GENOMNIA

Two dynamic detail levels

Overview track display shows methylation level calculated on the basis of progressively wider windows.

As you zoom enough, single methyl-cytosines will be displayed and pointing to a methylated cytosine on the track will display a popup with additional info.

Integration with canonical Genome browser functionalities

Savant Genome Browser provides many facilities to let ther user compare methylation level tracks with Gene annotations from Ensembl, Ucsc, Refseq genes, 1000 Genomes Browser and many others. Moreover there are several tools that allow in browser data analysis such as SNP discovery, RNA seq analysis, differential expression and others.

Area chart describes the distribution of methyl-cytosines in each sequence context.

Pie chart describes the percentage of methyl-cytosine in each sequence context.

Static on-paper charts are reproduced and updated dynamically using the Radiant Framework.

Track loading functionalities

Possibility to display your local data in well known bioinformatics formats, such as BED, BAM, WIG and many others.
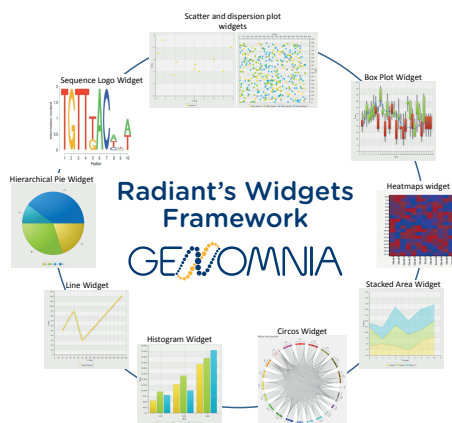
Radiant Genome Browser
Exploring Methylseq Datasets in a Genome Browser

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The Radiant Genome Browser is able to load and visualize methyl seq data analysed with the MethylPipe Package, available from Bioconductor (Kishore, 2014). MethylPipe analyses base resolution DNA methylation data in both the CpG and non-CpG sequence context. Usually single based methylation maps can be described by methylation level distribution, as in R. Lister, M. Pelizzola et al, 2009. Radiant genome browser provides a pie chart that describes the percentage of methylcytosines identified for the sample in each sequence context and an area chart that describes the distribution of the methylation level in each sequence context. Those charts can be related to the whole chromosome or the region actually displayed by the browser and are updated at each scrolling action.
The Radiant Genome browser also shows on track information, displaying the methylation level as an average statistic of progressively wider windows or in detail, with additional calling properties for every single methyl-cytosine.

The software is freely available at **http://radiant-project.eu/Visualisation/Download.html**

Radiant's Widgets Framework
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Scatter and dispersion plot widgets

Sequence Logo Widget

Box Plot Widget

Hierarchical Pie Widget

Heatmaps widget

Line Widget

Stacked Area Widget

Histogram Widget

Circos Widget

Savant is a Genome Browser Desktop application. It is freely available for Windows, MacOS and Linux, can be downloaded locally and installed. Differently from a web browser, such architecture allows more flexibility and is potentially best suited to manage large files such as alignments related to genomes because they don't need to be uploaded over the internet. Moreover, working locally is a plus when data must be kept private.

RADIANT

The Radiant plugin for the Savant Genome Browser is composed by a collection of modules and a framework of reusable components. The Radiant Framework was designed to reproduce static on-paper charts to provide dynamically explorative charts of on-track visualized data. Utilizing any combination of the widget displayed in the picture along with basic elaborations, it is possible to have descriptive statistics updated on-the-fly as the genome browsing window is shifted.

This project has been developed in the framework of the FP7 bioinformatics project Radiant (http://radiant-project.eu) which is aimed at developing novel statistical methods. Genomnia's work is to develop a graphical browser that makes it easy to display, explore and elaborate interactively tracks and other types of visualizations for multivariate data along genomic coordinates. We have interpreted this browser as a visualization tool for the rest of RADIANT Project work packages outputs.
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K. Kishore, M. Pelizzola (2014). MethylPipe: Base resolution DNA methylation data analysis. R package version 0.99.9.