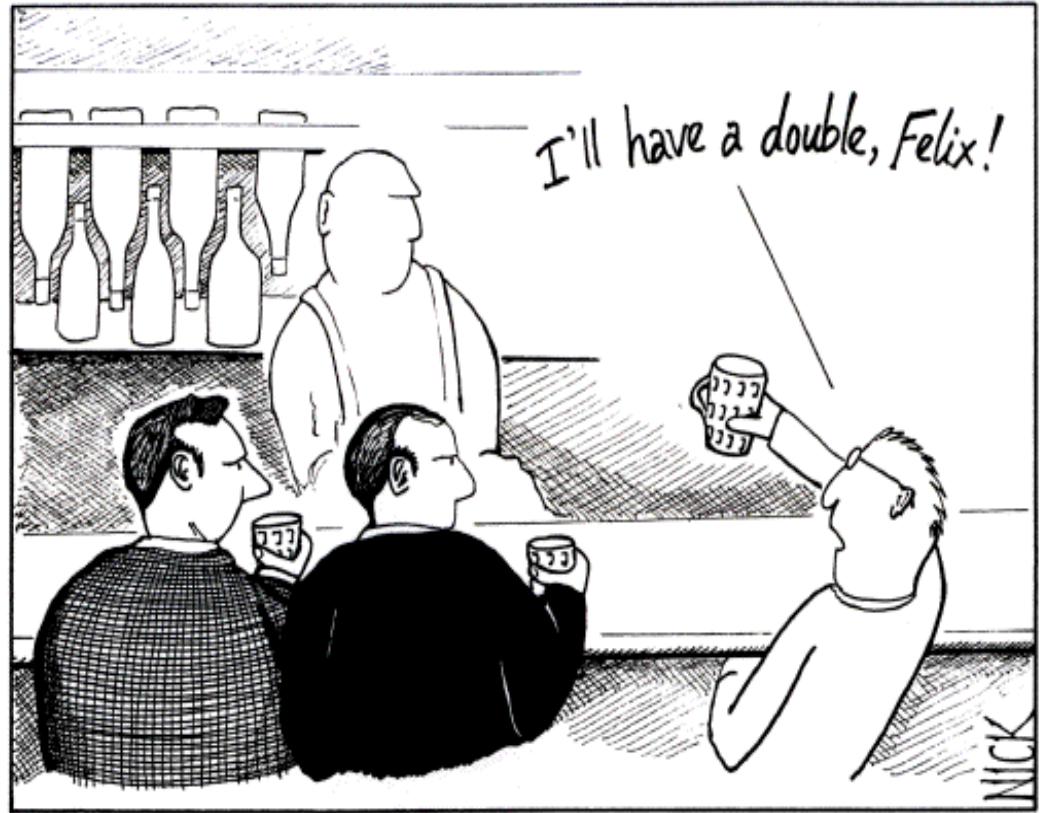


Module 1

Artemis

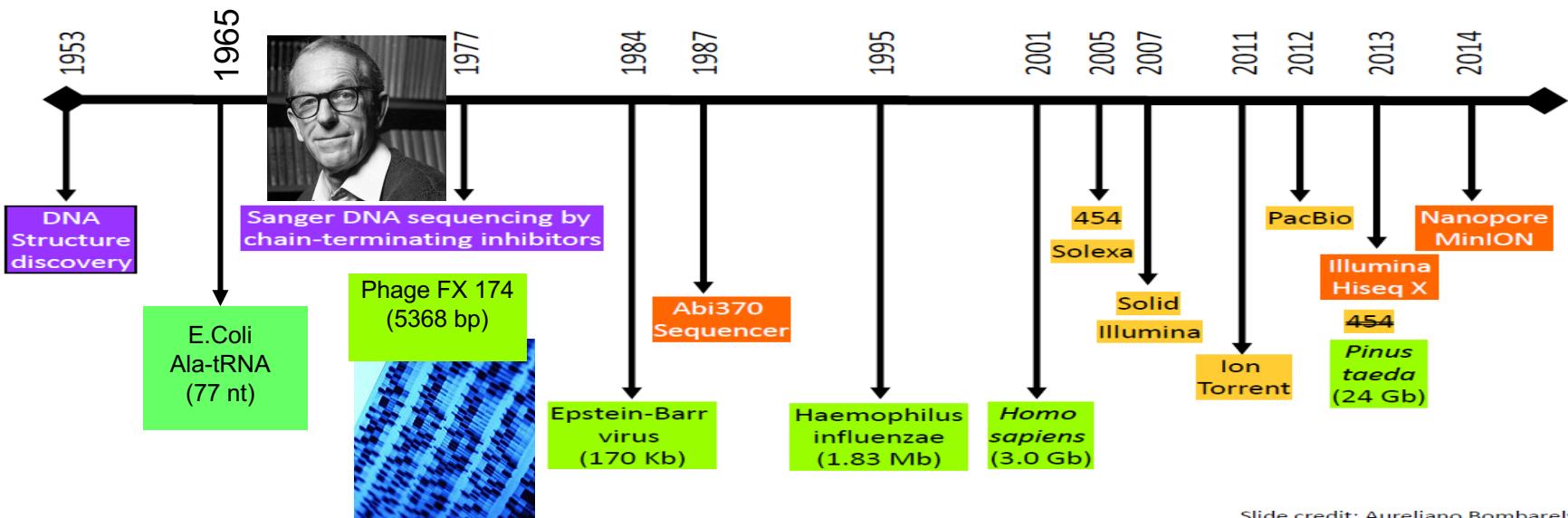
It all started at the pub...



