Ensembl: How far will Elastic stretch?



Data in Ensembl



- We offer...
 - 10,000s of genomes from 1000s of species
 - Gene model annotation or third-party import
 - Comparative genomics e.g. gene trees, alignments
 - Variation annotation
 - Regulatory elements
 - Cross-references, ontologies and protein features

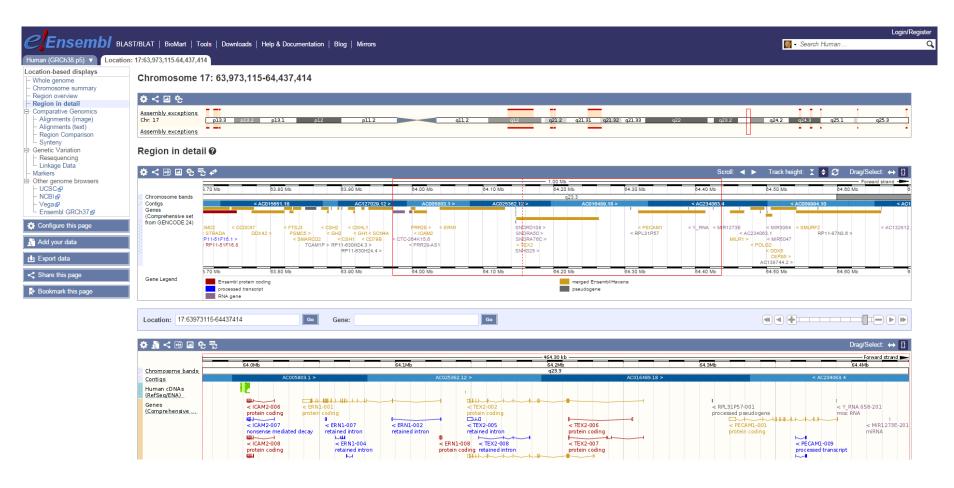
Ensembl as a platform



- We provide...
 - A genome browser
 - Six sites for different parts of the taxonomy
 - MySQL databases
 - FTP flatfiles
 - Perl API
 - REST API

Ensembl: The browser







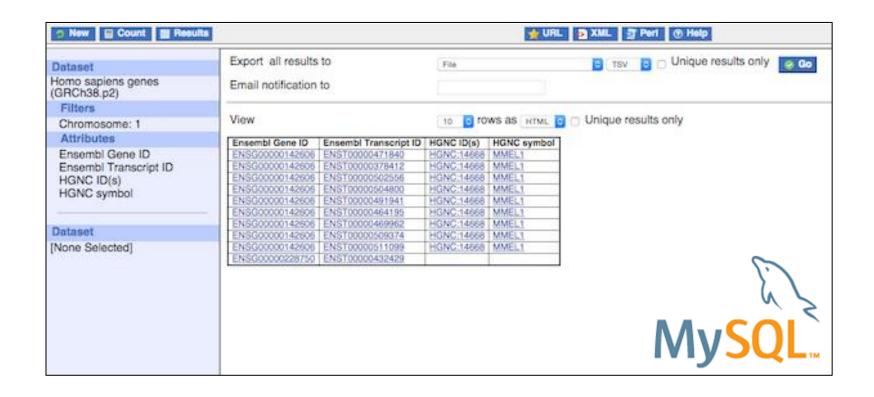
Beyond the browser: user needs



- Bulk export
 - e.g. names and descriptions on all genes from chr 1
- ID conversion
 - e.g. Ensembl IDs for a set of UniProt accessions
- Support for taxonomies and ontologies
 - e.g. all MAPK genes from Ascomycota
- Structured queries
 - e.g. genes annotated as involved in virulence in barley



Beyond the browser: BioMart



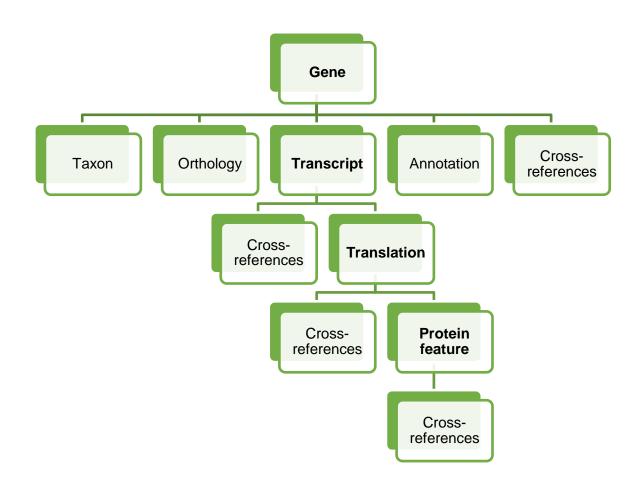




- Gene-centric searching
 - >100 million genes from >30,000 genomes
- Retain data structure
 - Support for nested queries
- Web interfaces to support wide variety of use-cases
- Programmatic APIs to support different languages e.g. R, Python, Java
- Use of search service in project-specific interfaces e.g. EBiSC, HipSci

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Beyond the browser: what next?



Beyond the browser: what next?





















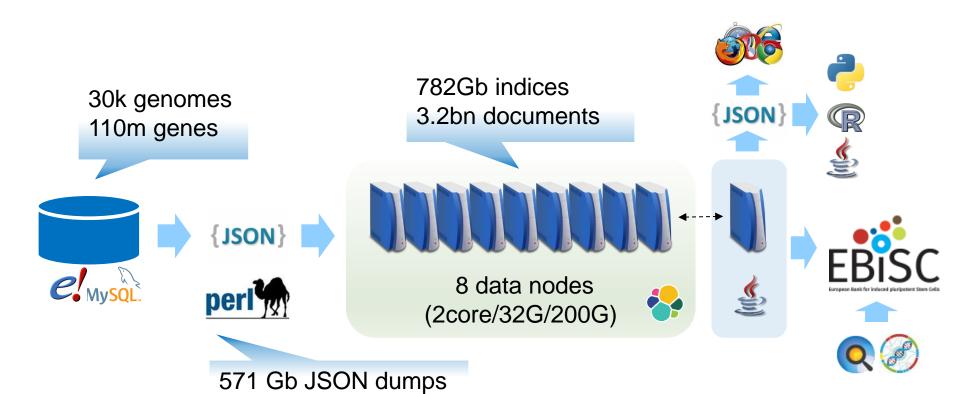
Beyond the browser: what next?





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Elasticsearch: Taking it for a spin





Elasticsearch experiences: The best...

- ✓ Very easy to get started
- ✓ Excellent documentation
- ✓ Strong community
- ✓ Good support for nested data & aggregations
- Decent query and retrieval performance
- ✓ Comprehensive REST APIs
- ✓ Fast bulk loading via Perl API
- ✓ Nice ecosystem of free and commercial plugins
 - ✓ e.g. Marvel, elasticsearch-head





Elasticsearch experiences: The rest...

- Resource hungry
 - Cluster sizing feels like a dark art
 - Node failures can be very hard to recover from
- Some *very* unexpected behaviour acts as a roadblock
 - ➤ 100x leap in index size for some docs 2.0->2.1 (maybe norms?)
 - Unexplained spikes in heap size on some VMs (FS related?)
- No support for ontologies and taxonomies
- Parent-child type relationships aren't very performant
- Marvel & co are not free



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