

chromozoom

chromozoom.org

rethinking the UI
of genome browsers



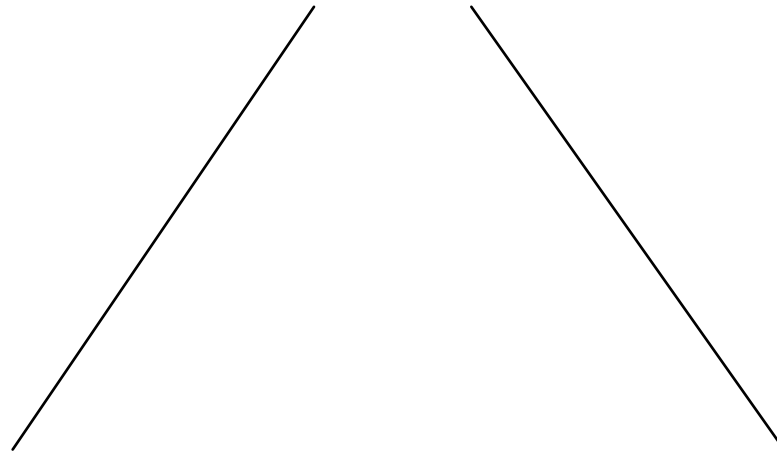
MOUNT SINAI HOSPITAL
Joseph and Wolf Lebovic Health Complex
Samuel Lunenfeld Research Institute

Ted Pak
Roth Laboratory
Donnelly Centre, University of Toronto
Samuel Lunenfeld Research Institute,
Mt. Sinai Hospital



genome browsers:

lots of data



small viewable area

UCSC, GBrowse, etc.



Search

Landmark or Region:

chrI:83,567..105,388

Examples: chrIII, chrV:80,000..120,000, SGS1, RPL28, YCR065W, flocculation.

Data Source

Saccharomyces cerevisiae S288C Genome

Annotate Restriction Sites

Scroll/Zoom:



Show 21.82 kbp



☐ Flip

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

position/search chrIV:765,966-775,965

size 10,000 bp.

Configure Image

image width: 917 pixels

label area width: 17 characters

text size: 10

- | | |
|-------------------------------------|---|
| <input type="checkbox"/> | Show light blue vertical guidelines |
| <input checked="" type="checkbox"/> | Display labels to the left of items in tracks |
| <input type="checkbox"/> | Display description above each track |
| <input checked="" type="checkbox"/> | Show track controls under main graphic |
| <input type="checkbox"/> | Next/previous item navigation |
| <input type="checkbox"/> | Next/previous exon navigation |

☒ Show grid

Image Width

☐ 450 ☐ 640 ☒ 800 ☐ 1024 ☐ 1600

☒ Cache tracks

☒ Show tooltips

★ ☐ ☐ ☐ ☐ ☐ ☐ ☐ ☐ Adr1 and Cat8 ChIP chip: Tachibana et al. (2005)

★ ☐ ☐ ☐ ☐ ☐ ☐ ☐ ☐ Transcribed regions (ab initio): Yassour et al. (2009)

track search default tracks default order hide all add custom tracks track hubs configure reverse resize refresh

collapse all expand all

Use drop-down controls below and press refresh to alter tracks displayed.
Tracks with lots of items will automatically be displayed in more compact modes.

Mapping and Sequencing Tracks

refresh

Base Position	Assembly	Gap	WashU Clones	GC Percent	Short Match
dense <input type="button" value=""/>	hide <input type="button" value=""/>	[No data-chrIV]	hide <input type="button" value=""/>	hide <input type="button" value=""/>	hide <input type="button" value=""/>

[Restr Enzymes](#)

hide

Genes and Gene Prediction Tracks

refresh

SGD Genes	SGD Other	Ensembl Genes	Human Proteins
squish <input type="button" value=""/>	hide <input type="button" value=""/>	hide <input type="button" value=""/>	hide <input type="button" value=""/>

mRNA and EST Tracks

refresh

S. cer. mRNAs	Spliced ESTs	S. cer. ESTs
hide <input type="button" value=""/>	hide <input type="button" value=""/>	hide <input type="button" value=""/>