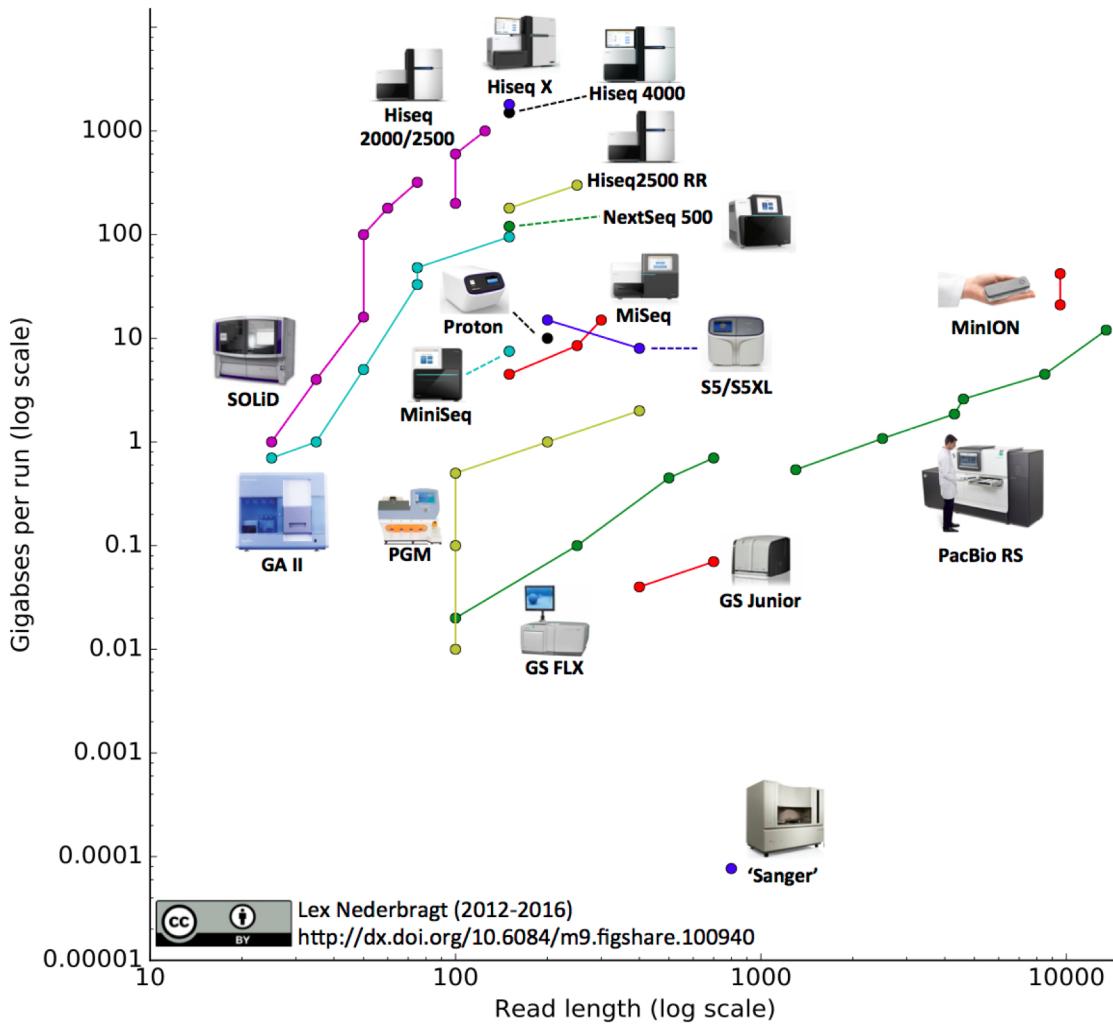
Cambridge, 1953. Shortly before discovering the structure of DNA, Watson and Crick, depressed by their lack of progress, visit the local pub.

