

Software licencing: UCSC Genome Browser

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CI4CC symposium

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@GenomeBrowser



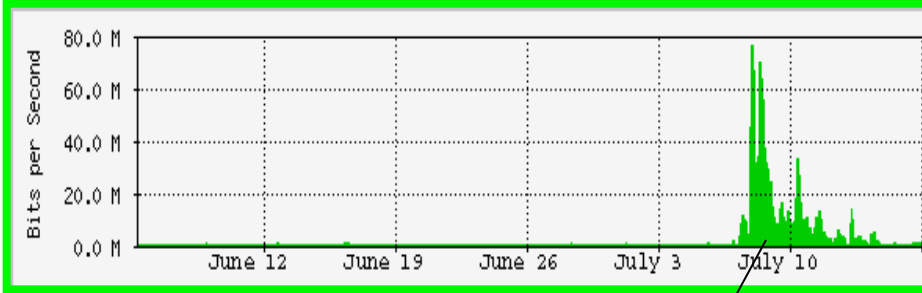
UCSC Genome Browser

Database + files: ~40 Tb

web site: 1 million hits per day

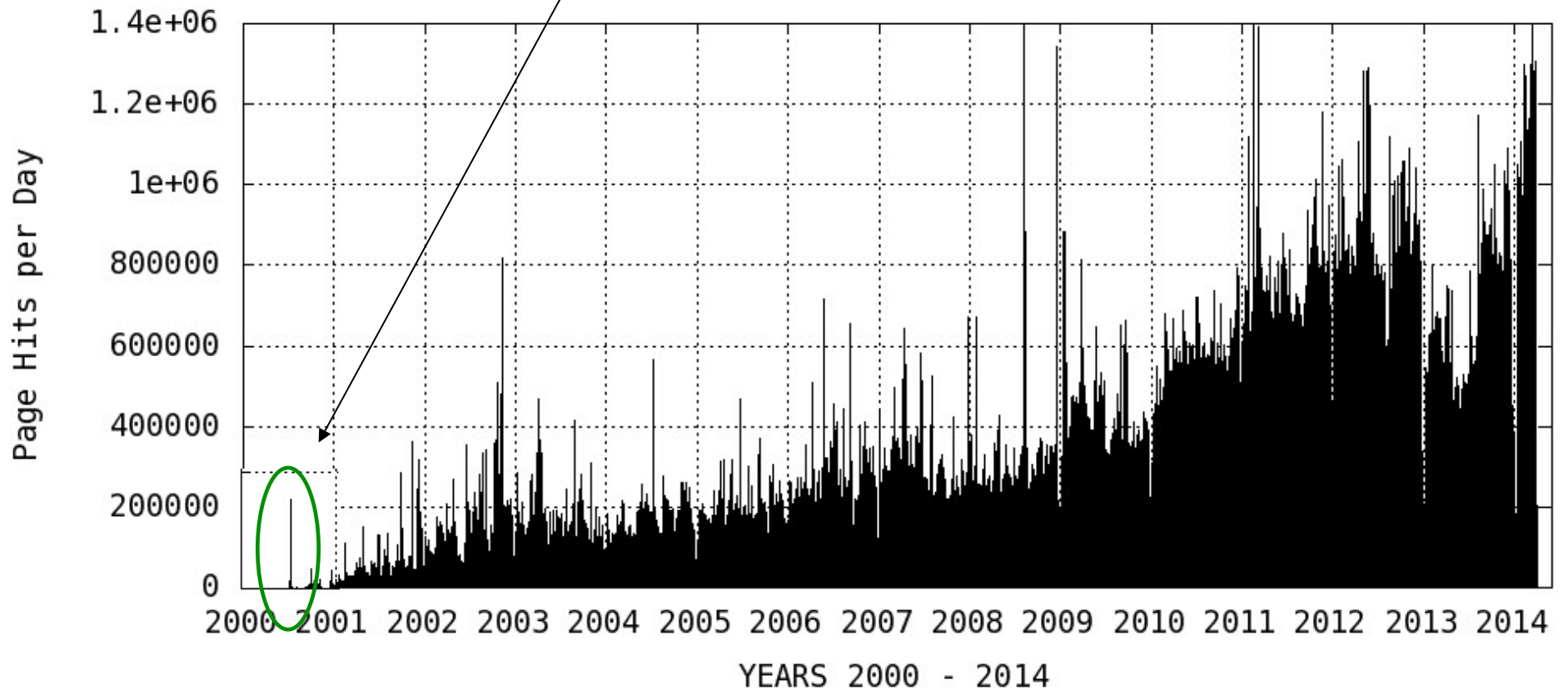
~200,000 regular users

~400 known mirrors

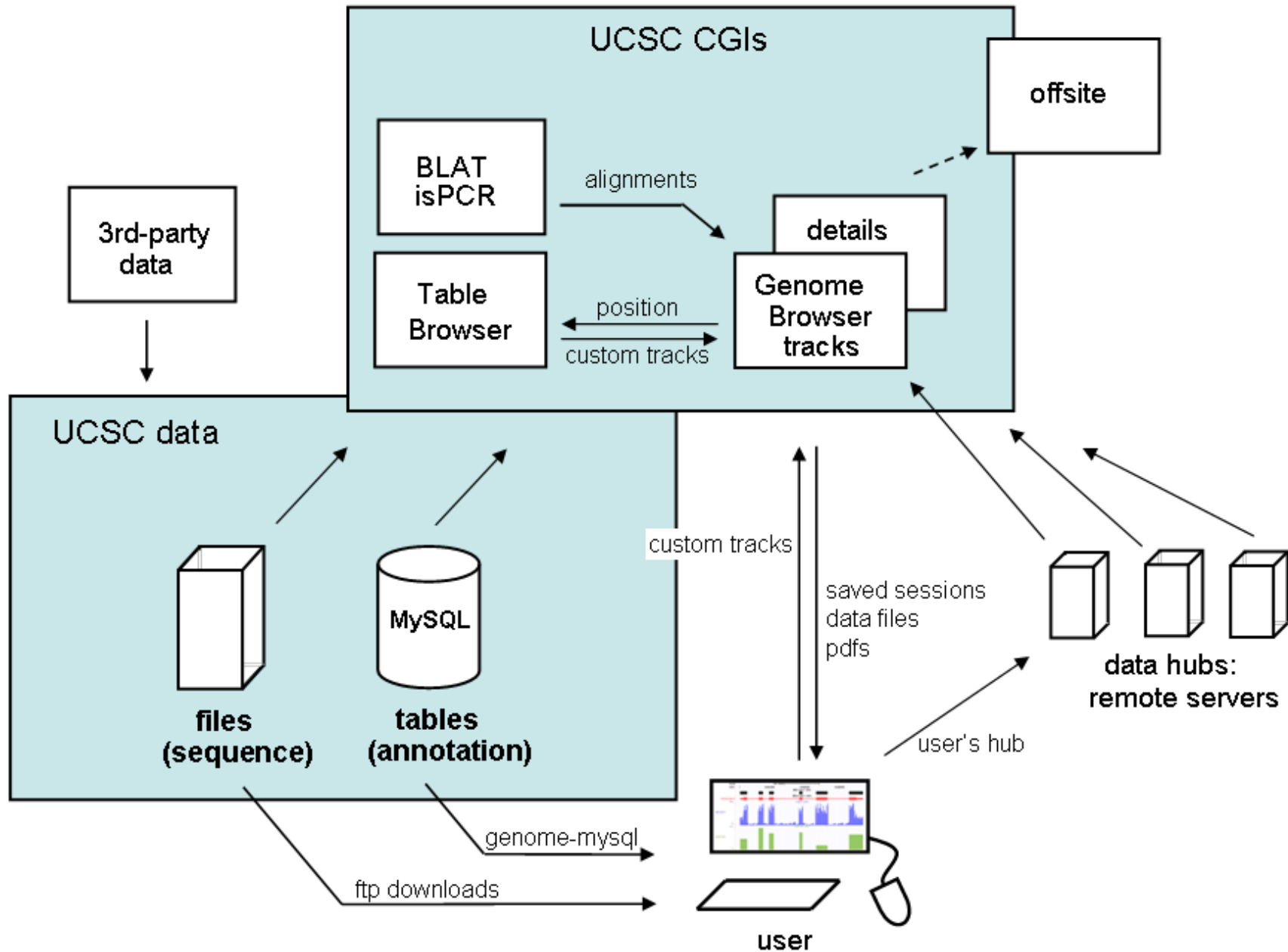


- 7,000,000 hits a week.
- ~200,000 regular users.