Annotations for SGD curated features ☐ All on ☐ All off

- ★ 3-frame translation (forward) ☐
- ★ 3-frame translation (reverse) ☐
- ☒ ★ All Annotated Sequence Features ☐
- ★ DNA/GC Content
- ★ Genomic Clones ☐
- ★ Non-coding RNA Genes ☐
- ★ Protein-coding Genes ☐
- ★ ResGen primer products ☐

Chromatin structure

DNase I hypersensitive sites ☐ All on ☐ All off

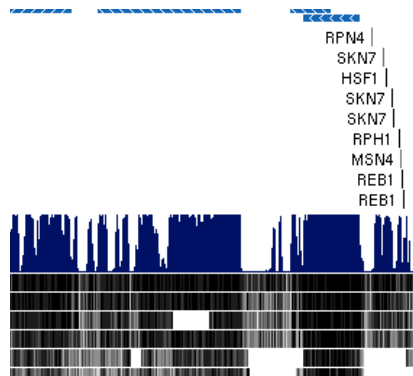
- ★ Digital genomic footprinting: Hesselberth et al. (2009) ☐

Histone modifications ☐ All on ☐ All off

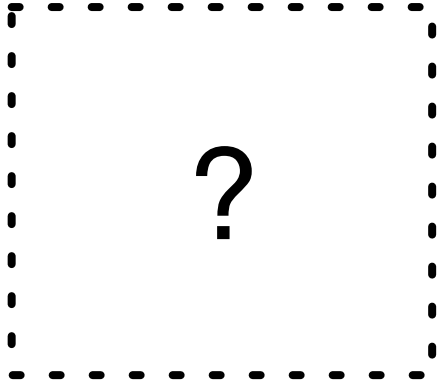
- ★ Histone modifications (chrIII & other promoters): Liu et al. (2005) ☐ [2 of 15 subtracks selected]
- ★ Histone modifications: Guillemette et al. (2011) ☐ [4 of 4 subtracks selected]
- ★ Histone modifications: Kirmizis et al. (2007) ☐ [2 of 18 subtracks selected]
- ★ Histone modifications: Pokholok et al. (2005) ☐ [10 of 19 subtracks selected]

Histone variants ☐ All on ☐ All off

- ★ H2AZ Nucleosome occupancy: Guillemette et al. (2005) ☐ [3 of 3 subtracks selected]
- ★ H2AZ Nucleosome positions: Albert et al. (2007) ☐
- ★ Nucleosome organization ☐ All on ☐ All off
- ★ Nucleosome occupancy: Field et al. (2008) ☐ [3]
- ★ Nucleosome occupancy: Lee et al. (2007) ☐ [2]







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move zoom in base zoom out

position/search chrIV:765,966–775,965 size 10,000 bp.

Configure Image

image width: pixels

label area width: characters

text size:

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Mapping and Sequencing Tracks

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Restr Enzymes

hide

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- ★ DNA/GC Content
- ★ Genomic Clones ☐
- ★ Non-coding RNA Genes ☐
- ★ Protein-coding Genes ☐
- ★ ResGen primer products ☐

Chromatin structure

DNase I hypersensitive sites ☐ All on ☐ All off

- ★ Digital genomic footprinting: Hesselberth et al. (2009) ☐

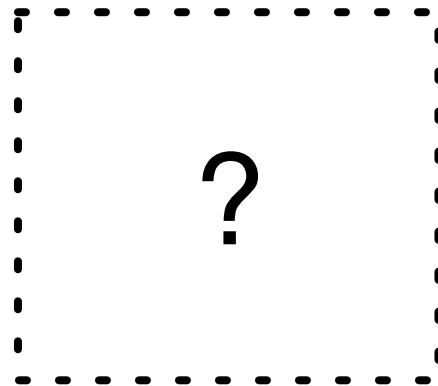
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[Restr Enzymes](#)

