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CfMR
Centre for Musculoskeletal Research

Integration of Research IT services within the Centre for Musculoskeletal Research

John Bowes
Research Fellow

Arthritis Research UK | centre for genetics & genomics

NHS
National Institute for Health Research

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Aim...

1. .. to show how as a centre we have adopted core set of Research IT services as our routine analysis platform

2. Two examples where collaborating with Research IT has enabled to develop projects not previously possible

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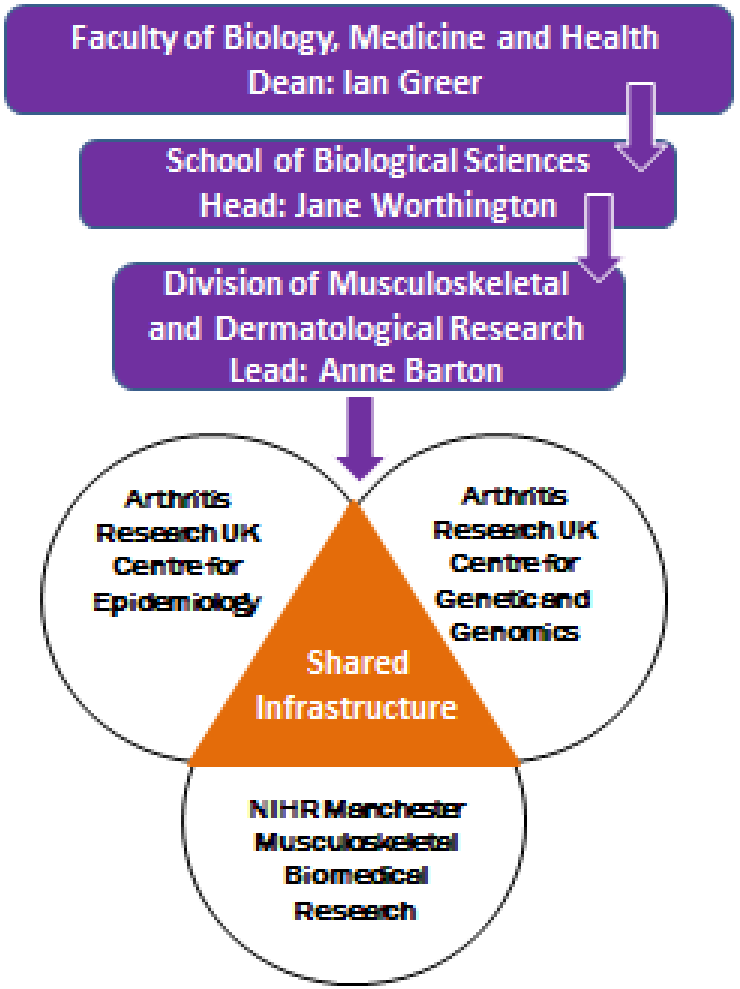
Centre for Musculoskeletal Research



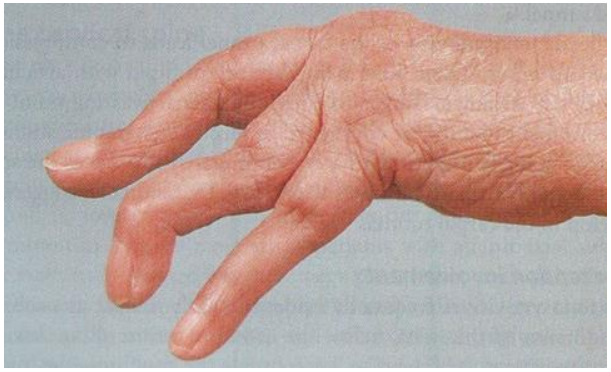
Centre for Genetics and Genomics

Study genetic basis of musculoskeletal disorders:

1. Rheumatoid Arthritis
2. Juvenile Idiopathic Arthritis
3. Psoriatic arthritis

Autoimmune diseases:

- significant disability
- increased morbidity
- increased mortality



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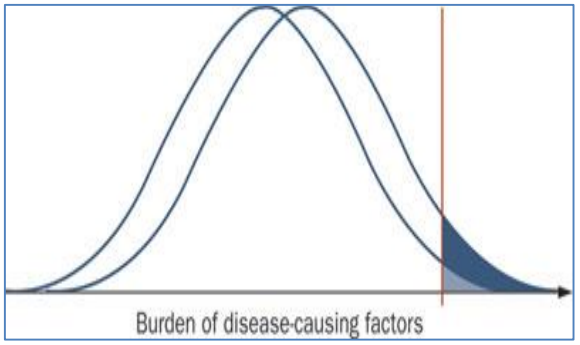
Common complex diseases