YEARS 2000 - 2014 - genome.ucsc.edu WEB Page Hits per day

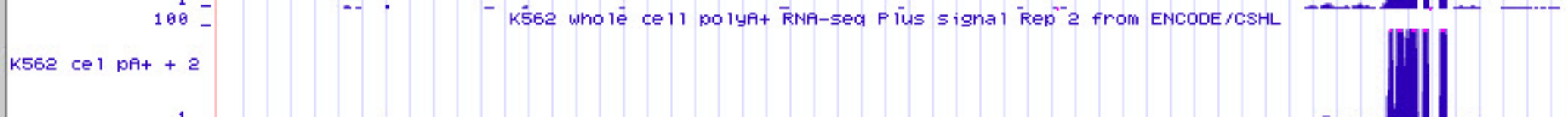
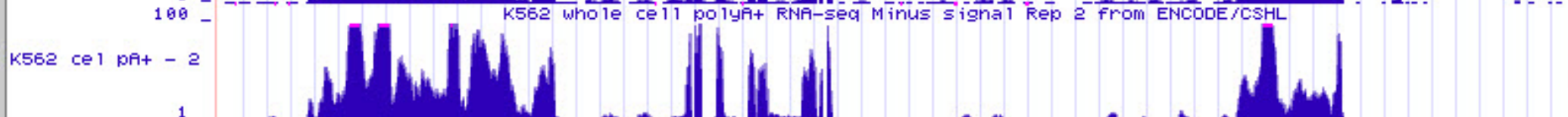
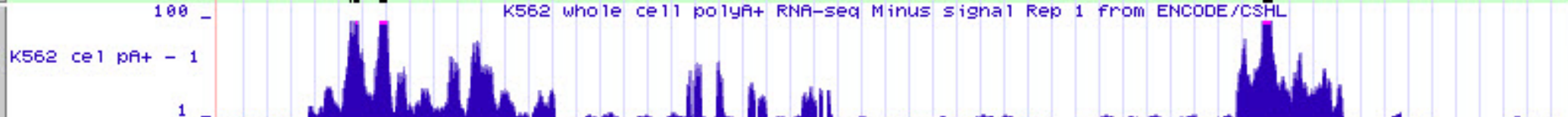
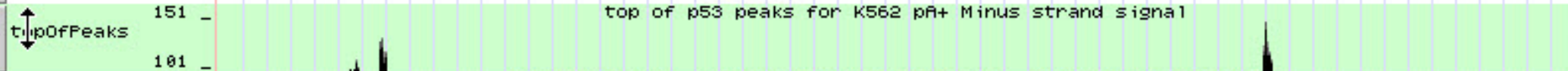
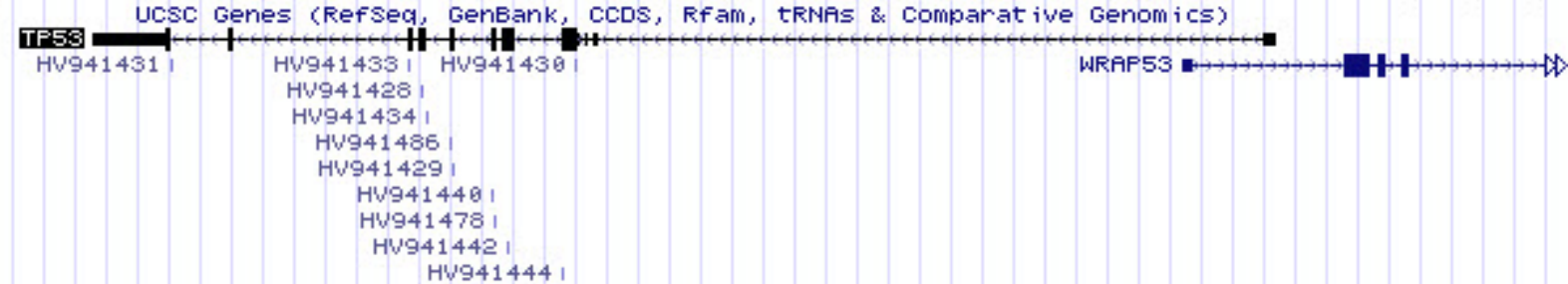


architecture



chr17 (p13.1) 3.1 17p12 17p11.2 q11.2 17q12 17q22 24.3 25.1 q25.3

Scale 10 kb hg19
chr17: 7,570,000 | 7,575,000 | 7,580,000 | 7,585,000 | 7,590,000 | 7,595,000



Genome Browser Licenses

Genome Browser mirrors

Genome Browser in a Box (GBiB)

Sold to commercial entities

Free for academic use

License: how decide to sell?

open-source project, but companies were trying to commercialize genome annotation, so it made sense to capture some of that income if they planned to capitalize on UCSC software

Licenses: how many?

several

License: significantly fund the group?

NO – The license money goes to the authors, HHMI and the University, not the project

Project has ~ 200 FTE-years of effort in it – even if the money came the project, would not be “significant”.

License: unauthorized use?

Yes – anecdotally

Have considered making detection possible, but that costs time/effort as well

**License: does charging for software
deter adoption?**

**Probably – though some are probably
doing it clandestinely**

License: do we treat licensees differently?

Yes, slightly. They pay for support. And our QA staff know who they are and give them slightly faster response.

License: other effects?