Brief history of sequencing ... and bioinformatics

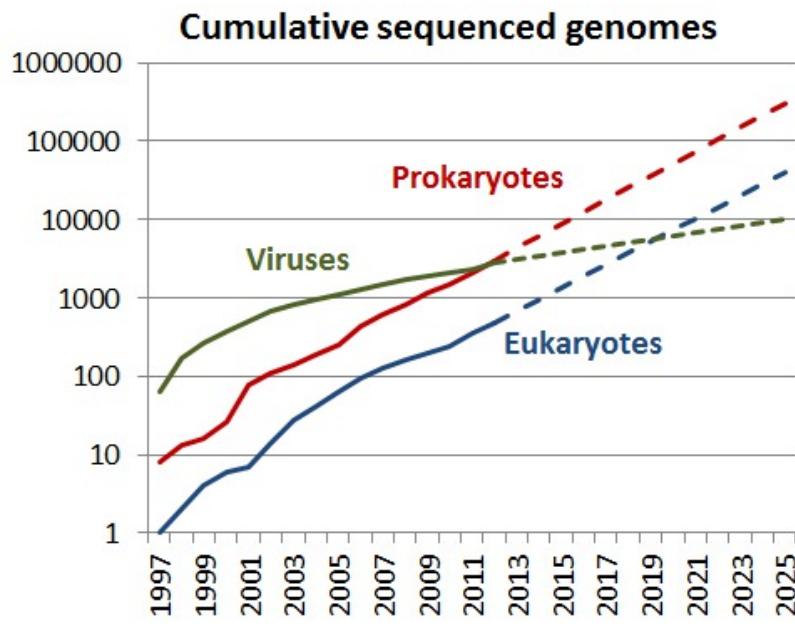
1965	Atlas of protein sequences (Dayhoff)
1977	First program to collect φX174 sequence data (McCallum & Smith)
	Sequence data handling by computers (Staden)
1980	EMBL Data bank
1981	1st Nucleic acid sequence database (Dayhoff)
1982	GenBank started @ NCBI
1988	FastA (Pearson & Lippman)
1990	BLAST (Altschul & Pearson)
1995	Phred (Green)
	TIGR Assembler



Sanger, NGS, 3rdGen



Lex Nederbragt (2012-2016)
<http://dx.doi.org/10.6084/m9.figshare.100940>



Su, Andrew (2013): Cumulative sequenced genomes. figshare.
<http://dx.doi.org/10.6084/m9.figshare.722952> Retrieved 14:45, Nov 29, 2015 (GMT)

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Home > News > Posts > UK leads the world as 100,000 Genomes Project hits the 50,000 genomes landmark to transform NHS patient care

UK leads the world as 100,000 Genomes Project hits the 50,000 genomes landmark to transform NHS patient care

Posted on February 20, 2018 at 10:03 am

The Department of Health and Social Care, NHS England and Genomics England today announced reaching the 50,000 whole human genome sequences landmark within the 100,000 Genomes Project.

It is a milestone that sets the UK on track to fully realise the potential of genomic medicine, deliver better care for patients and establish the UK as the global 'go to' destination in the fast emerging

Genomes Sequenced
5 0 0 6 5

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- [Rare Disease](#) • [Research](#)
- [Sir John Chisholm](#) • [Surveys](#)
- [Vivienne Parry](#)

We have a sequence, now what?