- Complex disease

  1. Genetic risk factors
  2. Environment risk factors
  3. G+E = liability

- Goal: identify genetic variants that underlie disease

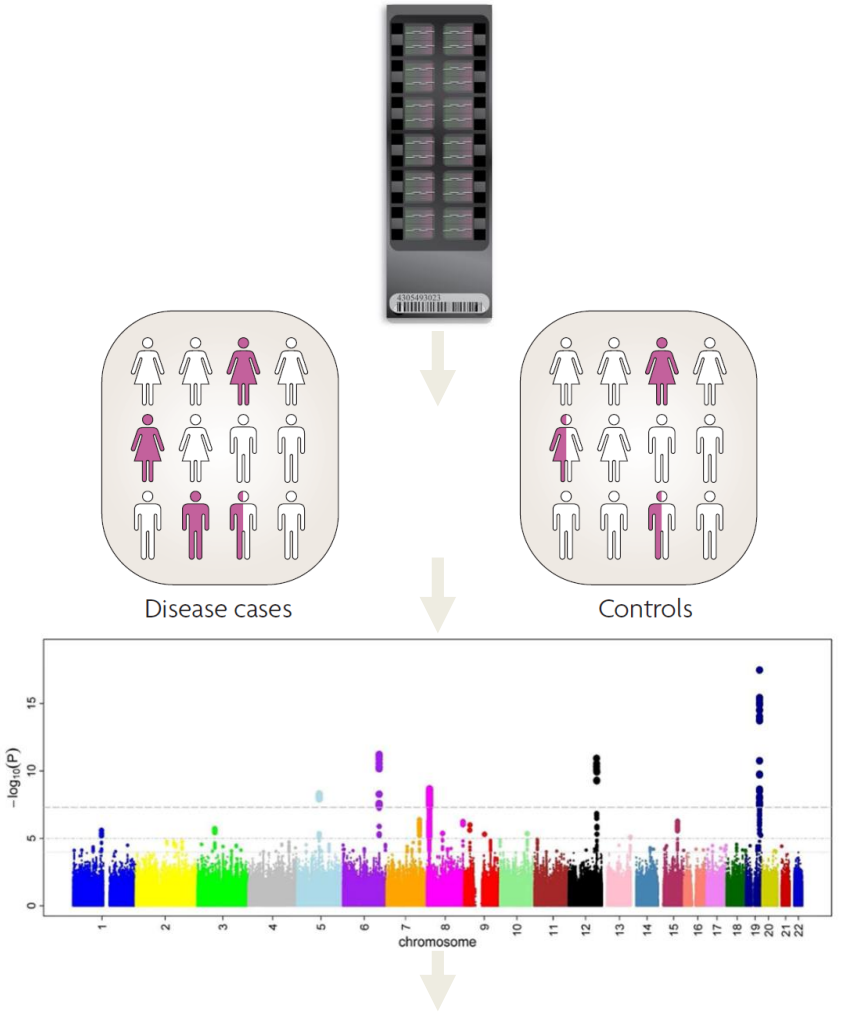


Genome-wide association studies (GWAS)

Genotyping
~1 million genetic variants randomly distributed in the genome typed in high-density arrays

Case-control study
Compare frequencies of genetic variants between disease cases and controls

Genome scan results
Significant differences in SNP allele frequencies indicate possible new disease genes and loci



Genotype-associated SNPs in independent case-control sample

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Research interests:

1. **Understanding susceptibility**
   - risk prediction
2. **Disease outcome**
   - Longitudinal – disease severity
3. **Treatment**
   - drug response/repositioning
4. **Biology – functional genomics**
   - Chromatin confirmation, RNA-seq, CRISPR