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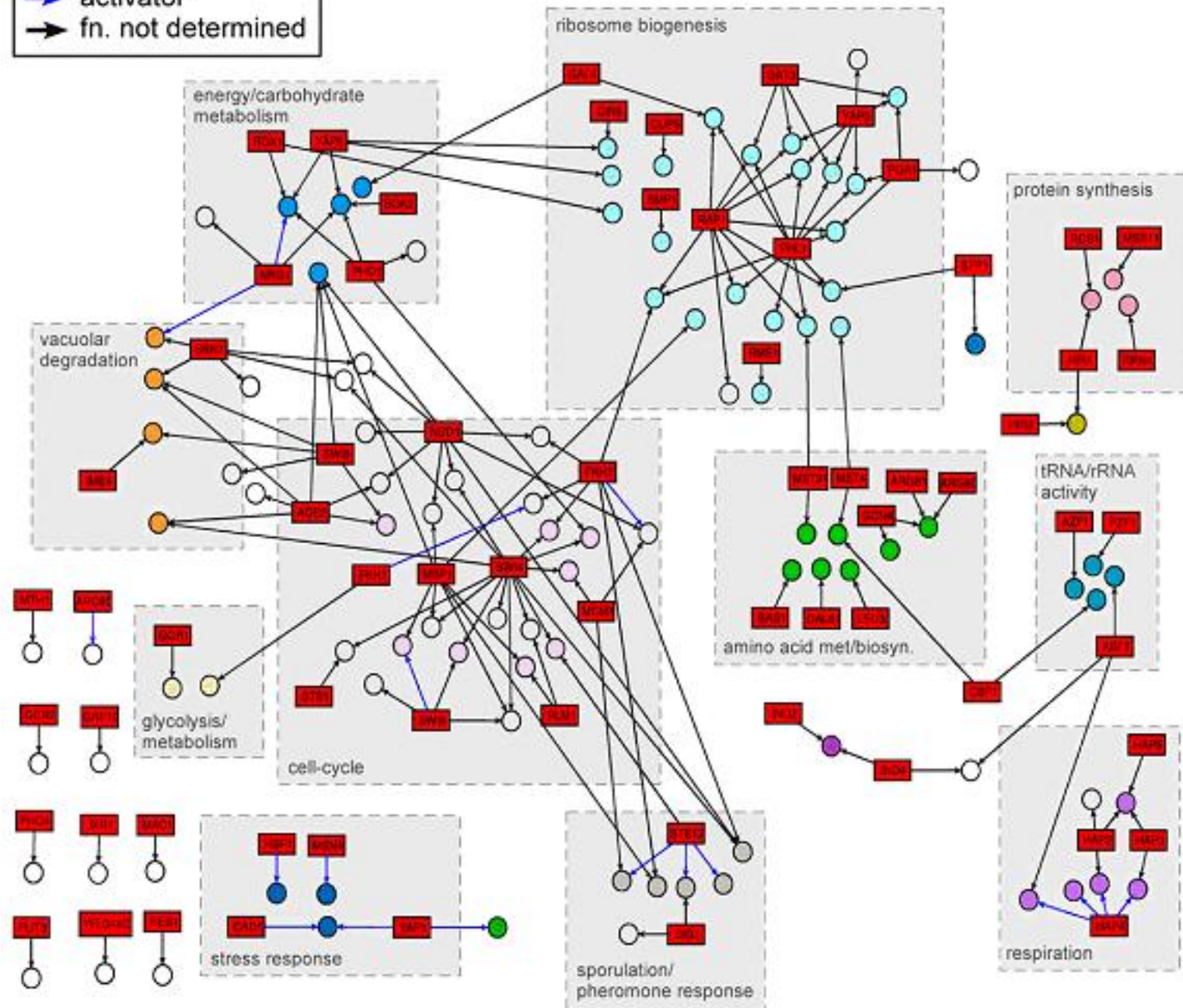
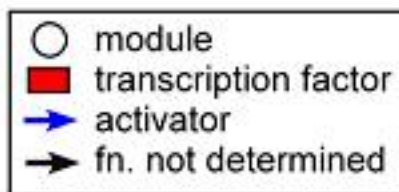
Histone modifications ☐ All on ☐ All off

