Prove your point!

The Genomic HyperBrowser

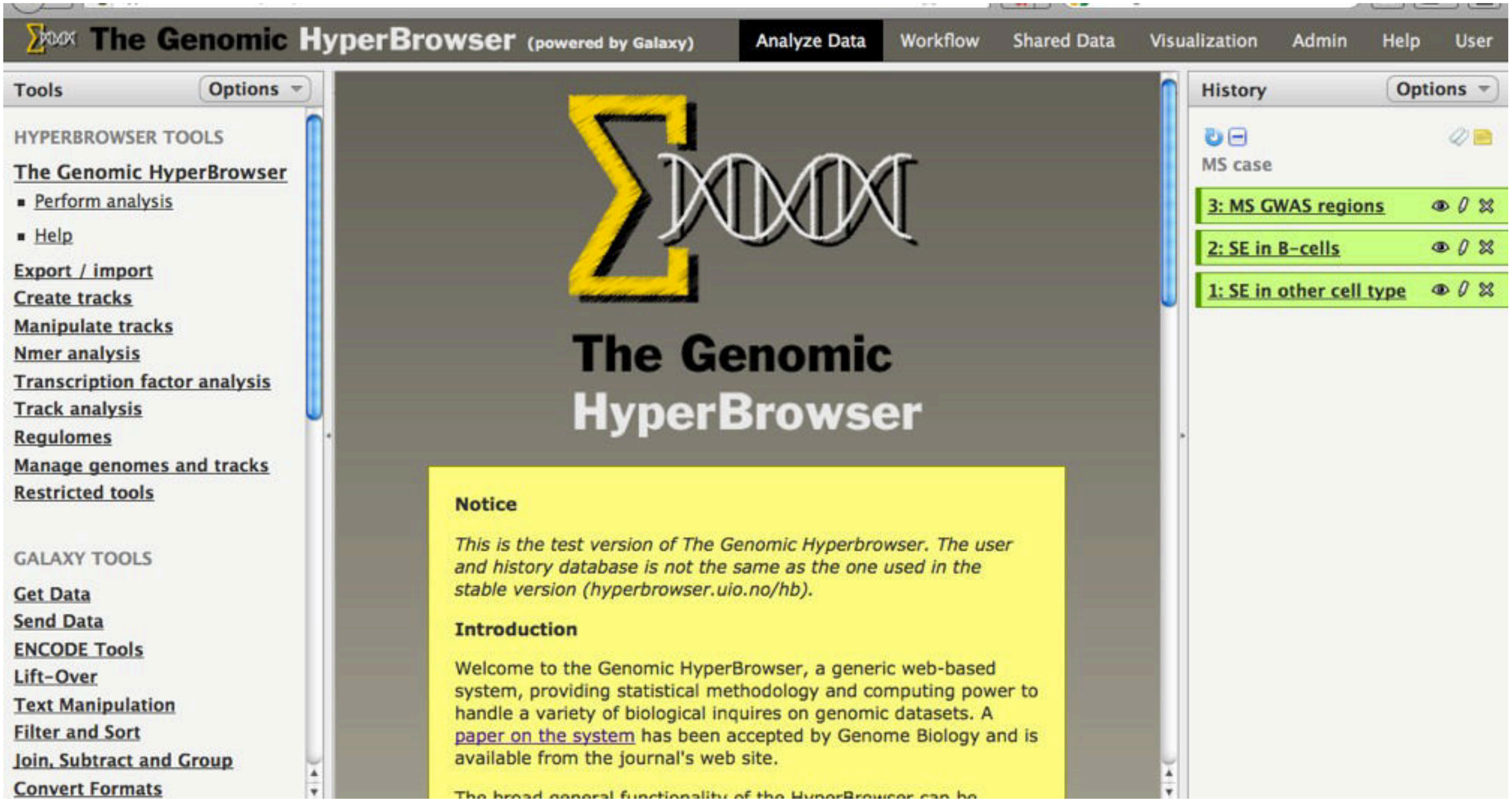
- Web system for *analysis* of genomic tracks
  - Tens of custom-built tools
    - Thousands of collected tracks
- But mainly:
  - A single tool hiding nearly 100 statistical analyses and hypothesis tests

The aim

- Analyze any kind of genomic track data
- Cover every non-standard investigation
- Robust statistical analysis

Enough talk..

(internet worked!)


The Genomic HyperBrowser (powered by Galaxy)
Analyze Data
Workflow
Shared Data
Visualization
Admin
Help
User
Tools
Options
HYPERBROWSER TOOLS
The Genomic HyperBrowser
Perform analysis
Help
Export / import
Create tracks
Manipulate tracks
Nmer analysis
Transcription factor analysis
Track analysis
Regulomes
Manage genomes and tracks
Restricted tools
GALAXY TOOLS
Get Data
Send Data
ENCODE Tools
Lift-Over
Text Manipulation
Filter and Sort
Join, Subtract and Group
Convert Formats
The Genomic HyperBrowser
Notice
This is the test version of The Genomic Hyperbrowser. The user and history database is not the same as the one used in the stable version (hyperbrowser.uio.no/hb).
Introduction
Welcome to the Genomic HyperBrowser, a generic web-based system, providing statistical methodology and computing power to handle a variety of biological inquires on genomic datasets. A paper on the system has been accepted by Genome Biology and is available from the journal's web site.
History
Options
MS case
3: MS GWAS regions
2: SE in B-cells
1: SE in other cell type

The Genomic HyperBrowser (v1.1)

Genome build: Human Mar. 2006 (hg18/NCBI36)

First Track

-- From history (bed, wig, ...) -- | 3 - MS GWAS regions

?