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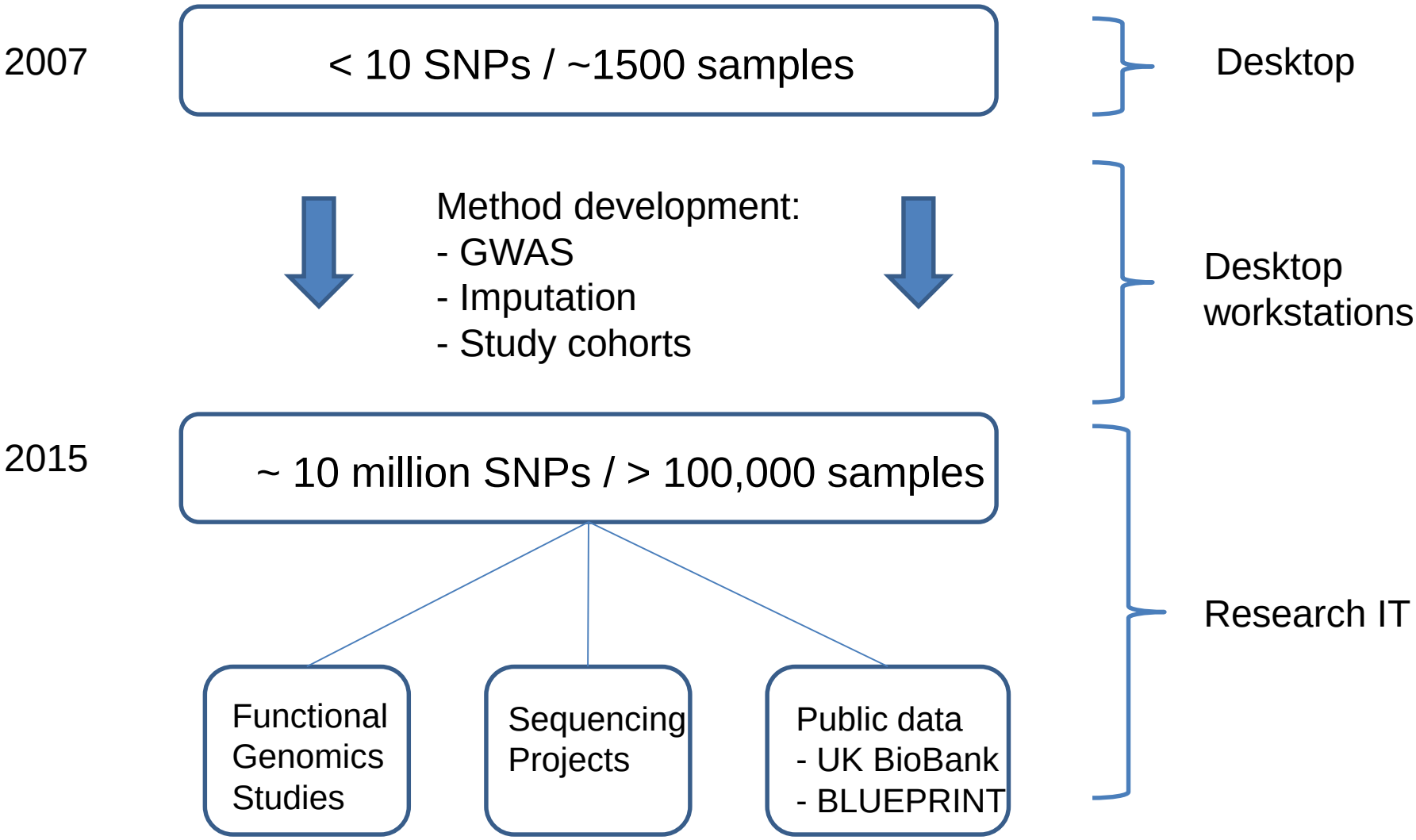
Acceleration of data collection