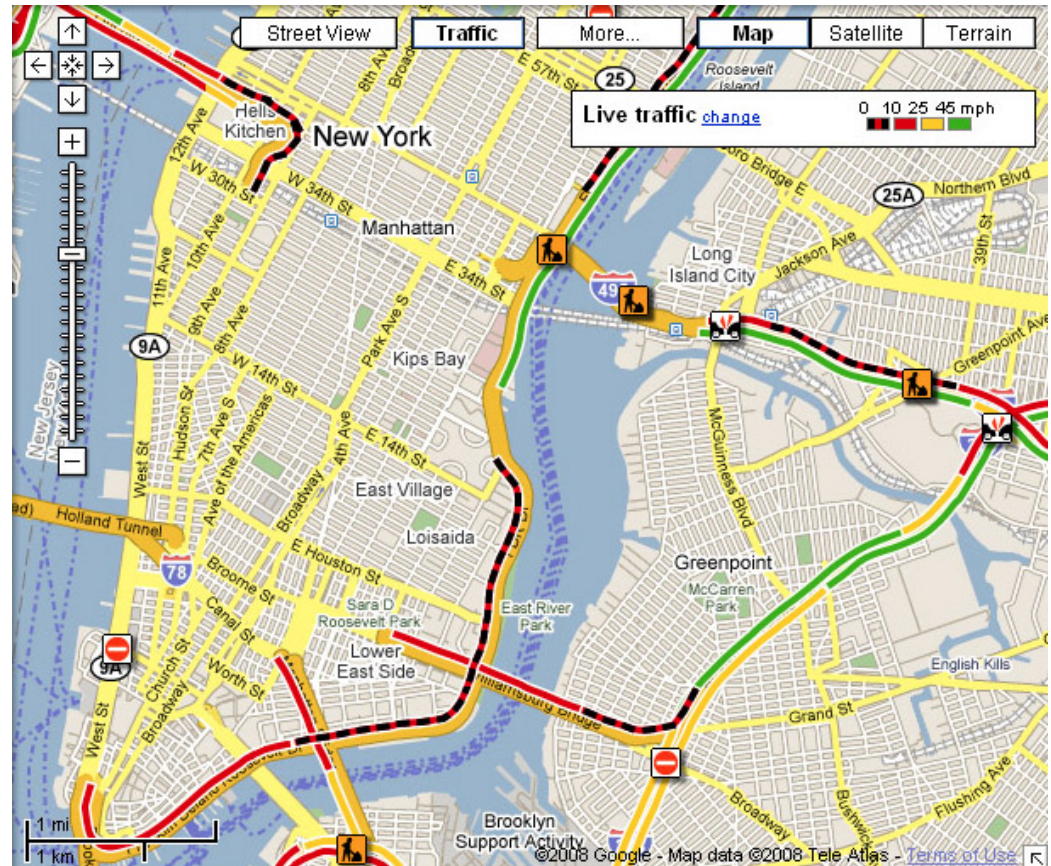
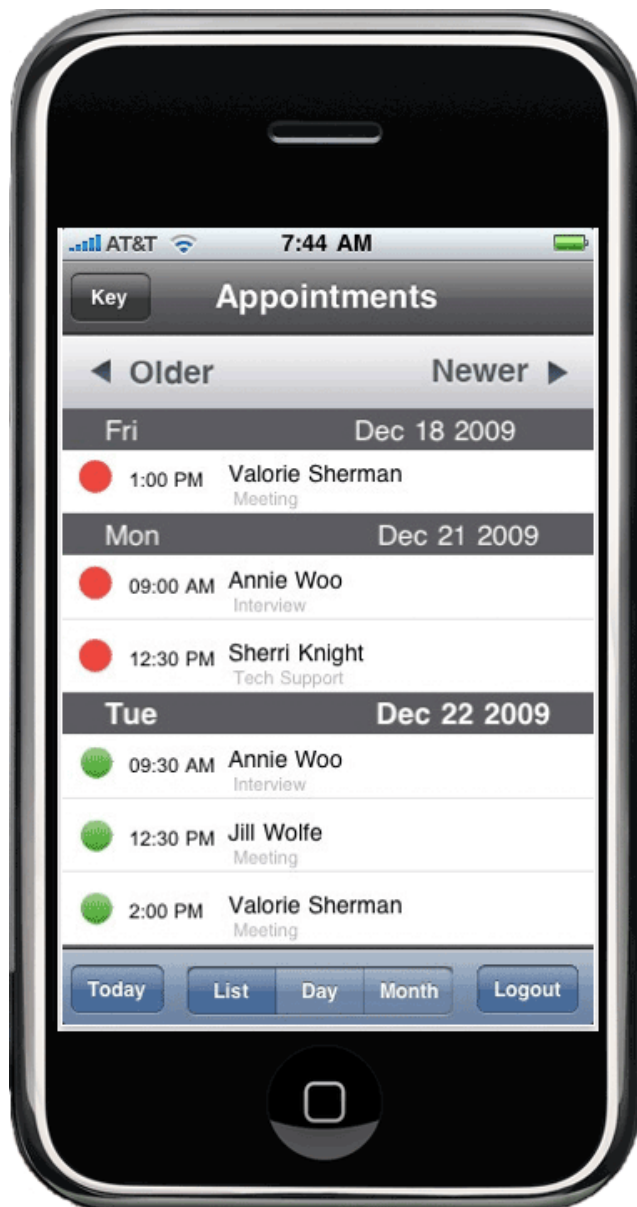
