# CREACIÓN DE GRÁFICOS INTERACTIVOS EN R:

# APLICACIÓN AL ANÁLISIS DE DATOS GENÓMICOS DE GLIOMAS

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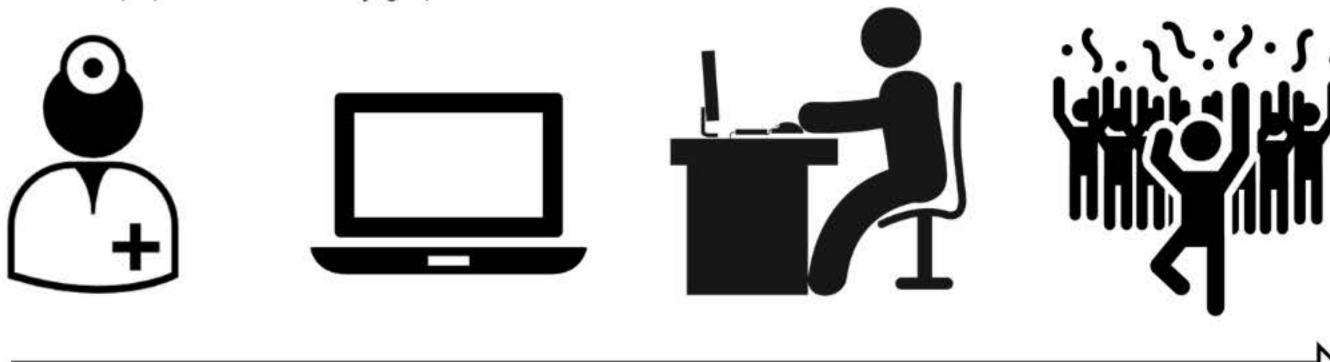






#### **BIOINFORMATICS SERVICE**

- Our main objective is to transform biological data from experimental techniques into valid knowledge.
- Bioinformatics data analysis of:
  - Next Generation Sequencing: De Novo seuencing, RNA-Seq, Identification/association of variants, ChiP-Seq, etc.
  - Expression microarrays: differential expression, co-expression, temporal series, marker selection.
  - Protein panels: differential analysis and correlation with phenotypic variants.
  - Sequences: functional annotation, location of transcription factors, phylogenetic studies.
  - List of genes: functional studies, analysis of biological networks, functional enrichment analyses, etc.
- Visualization of results is a key aspect for a bioinformatics service:
  - Easy understanding of results
  - Graphs allow to achieve new discoveries
  - Scientific papers are driven by graphs





#### INTERACTIVE GRAPHS IN R

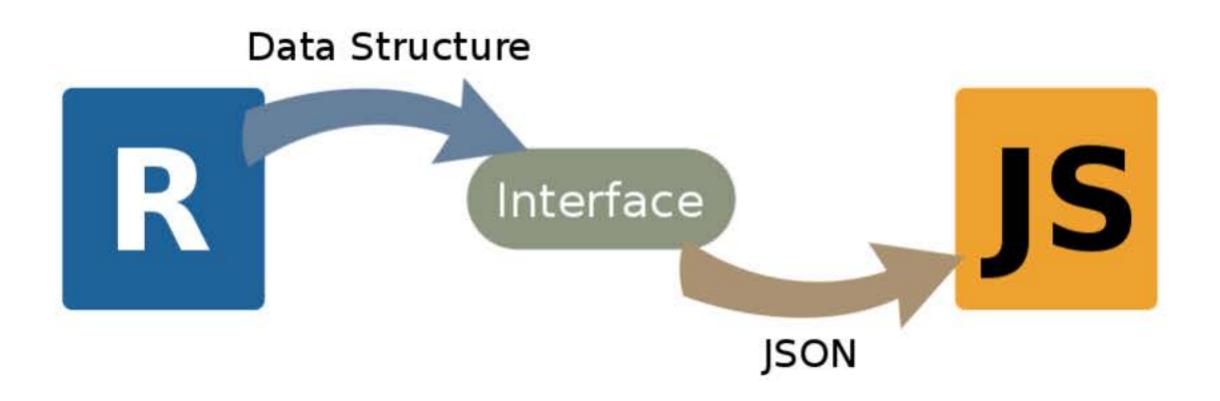
- Main R packages of Interactive Graphs:
  - Leaflet: Geo-spatial mapping
  - dygraphs: Time series charting
  - MetricsGraphics: Scatterplots and line charts with D3
  - networkD3: Graph data visualization with D3
  - d3heatmap: Interactive heatmaps with D3
  - DataTables: Tabular data display
  - threejs: 3D scatterplots and globes
  - DiagrammeR: Diagrams and flowcharts
- Javascript Advantages
  - Dynamic and interactive representations
  - Vector graphics (easy to get a SVG and a PDF format)
  - Extended functionality to web pages
  - Growing number of JS programmers and public open source projects
  - Active JavaScript graphs libraries: D3, BioJS, etc.
  - Multiplatform: Only a Web Browser is needed for visualization