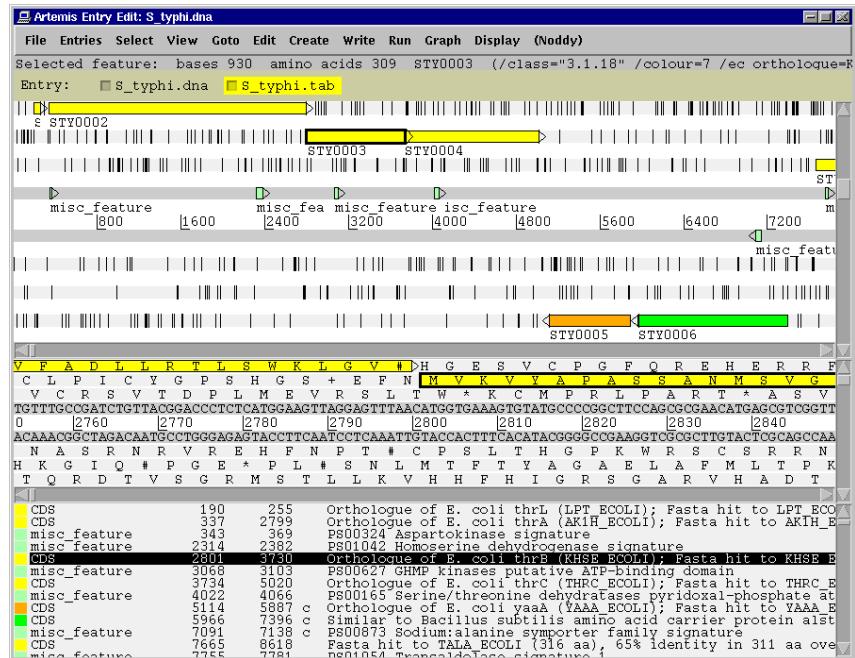




Artemis

Genome browser and annotation tool

- visualization of sequence
 - DNA
 - six frame translation
 - Panoramic and sequence view
- Annotation
 - Features
 - Mapped and listed
 - Editable
 - In layers (entry)
- perform and view analysis
 - basic analysis
 - Basic stats & index can be plotted
 - import and view the results of other searches/analysis
 - Different lines of evidence can be seen together



Artemis

Overview



Overview

Artemis is a free genome browser and annotation tool that allows visualisation of sequence features, next generation data and the results of analyses within the context of the sequence, and also its six-frame translation.



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Publications

Download and Installation

Please see our [GitHub page](#) for download and installation instructions.

Learn and Support

For information and advice on using this software please see our [GitHub page](#).

In addition, an email discussion list called [artemis-users](#) is available and posts to the list since September 2001 are archived at [mail-archive.com](#).

Chado

Artemis and ACT can be used to connect to [Chado](#) databases. They are being developed to store genomic data in the database and perform the same functions as the standard Artemis and ACT.

- [Chado overview](#)
- [Chado admin](#)
- [Chado practical guide](#)
- [Data storage](#)

Tool Type

- [Annotation](#)

Screenshots



- Genome browser and annotation tool (Rutherford et al, 2000)

Related Tools

- [Alien_Hunter](#)
- [Artemis Comparison](#)
- [BamView](#)
- [BLAST](#)
- [GeneDB](#)
- [Production and Curation of Reference Genomes](#)

Developed in JAVA in 1998

- Available for UNIX, Macintosh and Windows
- Developed for annotation and analysis of prokaryotic and small eukaryotic genomes
- Can be used simply as a sequence viewer allowing the visualization of sequence and annotation taken directly from EMBL or GeneBank.



Artemis

Files in Artemis

- It can read several file formats (FASTA, EMBL, GENE BANK, GFF).