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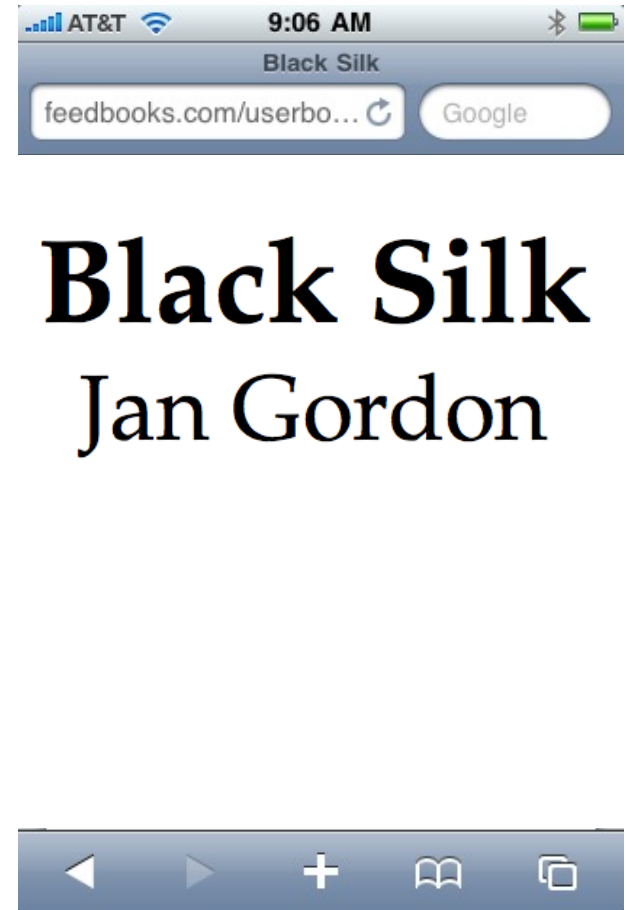
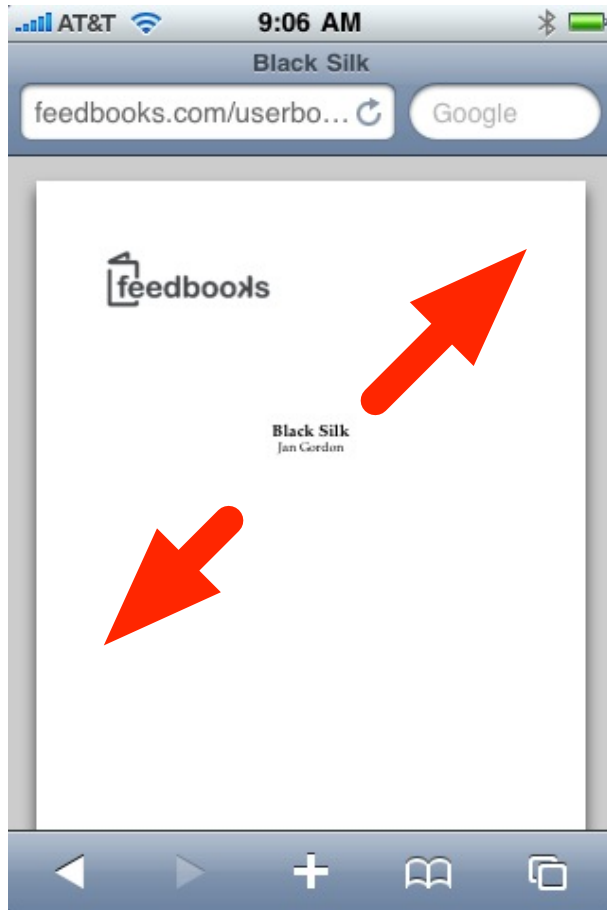