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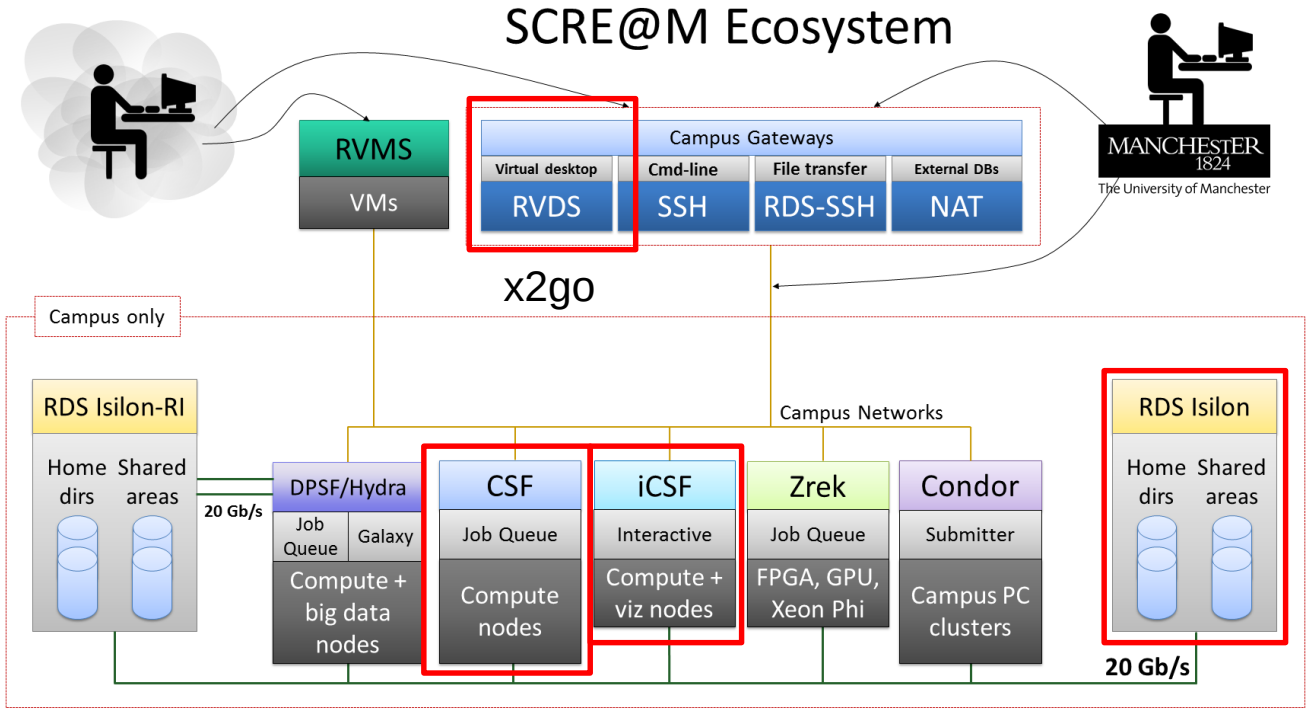
Computationally Intensive Resource (CIR) ecosystem



Rely on 4 core components:

1. RVDS
2. iCSF
3. CSF
4. Isilon

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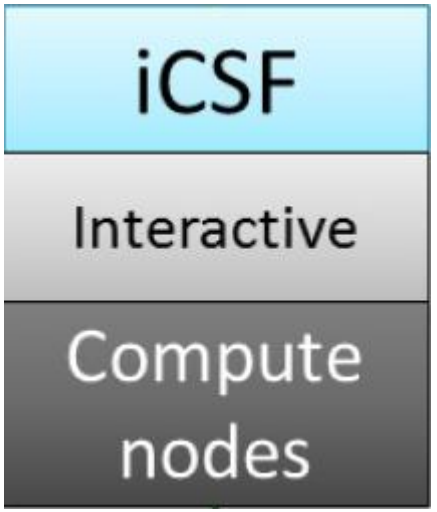
iCSF overview



- Main analysis platform
- GUI-based Interactive computational work
  - Stata, rstudio, MATLAB
- No SGE
  - Log directly onto back-end node (12)
- Multi-user workstation (>60 users)

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iCSF configuration

8 Standard Nodes	• 12 core nodes • 64 GB RAM
2 High-memory Nodes	• 16 core nodes • 256 GB RAM
1 Super-high-memory Node	• 2TB RAM • priority use for contributor
3 GPU nodes	• AMD FirePro v7800 GPUs