Sequence	Annotation
.fasta	.tab
.seq	
.dna	
	.embl

Fasta file

S_typhi.seq - Bloc de notas

Archivo Edición Formato Ver Ayuda

EMBL

Two-character line code indicates the type of information contained in the line

ECRSMA standard; DNA; PRO; 500 BP.
 L40173;
 L40173.1
 10-AUG-1995 (Rel. 44, Created)
 04-MAR-2000 (Rel. 63, Last updated, Version 4)
 Erwinia carotovora repressor (rsmA) gene, complete cds.
 repressor; rsmA gene.
 Pectobacterium carotovorum
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae;
 Pectobacterium.
 [1]
 1-500
 Cui Y., Chatterjee A., Liu Y., Dumenyo C.K., Chatterjee A.K.;
 "Identification of a global repressor gene, rsmA, of Erwinia carotovora
 subsp. carotovora that controls extracellular enzymes,
 N-(3-oxohexanoyl)-L-homoserine lactone, and pathogenicity in soft-rotting
 Erwinia spp";
 J. Bacteriol. 177(17):0-0(1995).
 GOA; Q47620; Q47620.
 SWISS-PROT; Q47620; CSRA_ERWCA.
 Key Location/Qualifiers
 source 1..500
 /db_xref="taxon:554"
 /organism="Pectobacterium carotovorum"
 /strain="71"
 /sub_species="carotovora"
 -10_signal 107..112
 /gene="rsmA"
 RBS 235..239
 /gene="rsmA"
 CDS 246..431
 /codon_start=1
 /db_xref="GOA:Q47620"
 /db_xref="SWISS-PROT:Q47620"
 /note="putative"
 /transl_table=11
 /gene="rsmA"
 /function="global repressor"
 /protein_id="AAA74502.1"
 /translation="MLILTRRVGETLIIGDEVTVLGVKGNQVRIGVNAPKEVSVHRE
 EIYQRIQAEKSQPSTY"
 Sequence 500 BP; 140 A; 101 C; 120 G; 139 T; 0 other;
 ggatccggca agcagggatag aaaaatgtttt accttcgat attctgaac tttatcatgt
 cagtctgtt gtttgtataaa caaaacgcata agctactgtt atccgataaaa ctaacaatgt
 gtgacaaacc gggatgtat ggtgttgat tttatccatgtc taggtttac ttccatcgac
 acatgtatggta taatggcgaa gagacagaga gaccgcac ttatataatct ttcacaggac
 aaaaatgtt tattttgtt ctgtcgatgtt gcgaaaccctt catatccgc gatggggat
 cggatccgtt attaggatgtt aaaggcaacc aggttgcgtt tttgtttatgc gacccatgt
 agttttgtt ccacatgtt gagatccatc aggttgcgtt ggcggaaatccatc
 cgtcatatgtt attggatgtt ctgtcgatgtt tcgcgggac gatggggat
 tccccccacac atttatcgat