#### DATA INTERFACE



- R interface to transform R Data Structures into JSON format
- It allows easy integration of JS graphs in R
- Enables future public open source project
- Easy generation of dynamic graphs with R



#### INPUT DATA

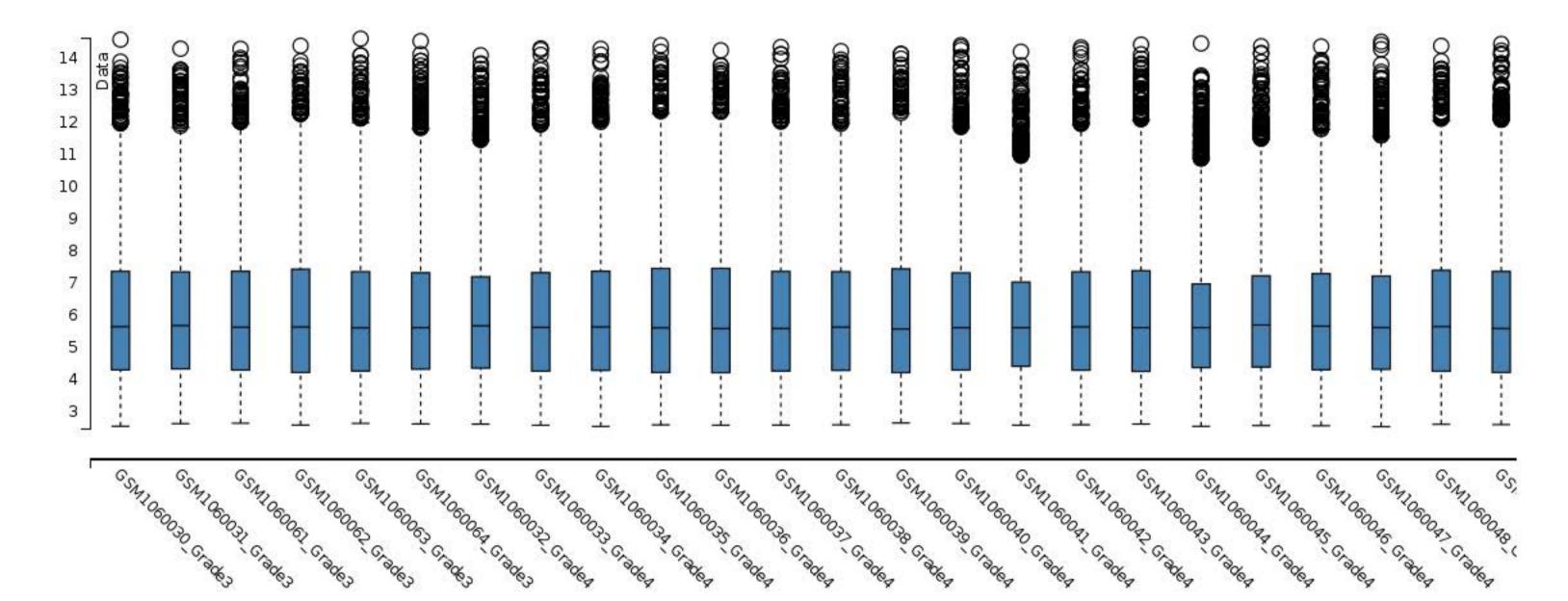
- Platforms: Expression and Cytoscan SNPs arrays (Affymetrix).
- Diseases: Gliome and Mielome (different grades)
- Summary of analysis protocol:



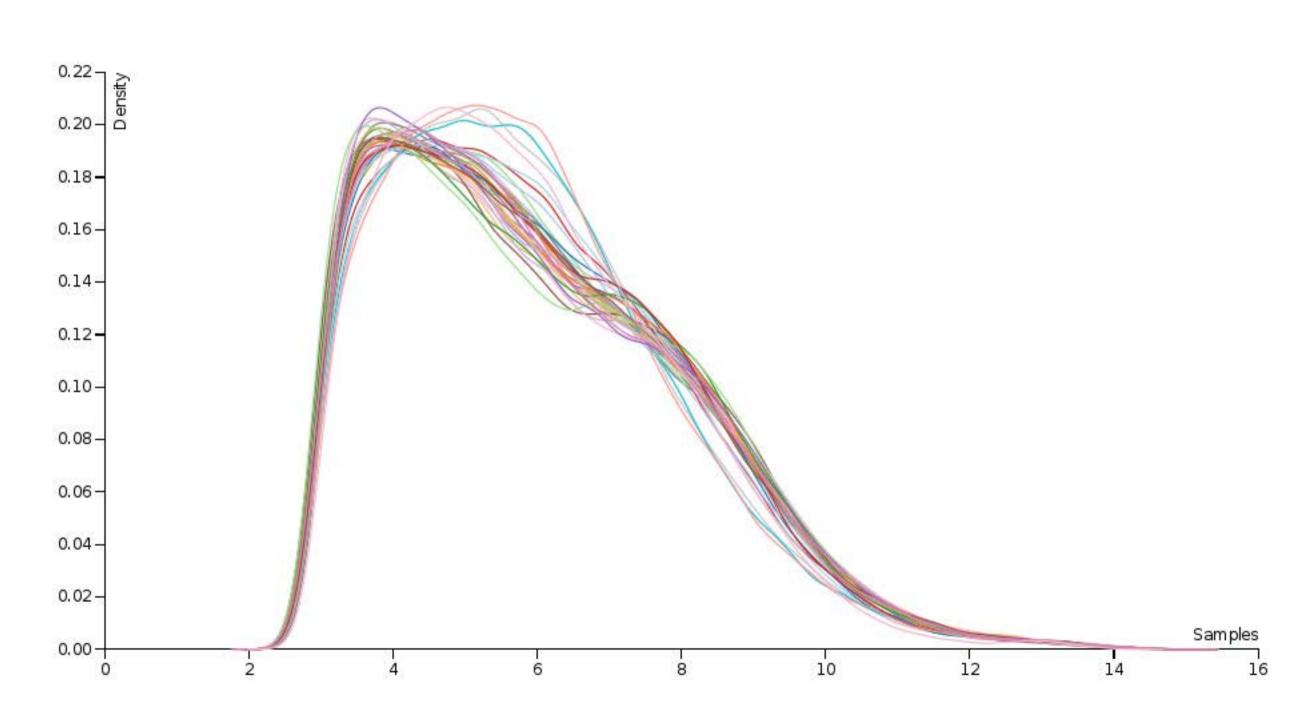
Servicio de Neurocirugía Unidad de Investigación del Hospital Universitario de Salamanca (HUS) Instituto de Estudios de Ciencias de la salud de Castilla y León (IECSCYL-IBSAL)