Second Track

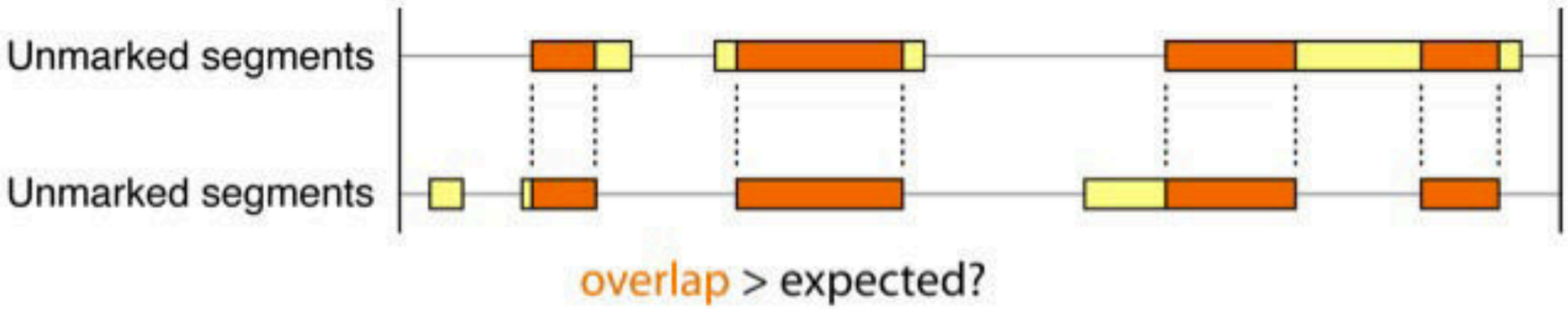
-- From history (bed, wig, ...) -- | 2 - SE in B-cells

?

Analysis

Category: Hypothesis testing | Overlap? ?

Are 'MS GWAS regions (3)' overlapping 'SE in B-cells (2)', more than expected by chance?



Toggle debug | Toggle run description

You asked:

Are 'MS GWAS regions' overlapping 'SE in B-cells', more than expected by chance?

Simplistic answer:

Yes - the data suggests this (p-value: 0.000)

Precise answer:

The p-value is 0.000 for the test

> **H0:** The segments of track 1 are located independently of the segments of track 2 with respect to overlap

vs

> **H1:** The segments of track 1 tend to overlap the segments of track 2

Low p-values are evidence against H0.

The test was also performed for each bin separately, resulting in 24 significant bins out of 26, at 10% FDR* (17 bins excluded from FDR-analysis due to lacking p-values).

Running workflow "Create case-control track"

Expand All | Collapse

remove overlapping segments from two tracks and write a target/control track

Step 1: Input dataset

Input Dataset

2: SE in B-cells

Step 2: Input dataset

Input Dataset

1: SE in other cell type

Step 3: Intersect

Step 4: Subtract

Step 5: Subtract

Step 6: Create target-control track

Send results to a new history

Run workflow

First Track

-- From history (bed, wig, ...) --

8 - Create target-control track on data 7

?

Second Track

-- From history (bed, wig, ...) --

3 - MS GWAS regions

?

Analysis

Category: Hypothesis testing

Preferential overlap?

?

Are 'Create target-control track on data 7 and data 6 (8)' marked as case overlapping unexpectedly more with 'MS GWAS regions (3)' than 'Create target-control track on data 7 and data 6 (8)' marked as control?

You asked:

Are 'Create target-control track on data 7 and data 6' marked as case overlapping unexpectedly more with 'MS GWAS regions' than 'Create target-control track on data 7 and data 6' marked as control?

Simplistic answer:

Yes - the data suggests this (p-value: 0.009901)

Precise answer:

The p-value is 0.009901.

Low p-values are evidence against H0.

The test was also performed for each bin separately, resulting in 14 significant bins out of 26, at 10% FDR* (17 bins excluded from FDR-analysis due to lacking p-values).

Publications

- Main publication
  - The Genomic HyperBrowser: inferential genomics at the sequence level
- Methodology publications
  - The differential disease regulome
  - Identifying elemental genomic track types and representing them uniformly
  - Sequential Monte Carlo multiple testing
- Application publications
  - Genomic Regions Associated with Multiple Sclerosis Are Active in B Cells
  - Vitamin D receptor binding, chromatin states and association with multiple sclerosis

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