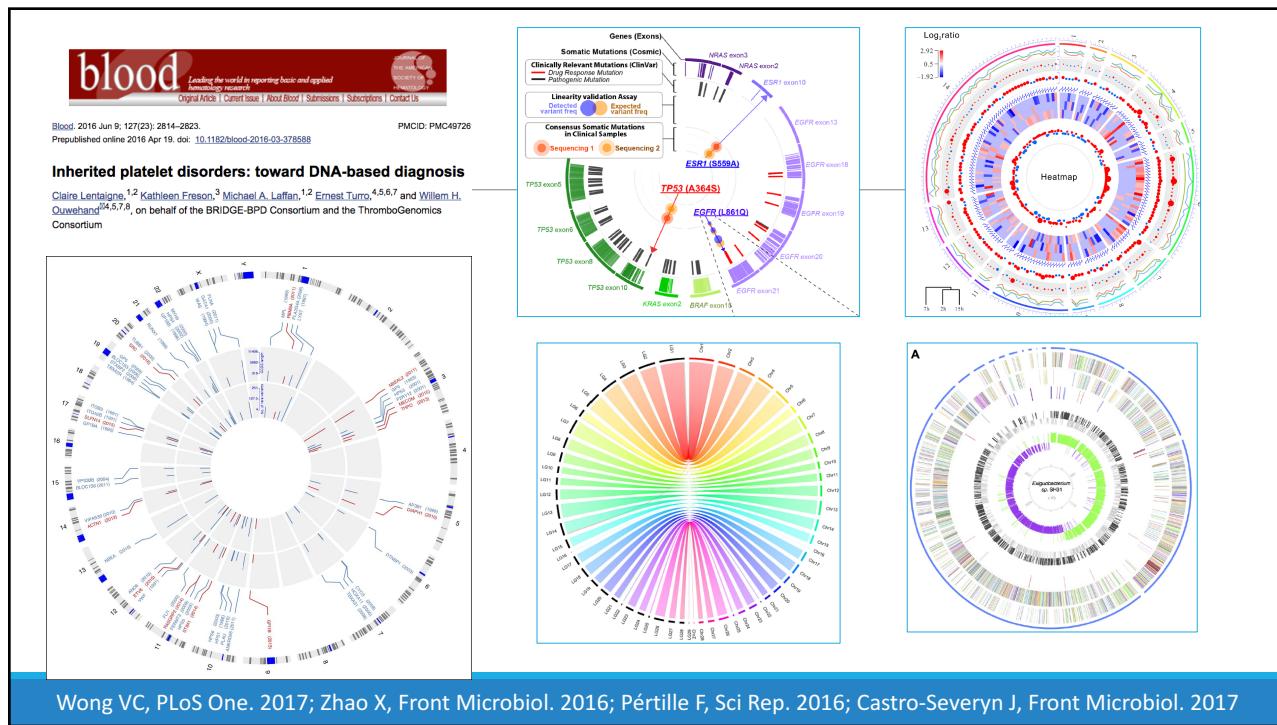
platforms all downloads top 20% posts 2 / 0.5 / 0.5 / 1 in Bioc 2.5 years
 build ok commits 0.83 test coverage unknown

[f](#) [t](#)

High-quality circular visualization of omics data

Bioconductor version: Release (3.2)
 OmicCircos is an R application and package for generating high-quality circular plots for omics data.
 Author: Ying Hu <yahu at mail.nih.gov> Chunhua Yan <yanch at mail.nih.gov>
 Maintainer: Ying Hu <yahu at mail.nih.gov>
 Citation (from within R, enter `citation("OmicCircos")`):
 <yanch@mail.nih.gov> YHCY (2015). *OmicCircos: High-quality circular visualization of omics data*. R package version 1.8.1.

<https://www.bioconductor.org/packages/release/bioc/html/OmicCircos.html>

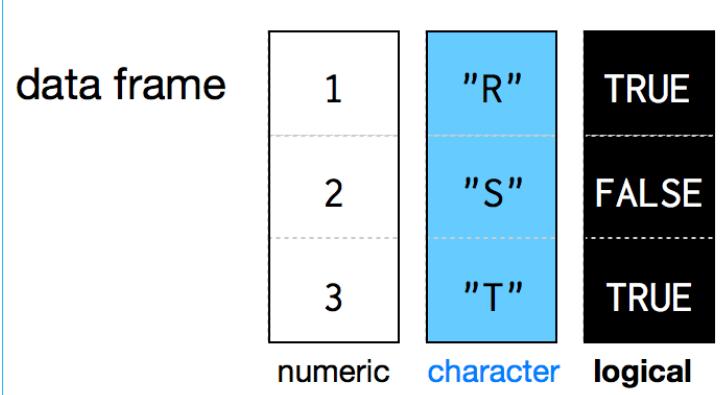


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Data frames used in OmicCircos

