Bioinformatics

- a definition ?

The design, construction and use of software tools to generate, store, annotate, access and analyse data and information relating to Molecular Biology

OR

Biologists doing "stuff" with computers?

Here we consider the <u>use</u> of Bioinformatics tools rather than their design and construction

Here we consider the <u>access</u> and <u>analysis</u> of data and information items rather than their generation, storage or annotation

Databases – Genes to Genomes

Primary DNA Sequence Databases

Original submission by experimentalists Content controlled by the submitter







NSDC International Nucleotide Sequence Database Collaboration

Primary Protein Sequence Databases









Protein knowledgebase consists of two sections:

- Swiss-Prot, manually annotated, reviewed.
- TrEMBL, automatically annotated, **not** reviewed.

Built from primary data



Submission by experimentalists Controlled by the submitter

akin to the primary research literature

akin to the review literature

RefSeq

non-redundant richly annotated DNA, RNA, protein diverse taxa

Protein domains, motifs, families



Protein domains/families represented as alignments and HMMs

Derived primarily from **UniprotKB** and **Genpept**



Aligned protein domains and consensus sequences

Derived automatically from UniprotKB



Conserved "blocks" of protein domain alignments

Derived from a subset of UniprotKB



Manually curated models for several hundred protein domains

Derived from proteins from completely sequenced genomes

Protein domains, motifs, families



Protein motifs/domains represented as **Patterns** and/or **HMM**s

Both derived from UniprotKB/Swissprot

Patterns are for highly conserved short regions. Example:

R-P-C-x(11)-C-V-S

HMMs are for less conserved longer regions.

Often there will be pattern(s) and an HMM for one domain.



Protein domains, motifs, families



Representations of domains by motif patterns (finger**PRINTS**)

Derived from UniprotKB

Each FingerPrint is compose of a series of conserved regions (motifs)

A match with a FingerPrint is thus an order set of motif matches



Residue Number

Percentage Sequence Identity to Motif

Database Access



Interpro is a consortium of member databases

Interpro defines protein families, domains, regions, repeats and sites according to matches against member databases

Interpro enables any subset of member databases to be searched together

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Genome databases



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EBI / Sanger Institute

Ensembl Species





Armadillo Dasypus novemcinctus



Caenorhabditis elegans



Clona savignyi



Chicken Gallus gallus





Dog Canis familiaris



Elephant Loxodonta africana





Gorilla Gorilla gorilla







Human Homo sapiens





Kangaroo rat Dipodomys ordii



Lesser hedgehog tenrec Echinops telfairi





Medaka Oryzias latipes





Mouse Mus musculus









Plg Sus scrofa



Ochotona princeps





Rabbit Oryctolagus cuniculus









Shrew Sorex araneus



Sloth Choloepus hoffmanni



Stickleback Gasterosteus aculeatus



Tarsler Tarsius syrichta



Tetraodon Tetraodon nigroviridis

Tree Shrew Tupaia belangeri

Wallaby Macropus eugenii







Zebra Finch Taeniopygia guttata





EnsemblPlants Species



Arabidopsis lyrata Gramene | Arabidopsis lyrata



Arabidopsis thaliana Gramene | Arabidopsis thaliana Columbia



Brachypodium distachyon Gramene | Brachypodium distachyon (L.) Beauv



Oryza sativa Gramene | Oryza sativa Nipponbare (Japonica rice)



Oryza sativa indica group Gramene | Oryza indica 93-11 (Indica rice)



Populus trichocarpa Gramene | Populus trichocarpa



Sorghum bicolor <u>Gramene</u> | Sorghum bicolor BTX623



Vitis vinifera Gramene | Vitis vinifera PN40024

NASC <u>e!</u>