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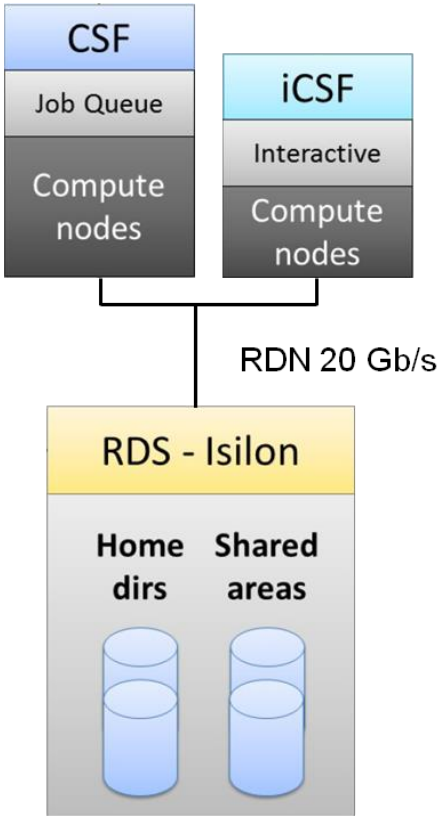
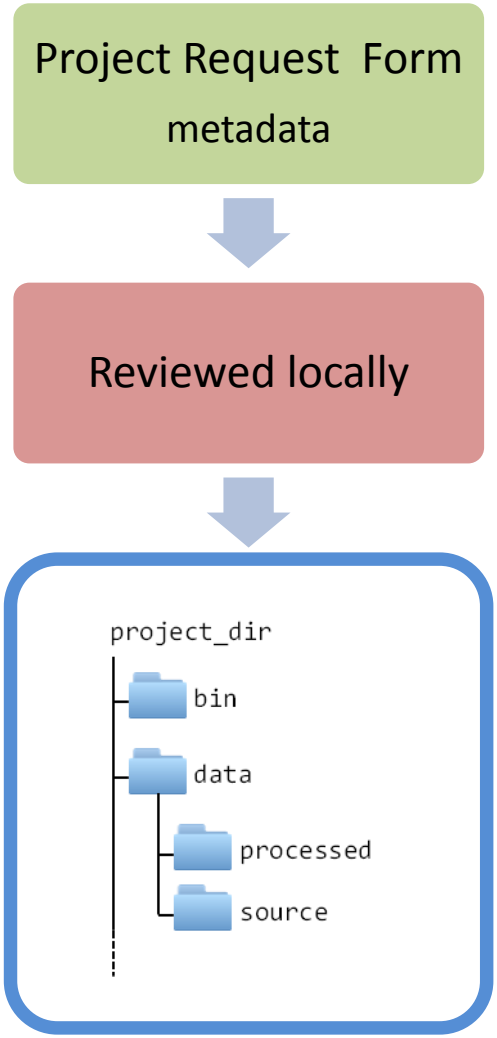
Research Data Storage

- Key feature: centralisation of compute and storage
- Tight integration of systems
- Storage linked to both clusters
  - High speed connection
  - Access home/project directories
- Highly resilient (snapshots and replication)
  - Not possible with our workstations



Project directory system

- Lots of users working on multiple projects (n=61)
- Important to organise this workspace
- Implemented a project directory system
- Currently have 89 projects (~20 TB)



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Transition

- Important transition period
  - Windows based systems to Linux
  - Most users had limited experience
- This was facilitated by a user workshop
  - Pen and George
- Core group of users
  - Now provide training/supervision to new users

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Three key issues

1. Dependent on existence
   - Changes would have an impact
   - Long term plans (cloud)

2. Maintaining access
   - Ad hoc grant contributions
   - Subscription (5 year access – multiple systems)

3. Archiving
   - Many completed projects
   - Interested in any centralised archiving processes

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Summary

Advantages of centralised systems:

1. No procurement, hosting, administration of local systems
2. Allows us to keep up the pace of data collection
3. Centralisation improves organisation
4. Not just about the hardware
   - access to expertise in Research IT is important

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Two projects:

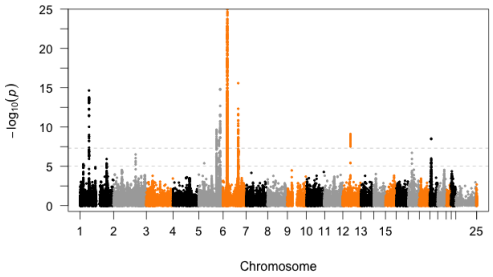
1. Data browser: RVMS and Research Software Engineers

2. Galaxy pipeline: DPSF and Centaurus server

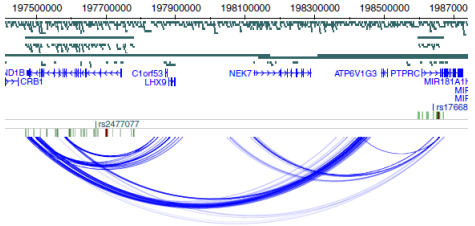
Data Browser

The Problem....

- We generate large volumes of data
- Not currently easy to browse in a unified way
- Sharing is ad hoc and with collaborators



Genetics



Genomics

Public data

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Data Browser

The Aim....