Header

Sequence



Artemis

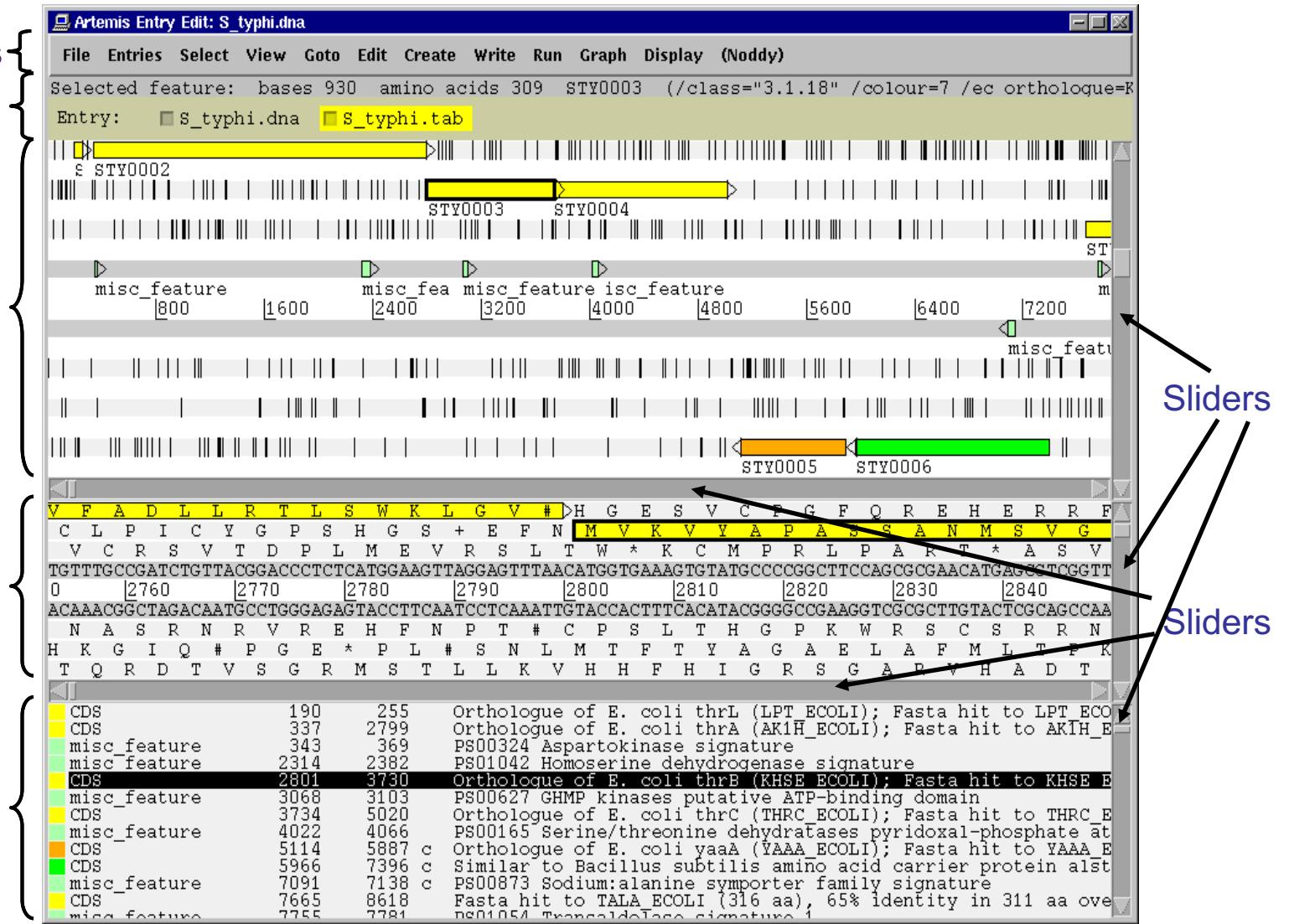
Drop Down Menus

Entry Button Line

Main Sequence View Panel

Magnified Sequence View Panel

Feature Menu





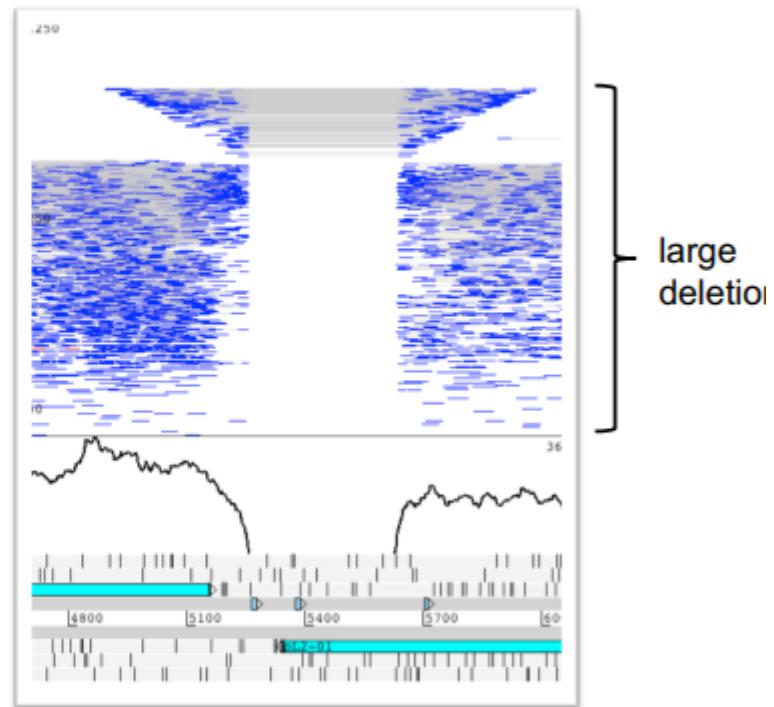
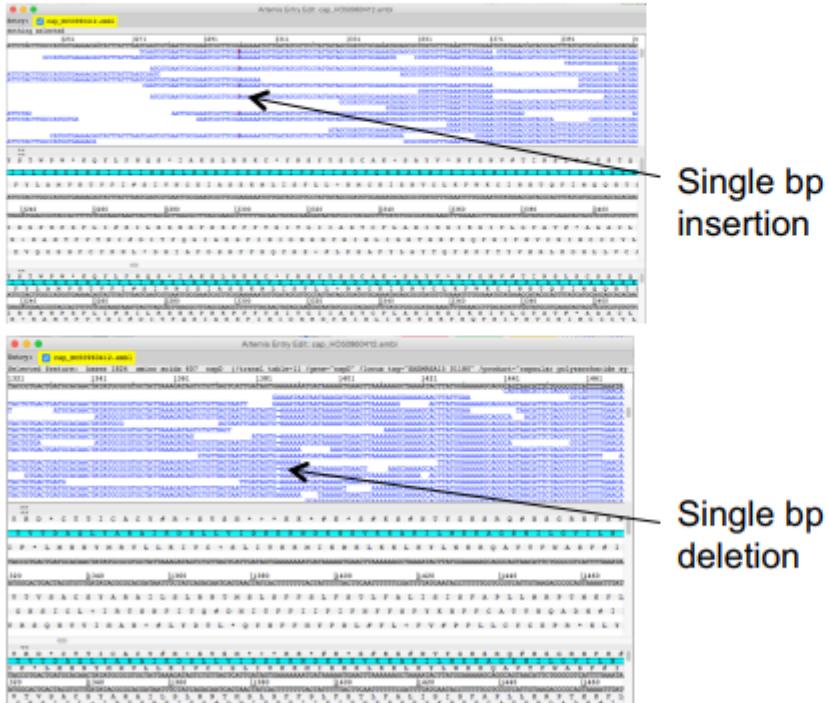
ARTE MUS

