A novel way of visualising eQTLs relative to SNP-SV pairs using Gosling.js

1. Introduction

Quantitative trait locus (QTL) studies connect genotypes with tissue/cell type specific cellular functions. Currently, QTL studies are mostly done on single nucleotide changes, but as SVs are bigger and have greater impact on traits, SV-QTL connections are of great interest.

2. Objective

How can the relations within SNP-SV-QTL data be efficiently visualised?

Legend

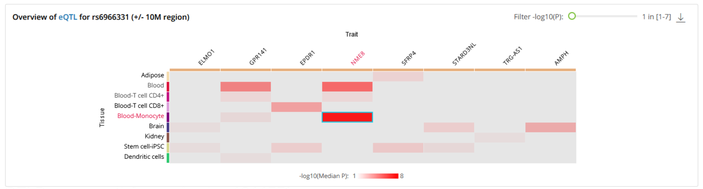
- **GWAS**: A **Genome-Wide Association Study** scans the genomes of many individuals to find genetic variants associated with specific traits.
- **SNP**: A **Single Nucleotide Polymorphism** is a single base-pair variation in the DNA sequence
- **SV**: A **Structural Variation** is a large-scale alterations of DNA.
- **eQTL**: An **expression Quantitative Trait Locus** is a genomic locus that correlates with variations in gene expression levels among individuals.

3. Related works

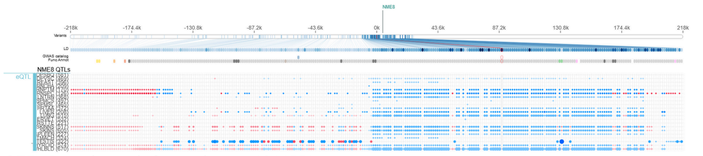
There are numerous tools to visualise the connections between:

- SNPs and SV
- Genes and their expression in tissues (eQTL)
- SNPs and diseases

These tools can however not visualise the connection between SVs and QTLs.



QTLBase, result for variant rs6966331



GTEx Portal, result for variant rs6966331

QTLBase and GTExPortal can show correlation of tissues with genes or individual SNPs within genes respectively, but not the correlation of SNPs to SVs.

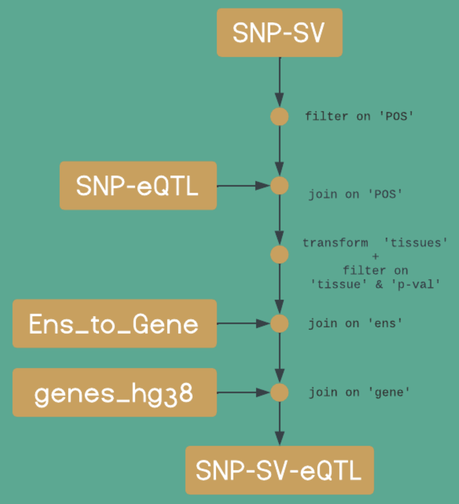
4. Materials and Method

The created visualisation is built as an extention on snpXplorer, a publicly available web-server for displaying GWAS associations. For the visualisation library, Gosling.js was chosen, as it offers a nice selection of functions for visualising genomic data.

Two main datasets were used:

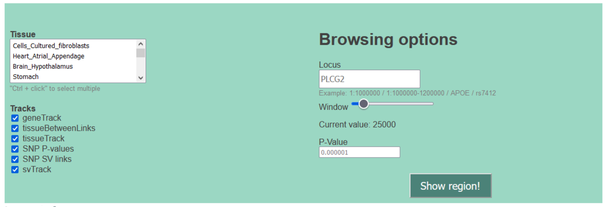
- SNP-SV data
- SNP-eQTL data

Upon querying:

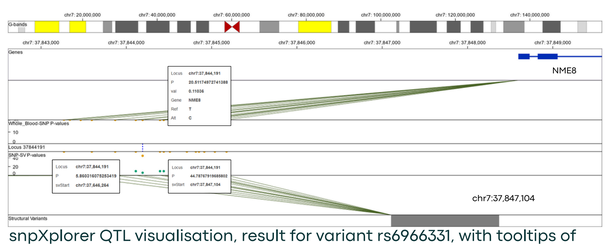


5. Results

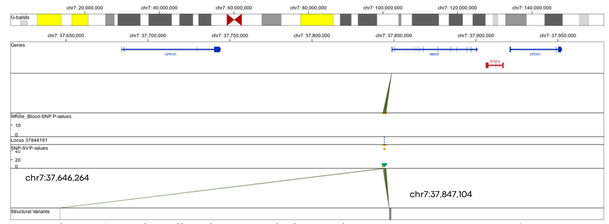
- The input form offers options for:
  - Tissues
  - Tracks to show
  - Target locus, range, gene, or variant
  - Window size
  - P-value for filtering
- The resulting plot displays at the top the chromosome of the target, and 7 main tracks containing:
  - genes
  - SNP-gene links
  - SNP-eQTL P-values
  - marker of the target
  - SNP-SV P-values
  - SNP-SV links
  - SVs
- Tracks can be deselected if unnecessary for a particular use case. This prevents data loading for these tracks, reducing query time.



Input form



snpXplorer QTL visualisation, result for variant rs6966331, with tooltips of the QTL and right SV related to the variant



snpXplorer QTL visualisation, result for variant rs6966331, zoomed out

6. Conclusion

The created tool succeeds in its original goal of overlapping and visualising the SNP-SV and SNP-eQTL datasets, which other tools failed to achieve.

Integration with snpXplorer codebase should be straightforward and no new dependencies were introduced.

Gosling.js offers integration of other visualisation libraries, so with this framework in place, new options for further development open up.

7. Discussion & Recommendation

- Pandas is a easy to use dataframe library, but isn't optimized for querying genomic data.
- The CSV format is a common data format, but it limits how Gosling.js can interact with it. Switching to another format, such as BEDDB, would eliminate the reformatting of data.
- The SNP-gene links, SNP-eQTL P-values, SNP-SV P-values and SNP-SV links tracks currently each retrieve data seperately, due to limitations in Gosling.js.

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