Vectors
Matrices
Arrays
Data frames
Lists
Factors



genome

chrom	chromStart	chromEnd	name	gieStain
chr1	0	2300000	p36.33	gneg
chr1	2300000	5300000	p36.32	gpos25
chr1	5300000	7100000	p36.31	gneg
chr1	7100000	9200000	p36.23	gpos25
chr1	9200000	12600000	p36.22	gneg

seg.name	seg.Start	seg.End	the.v	NO
1	1	4621656	NA	NA

Input Data

Points

chr	pos	NAME	TCGA.A1.A0SK.01A	TCGA.A1.A0SO.01A
1	939246	ISG15	-3.618	-2.286
1	2533140	MMEL1	-2.832	-3.093
1	6446321	TNFRSF25	2.559	-0.66
1	7832974	UTS2	1.708	-0.726
1	7912164	TNFRSF9	-0.189	-0.768

chr	pos	NAME	snp	vaf
8	33572686	DUSP26	rs28279	0.299330553
21	21563446	NCAM2	rs22707	0.494628791

Links

chr1	pos1	gene1	chr2	pos2	gene2
7	86200000	geneA1	19	30200000	geneB1
19	13800000	geneA2	9	136600000	geneB2
11	120700000	geneA3	15	65000000	geneB3
8	23400000	geneA4	8	29700000	geneB4
4	70400000	geneA5	8	117700000	geneB5

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Prepare R environment



<https://www.r-project.org>



<https://www.rstudio.com>



<https://www.bioconductor.org/packages/release/bioc/html/OmicCircos.html>

Installation

To install this package, start R and enter:

```
## try http:// if https:// URLs are not supported
source("https://bioconductor.org/biocLite.R")
biocLite("OmicCircos")
```

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OmicCircos

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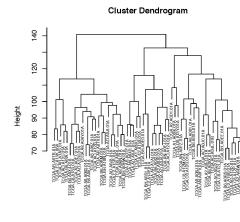
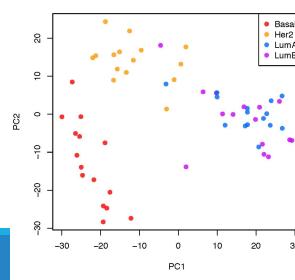
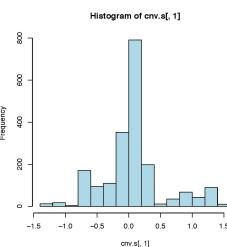
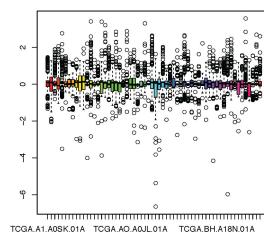
basic_plot_data_QC.R: QC plots

➤ Set working directory

➤ Load library

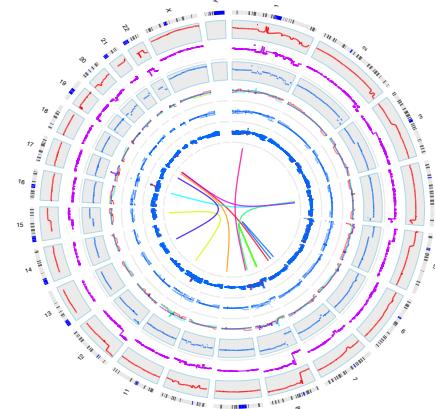
➤ Check data

- Table size
- Data structure
- Barplot
- PCA plot
- Cluster



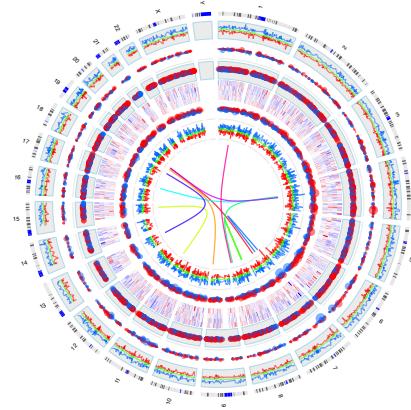
basic_plot_line.R: line plots

-
- "l": line
 - "ls": lines in stair step
 - "lh": horizontal lines
 - "ml": multiple lines (for more than 1 samples)
 - "ml2": multiple horizontal lines
 - "ml3": multiple lines in stair steps
 - "link": link lines based on Bezier curve



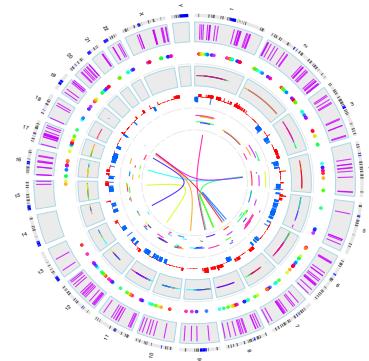
basic_plot_variation.R: data stats

-
- "quant90": 90% quantile lines
 - "sv": dot sizes proportional to the variance
 - "ss": dot sizes proportional to the values
 - "heatmap": heatmap
 - "s.sd": dots proportional to standard deviation
 - "ci95": 95% confidence interval line
 - "link": link lines based on Bezier curv