- Create a web-based data browser visualisation/exploration
- Publically available
- Mechanism for sharing data
- Encourage collaboration

WashU
EpiGenome
Browser

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Software engineers

- Developing with Rob Haines
- Team of professional software engineers
- Allows us to “hire” a RSE for a short period of time
- Not possible through conventional recruitment process

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RVMS

- Hosted on Research Virtual Machine Service (RVMS)
- Centrally hosted VMS
- Users maintain administrative control
- Tight integration with computing infrastructure

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CRAFT

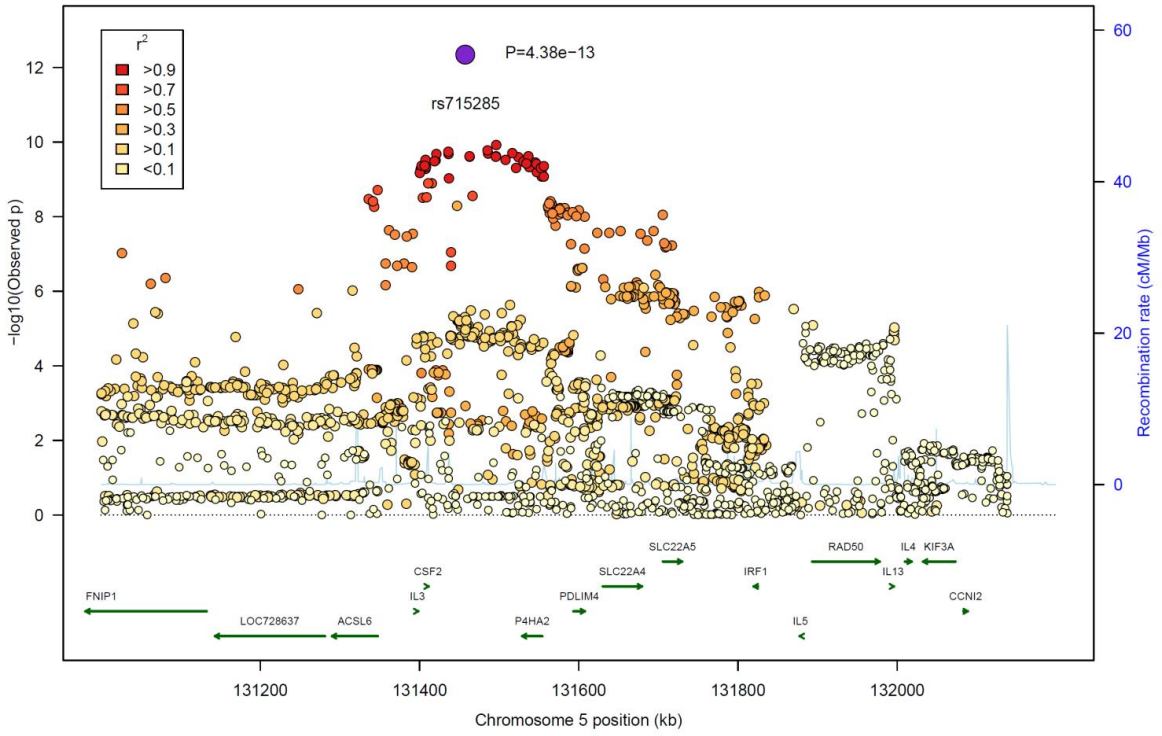
Galaxy

- **C**redible **R**efinement and **A**nnotation of **F**unctional **T**argets

- Pipeline for fine mapping genetic loci associated with disease

- Implemented in Galaxy
  - Bioinformatics platform for distributing workflows
  - Enables access for researchers without extensive computer experience

Fine mapping



- Large region
- Lots of genetic variants
- High correlation between variants
- Multiple candidate genes