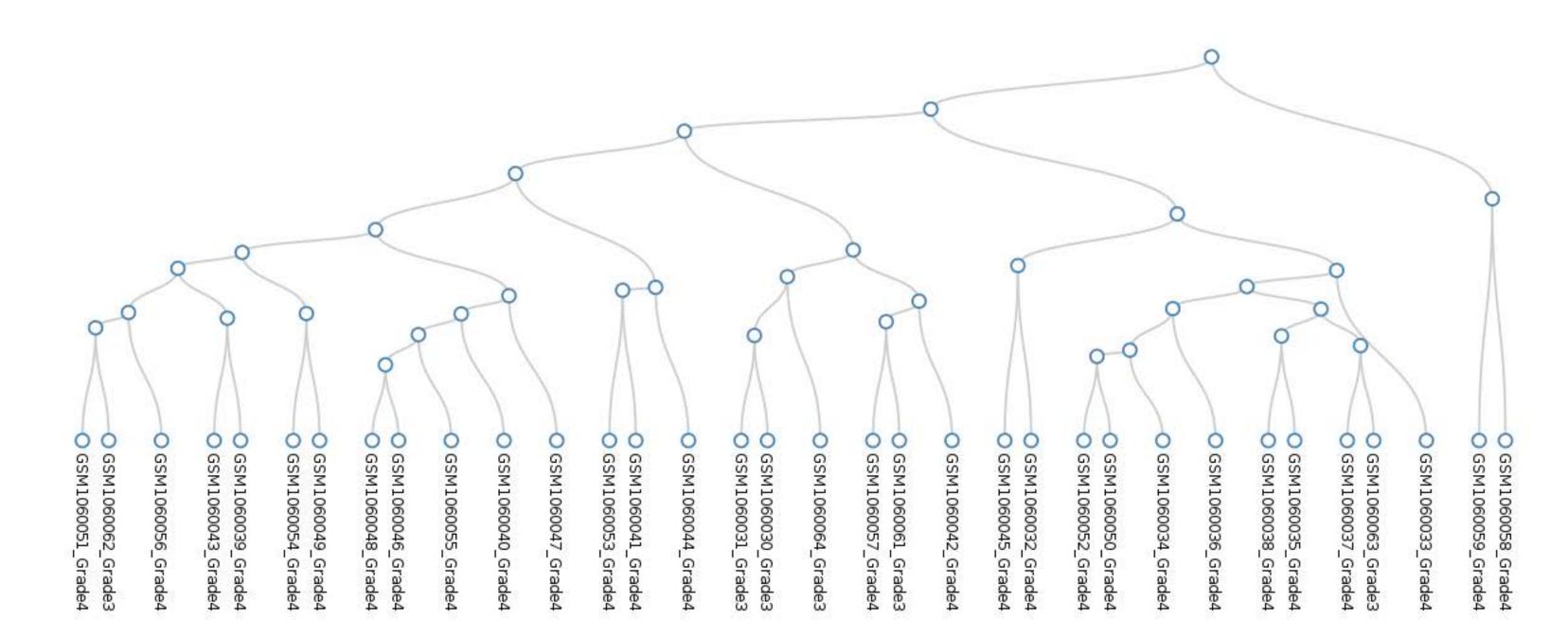
#### BOXPLOT



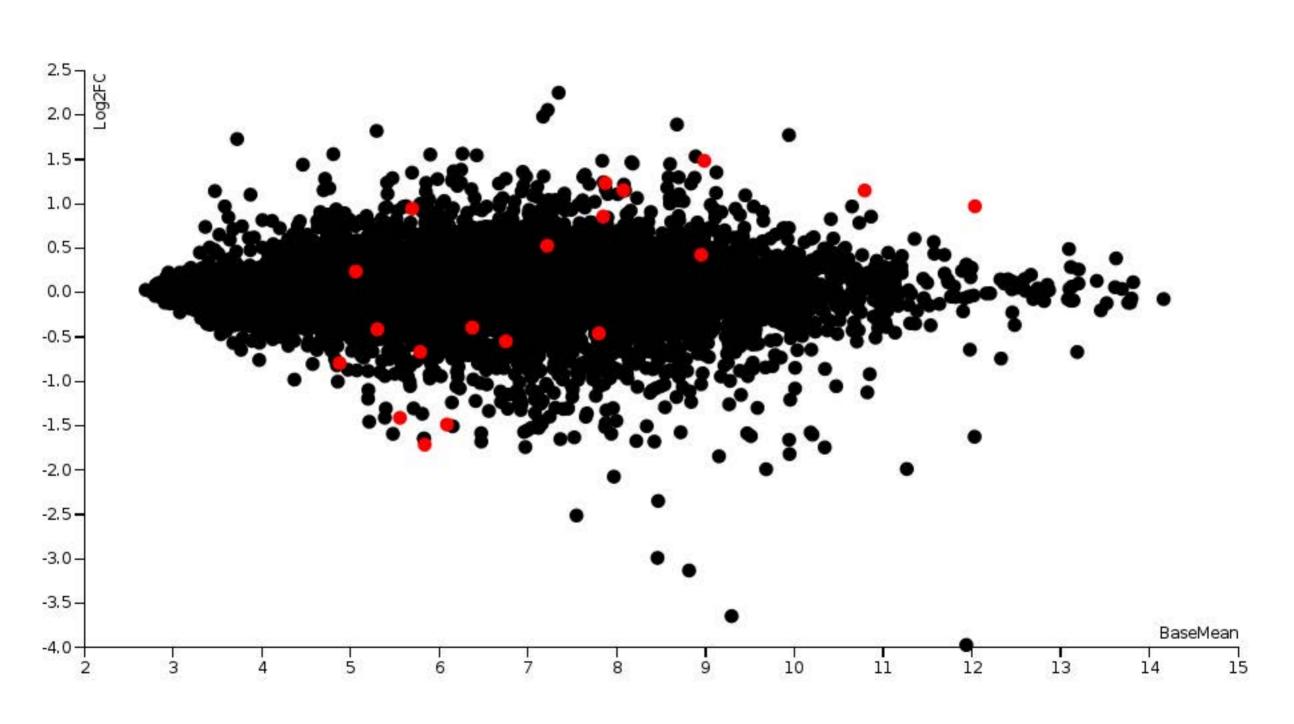
## **DENSITY PLOT**



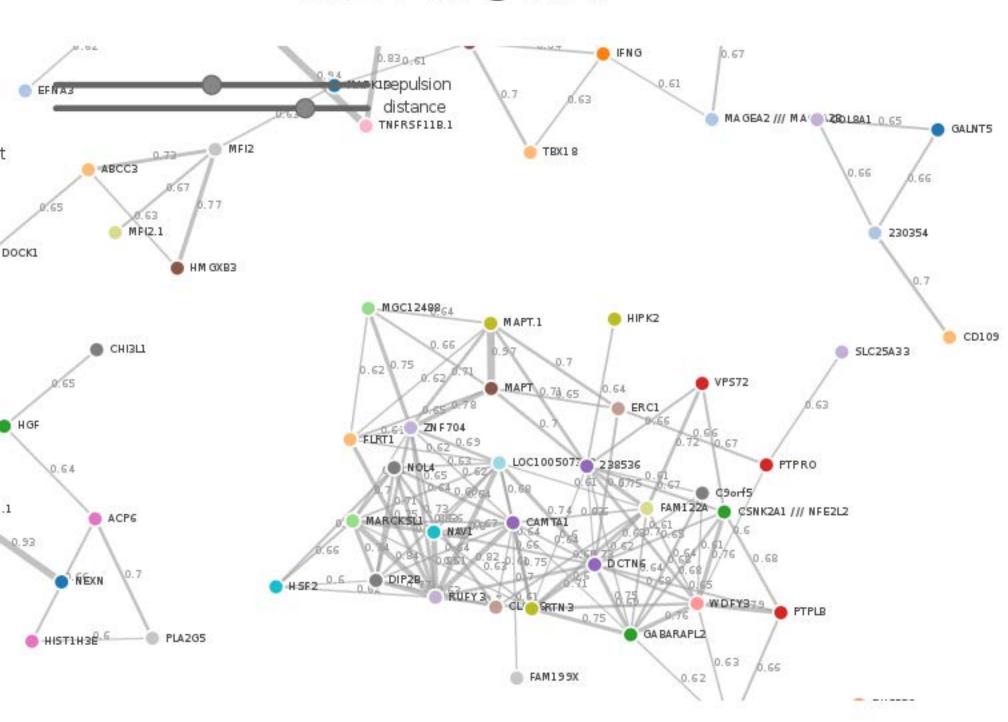
