

The System: Tools to enable Systems Biology for Veterinary Genomics
Michael Watson, Bioinformatics, IAH

EADGENE European Animal Disease Genomics Network of Excellence for Animal Health and Food Safety

Genomics for Animal Health: Outlook for the Future
13- 14th October 2009, Muséum National d'Histoire Naturelle, Paris, France



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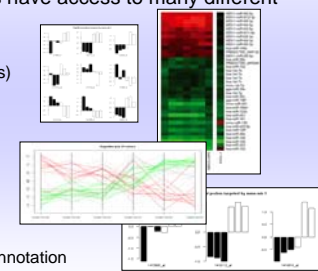
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BBSRC **IAH**

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Quantitative biology


- Biological researchers have access to many different datasets
 - Genome sequence
 - Genetic markers (SNPs)
 - Phenotype data
 - Knock out data
 - Microarray data
 - Expression studies
 - Genotyping
 - Copy number variation
 - Proteomics data
 - Pathways, functional annotation



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Data integration: SNPs

- Using Illumina beadstation, work from Pete Kaiser and Mark Fife
- 60,000 SNPs genotyped from 24 birds from each of IAH's lines
- Presented in GSCAN from Richard Mott's group



Taylor M et al Management, presentation and interpretation of genome scans using GSCANDB. *Bioinformatics*. 2007 23(12):1545-9.

- But, better presented when integrated with other data

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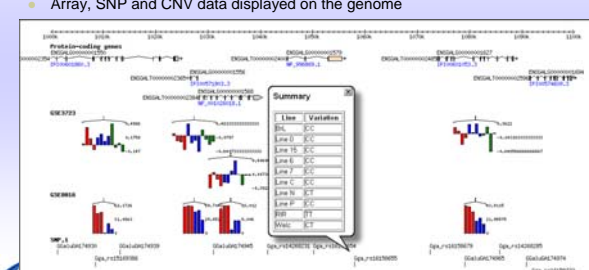
Data Integration: CNVs

- Copy number variation
 - Array based technique to quantify duplications/deletions in individuals compared to reference
 - Work again from Kaiser lab
 - CNV data on IAH chicken lines

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Focus: the quantitative genome

- Want to see how your gene behaved in one experiment? Or 30?
- Work done by Xikun Wu
- Array, SNP and CNV data displayed on the genome




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Qbrowse - example queries


- Show me all SNPs within a gene
- Show me all SNPs within 500bp of the start of that gene
- Show me all SNPs different between Lines 6 and N within 500bp of the start of that gene
- Show me all SNPs different between Lines 6 and N within 500bp of a gene that shows differential expression in an immune system experiment
- Show me all genes that are differentially expressed in an immune system experiment that are within regions of CNV between lines 6 and N
- Show me all SNPs that occur in deletions in line 6 compared to line N
- Etc
- Etc
- Have chicken up and running
- Plans for Porcine and bovine browsers by end of year

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Availability

- Alpha release available now
 - Microarray data only
 - <http://bioinformatics.iah.ac.uk/tools/gbrowse>
- Integrated with SNPs and CNV by Christmas
- Porcine browser by November
- Bovine by February next year
- Other tools coming soon
 - Enrichment analysis for chicken, pig and bovine gene lists
 - Web-services
 - Viral phylogenetics
 - Sequence databases – <http://bioinformatics.iah.ac.uk>



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