NEED: refine the association and prioritise functional variants

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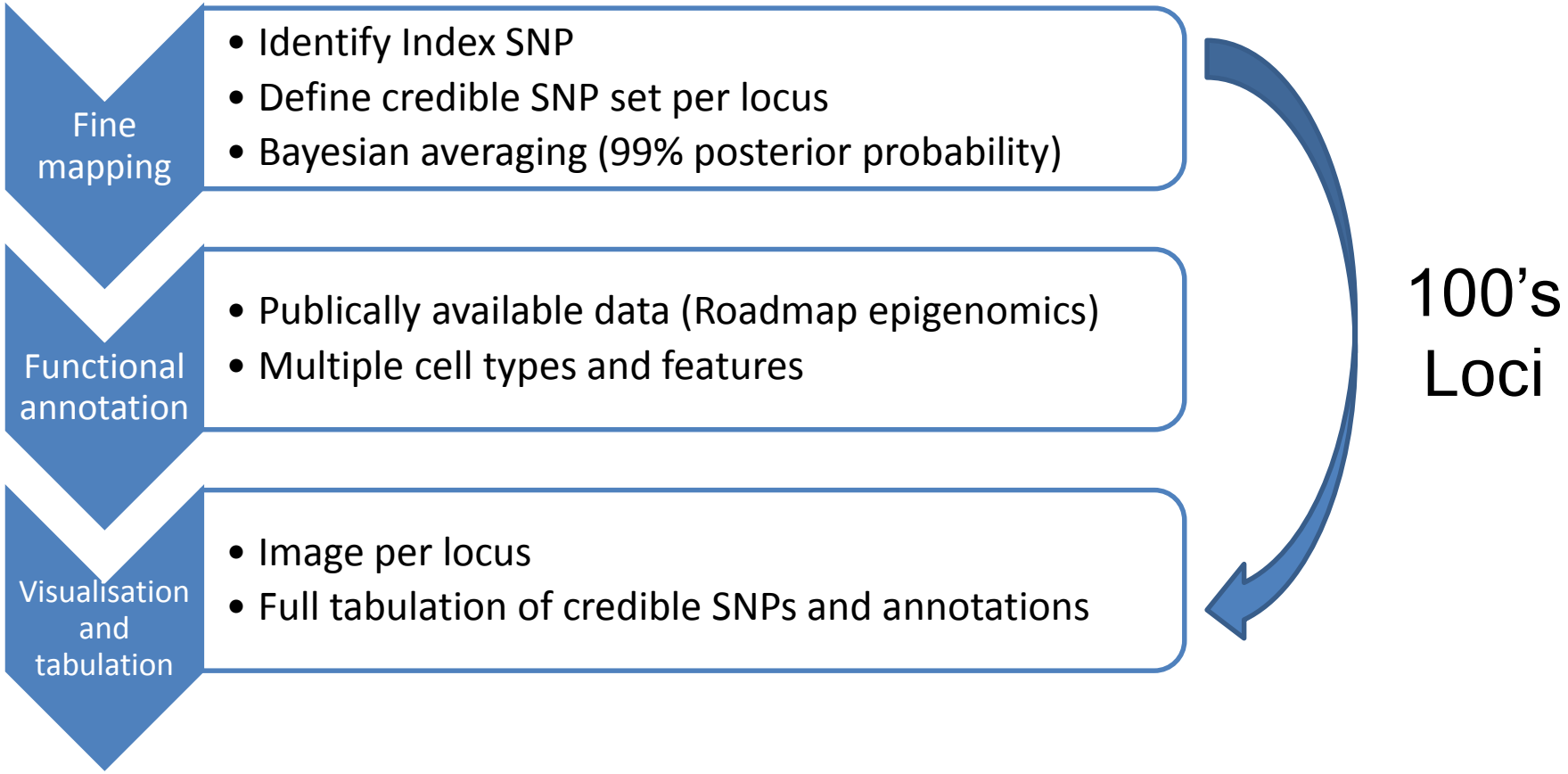
CRAFT stages



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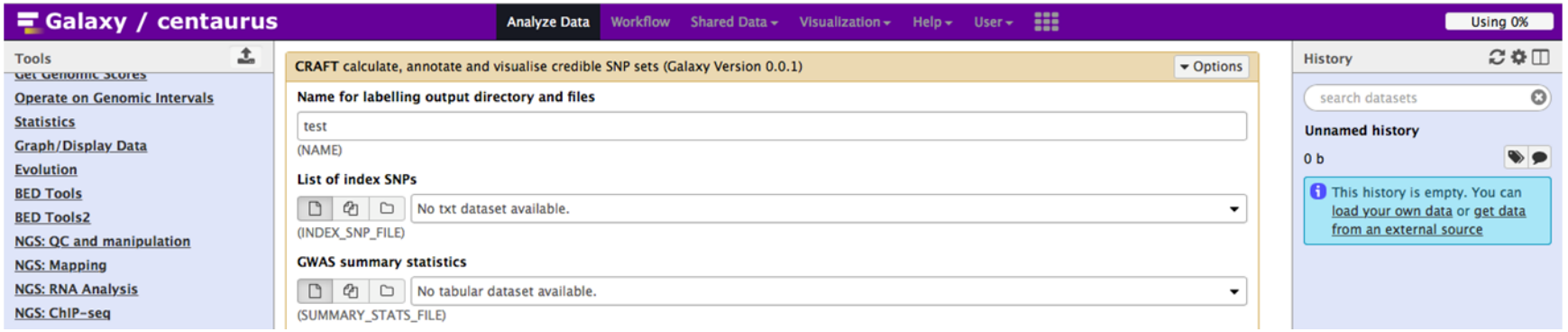
CRAFT: development