#### DENDROGRAM



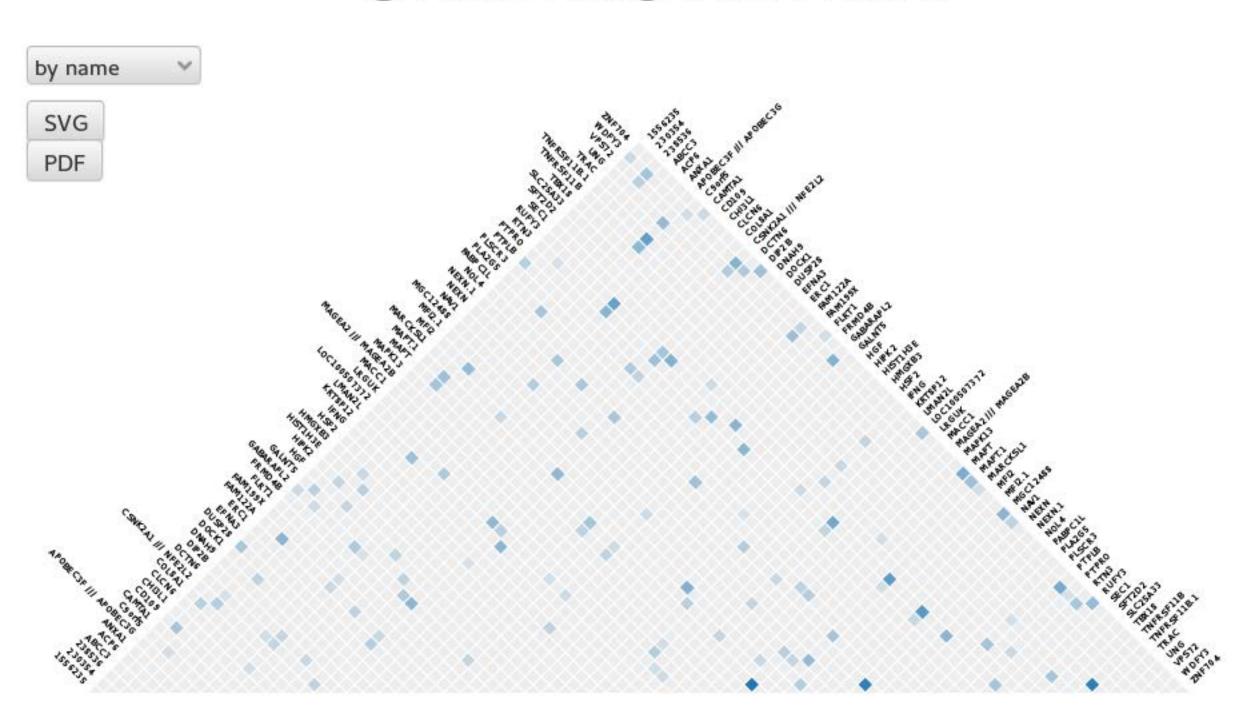
### SCATTER PLOT



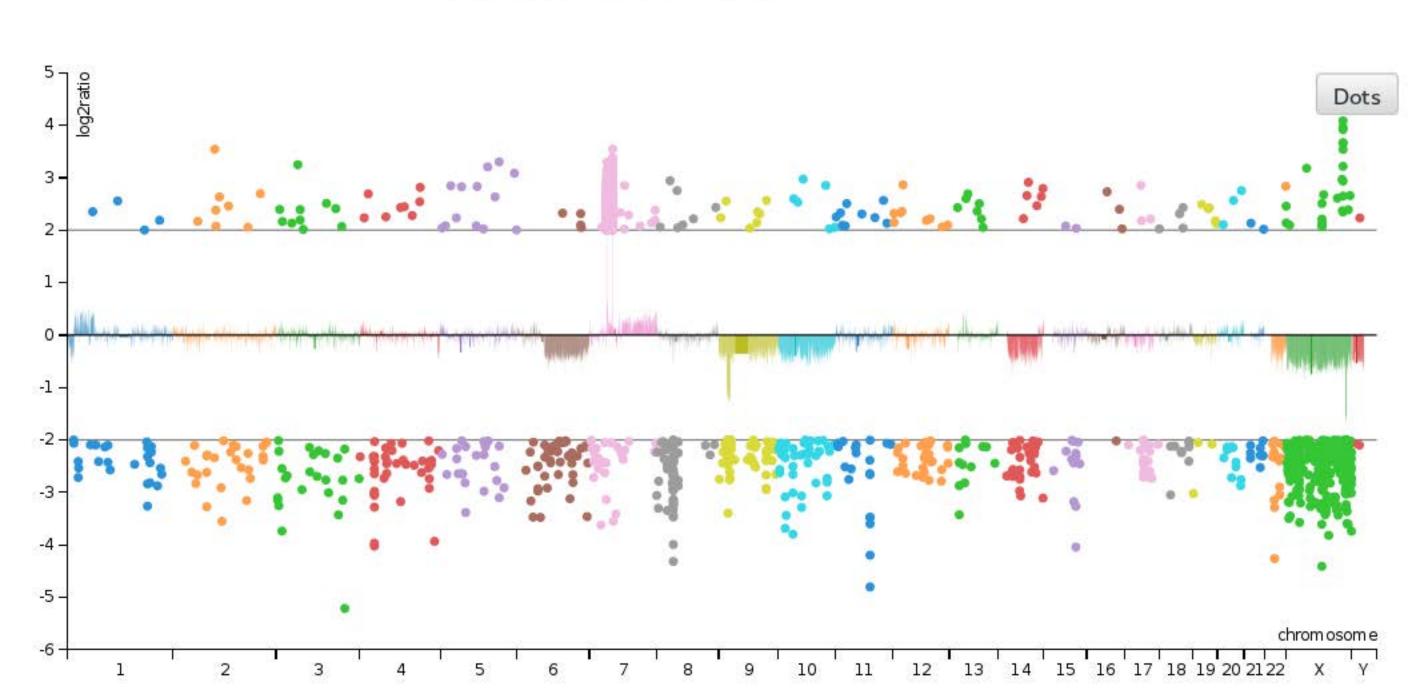