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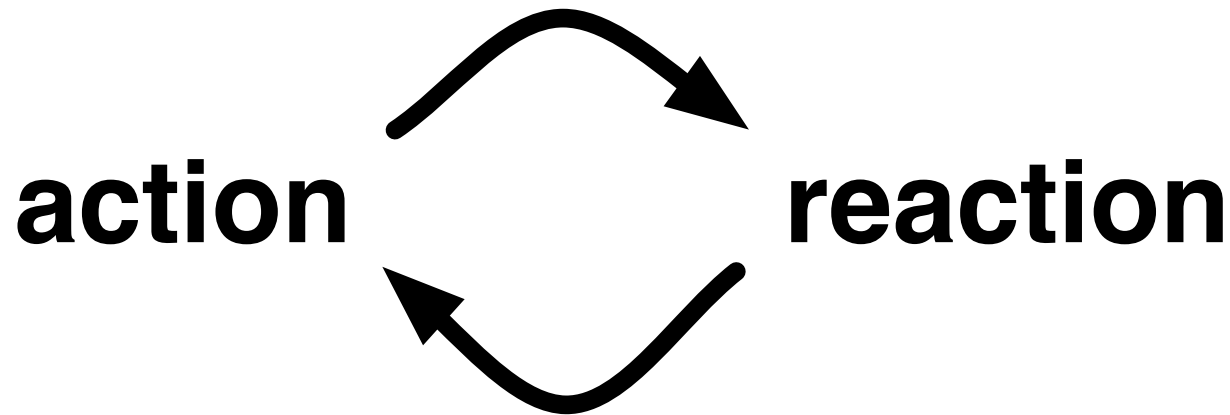