- Collaboration Peter Briggs (BCF)
- Hosted of Centaurus Galaxy Server
- Data Processing Shared Facility (DPSF)



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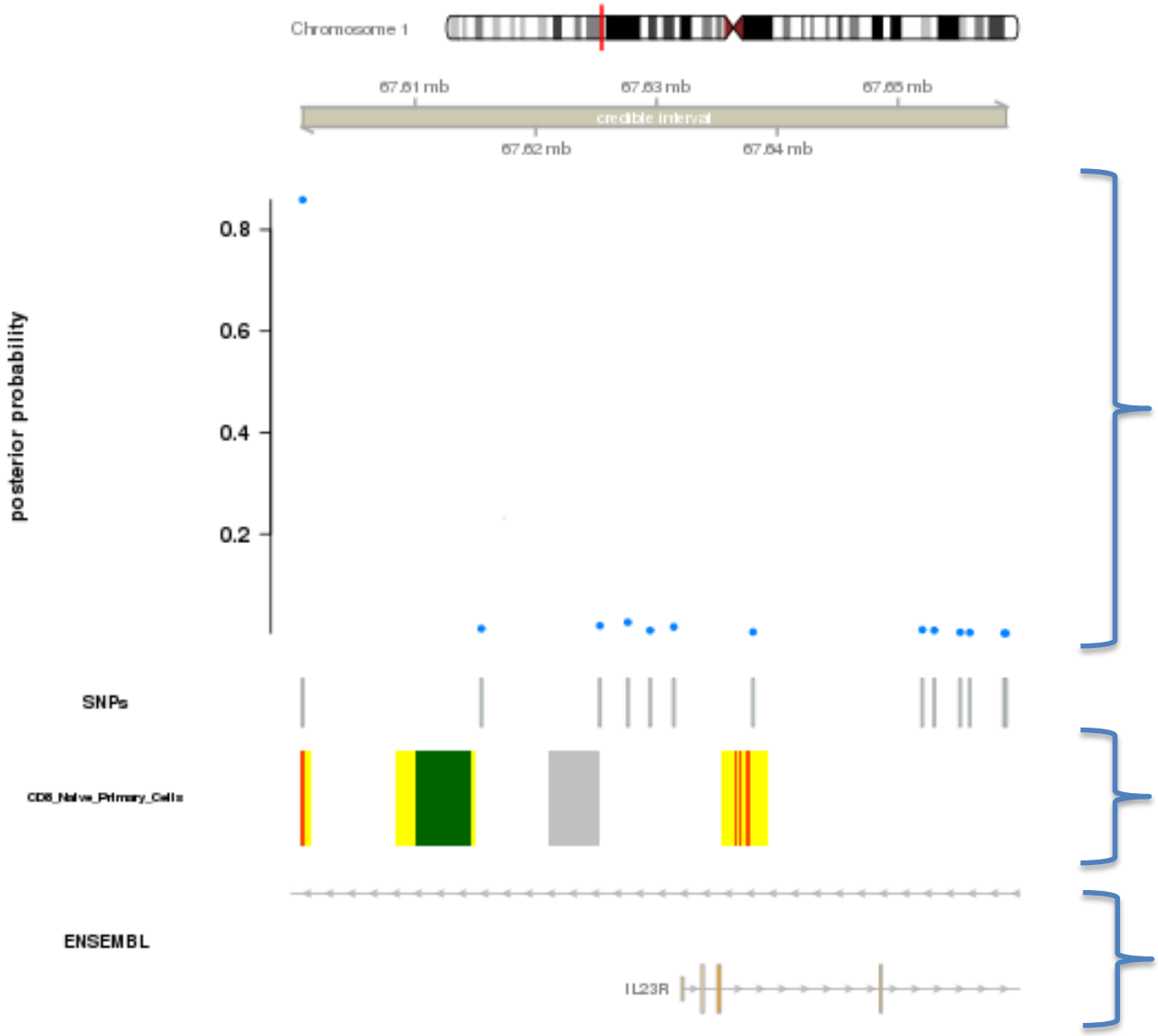
CRAFT: example



Credible SNP set (posterior probability)

ChrommHMM segmentations

Genes

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Conclusion

- Research IT systems now underpins the majority of our genetic research
- Access to both hardware and expertise has been important
- This has allowed us to keep pace with data collection

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