#### **NETWORK**



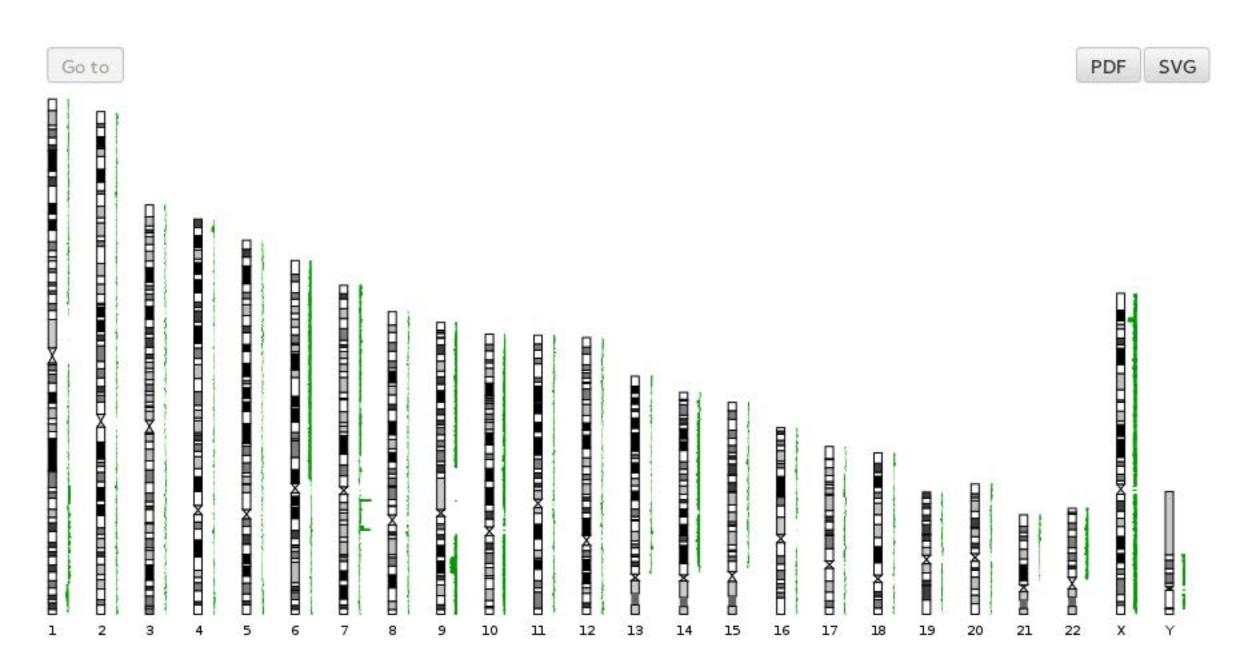
# SYMETRIC HEATMAP



#### **MANHATTAN PLOT**



#### **HUMAN GENOME BROWSER**





http://bioinfo.usal.es

Servicio de Bioinformática Sala 23.2 Edificio I+D+i C/ Espejo 2 37007 Salamanca (Spain)

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