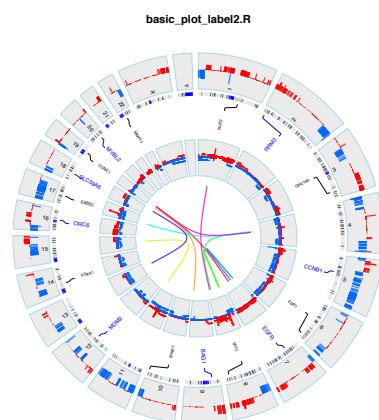
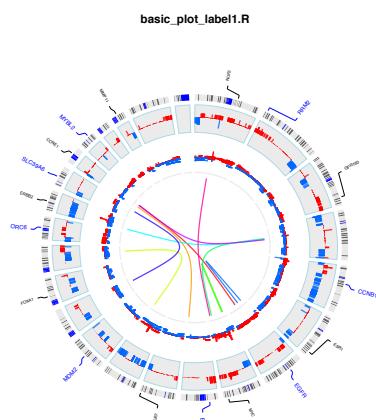
basic_plot_arc.R: arc plots

- "b3": bar charts with the same height
 - "s2": dots with the fixed radius
 - "arc2": arcs with the fixed radius
 - "b2": bi-directional bar charts
 - "arc": arcs with variable radius



basic_plot_label1/2.R: labels

"label": gene labels or text annotations

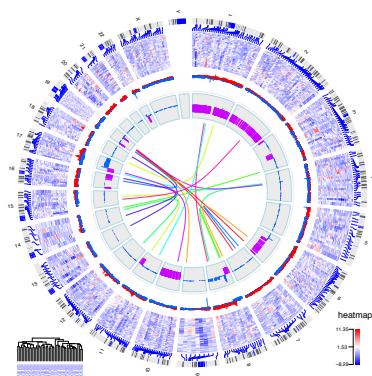


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advance_heatmap.R: heatmaps

- "heatmap2": heatmaps with genomic coordinates, cluster, and color key

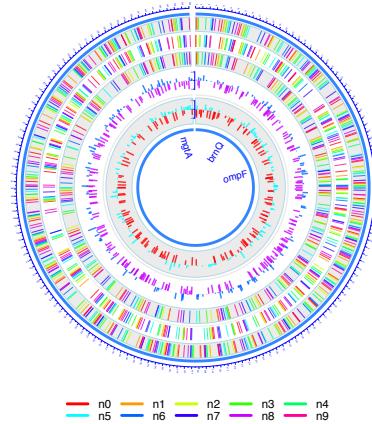


advance_user_genome.R: Ecoli

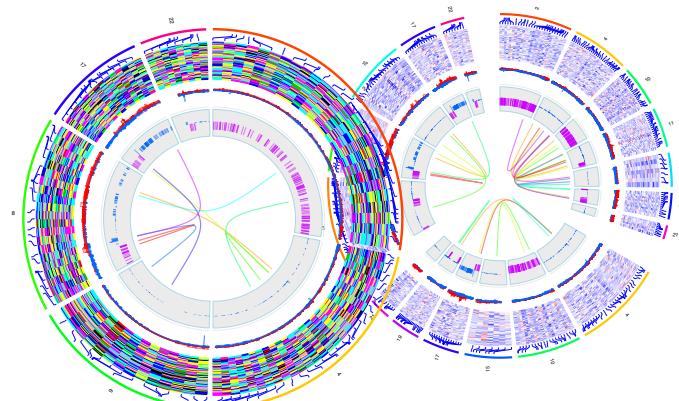
EColi K-12 GM4792

Define genome sizes

Create anchor circular location database



advance_zoom1/2.R: zoom

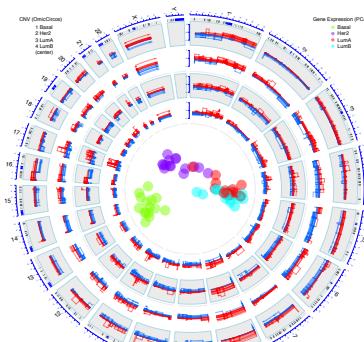
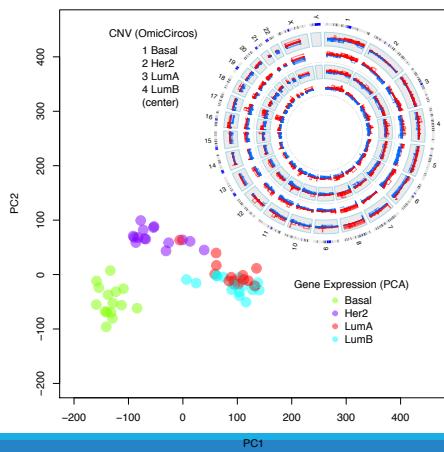


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integration_pca1/2.R: R graphics

- Different integration of PCA and omicCircos plots



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