THE NEXT GENERATION

artwork by Simon Harris

Artemis, the next generation

- Illumina data (bam files)
 - identification of indels

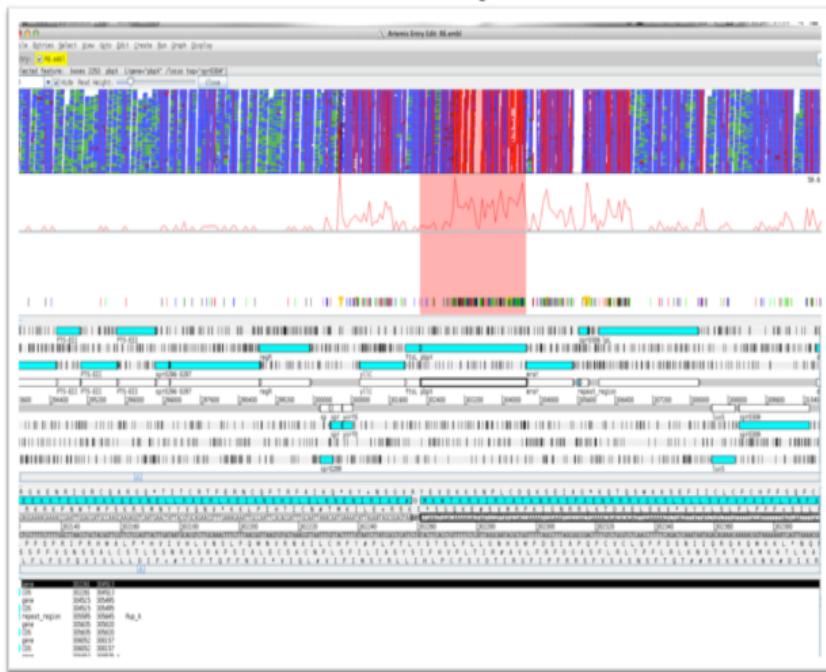


- we will see it on Module 4

Artemis, the next generation

auto-generation of SNP density and coverage plots

RNAseq mapping



Illumina data (bam files)



Features of the Artemis module

- Exercise 1 Familiarize with Artemis
 - Loading sequences and annotation files
 - changing the view
 - Searching and getting around
- Exercise 2
 - Graphs and plots
- Exercise 3
 - Basic analysis
 - Generating features
- Exercise 4 Feature editing
 - Adding and Modifying annotations
 - Finding evidence : Database searches



**hands
on**

The logo consists of the words "hands on" in a bold, black, sans-serif font. On the left side of the "h", there is a blue handprint. On the right side of the "n", there is another blue handprint. The handprints are composed of several blue ink-like smudges and splatters.