maintaining immersion



fluidity



positional awareness

no spinners
no progress bars
no loading screens
just drive



live demo

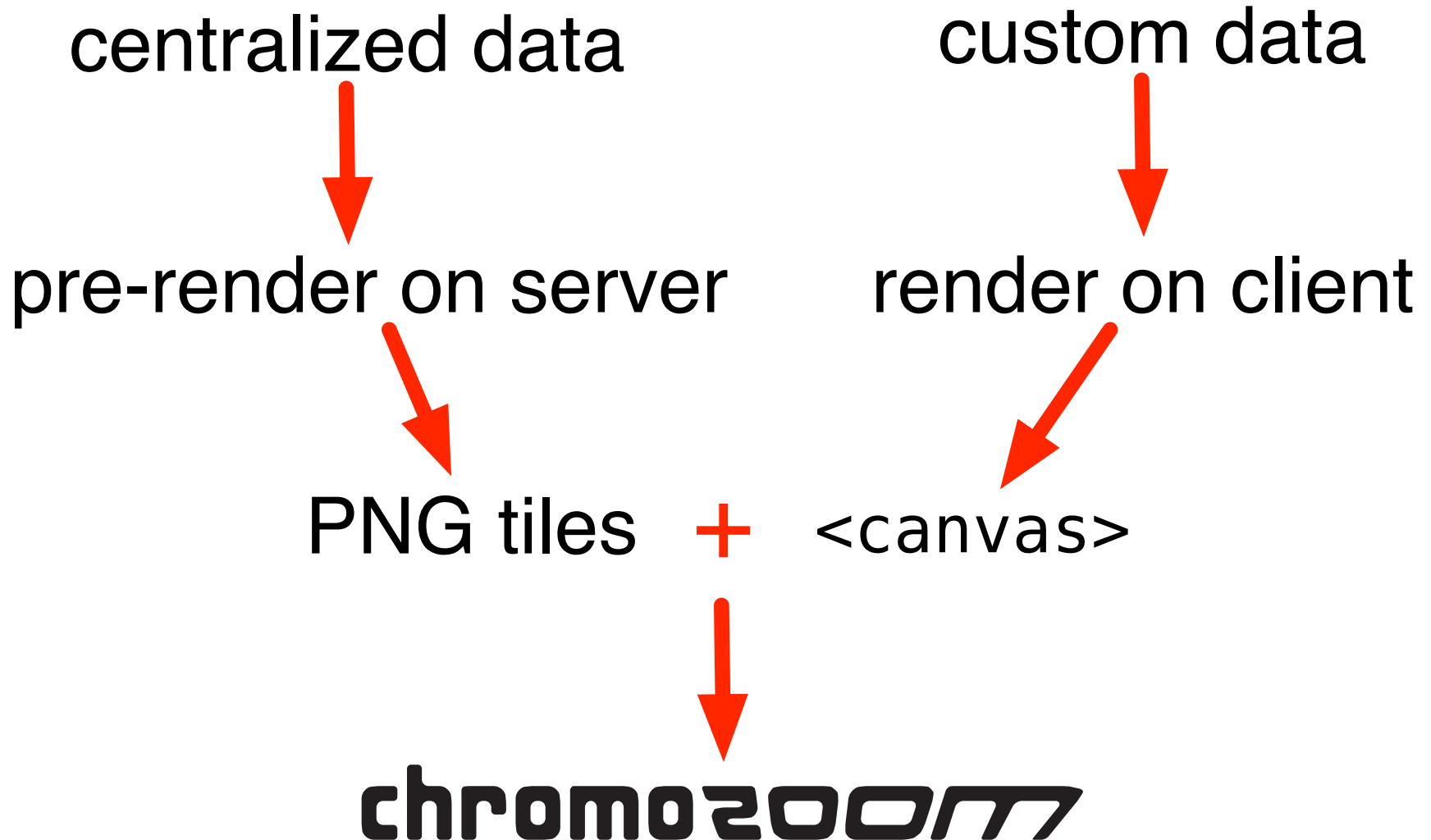
current highlights

- 19 yeast tracks from UCSC
- Search with autocomplete
- Speedy, smooth zoom & pan
- Contextual tooltips for regions
- Share links to exact views
- Open source
- Custom data supported...

custom tracks

- Drawn with JavaScript
- Can do:
 - **BED** and **bigBed** (exons only)
 - **WIG**, **bigWig**, and **bedGraph**
 - **VCFTabix**
- Should be easy to add more
- **big*** formats: best performance

division of labor



<http://chromozoom.org>

thank you!

in particular,
my advisor Fritz Roth
the entire Roth laboratory
and Michael Cherry, for inviting me.