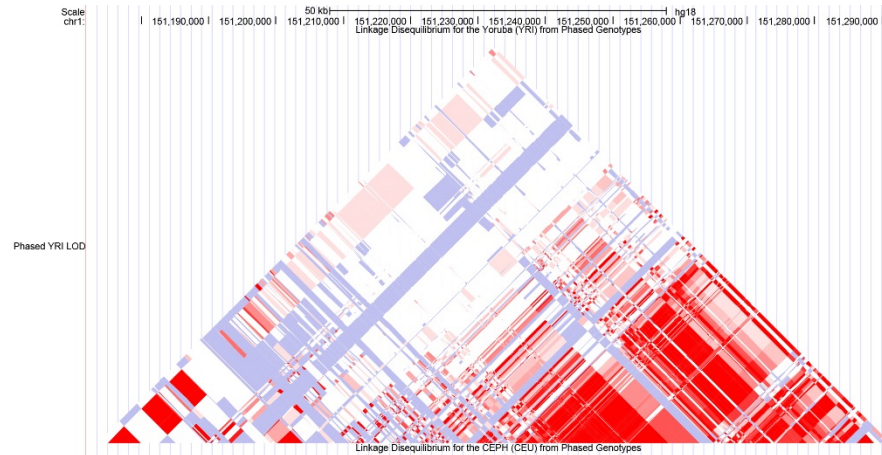
We do receive individually a small royalty from license fees – given to us by the original authors for contributing to updates and new development. This is a morale booster in the face of years of no raises from the University

Code Documentation and Maintenance

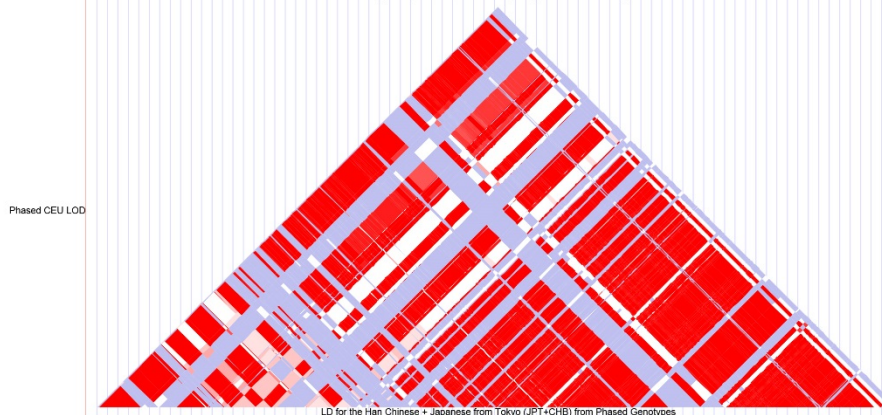
It is important to use code that is well supported. Many programs are written by grad students or postdocs who move on – leaving behind code that works until something in the pipeline changes.

Linkage Disequilibrium

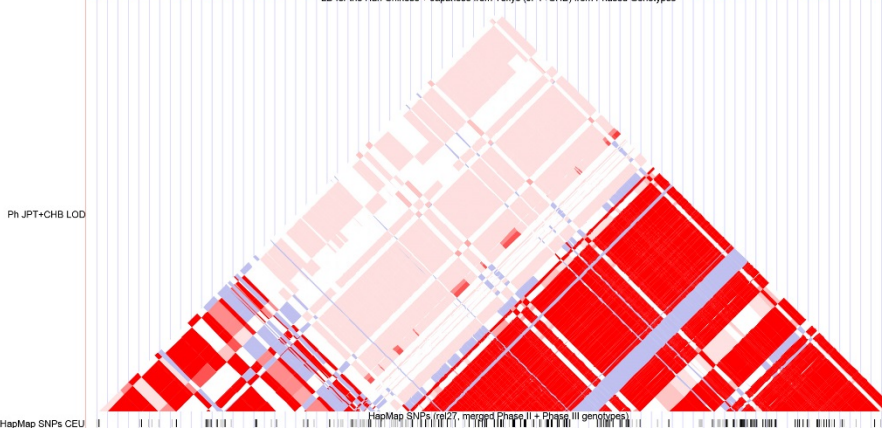
YRI



CEU



JPT+CHB



Haploview
software

No longer
works

Linkage
tracks now
only on
hg18

chr1:151,171,924-151,293,990

Acknowledgements

UCSC Browser team

- **David Haussler – co-PI**
- **Jim Kent – Browser Concept, BLAT, Team Leader, PI**

Engineering

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Cath Tyner
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Jorge Garcia
Erich Weiler
Gary Moro

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Donna Karolchik
Ann Zweig

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