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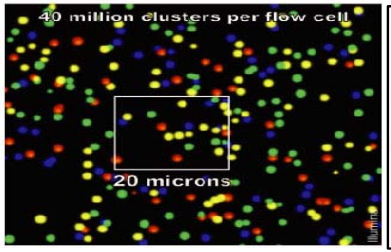
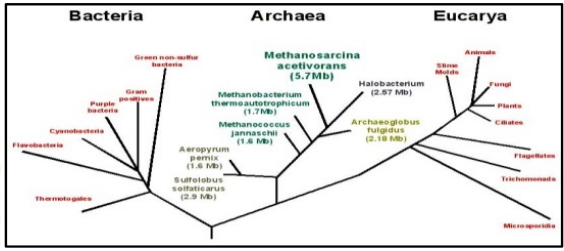


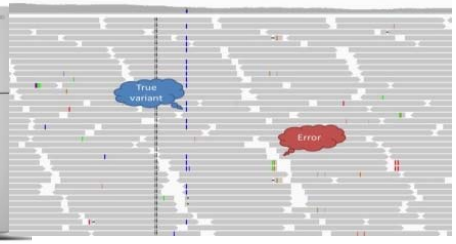


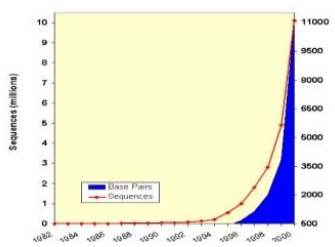
Ontology, and Identification of Molecular Pathways

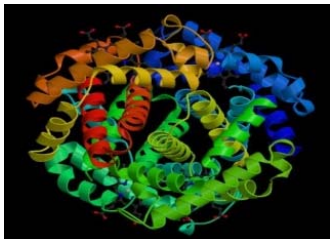
北京大学生物信息学中心 魏丽萍

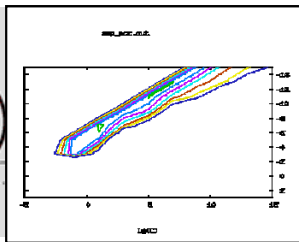
Liping Wei, Ph.D.

Center for Bioinformatics, Peking University









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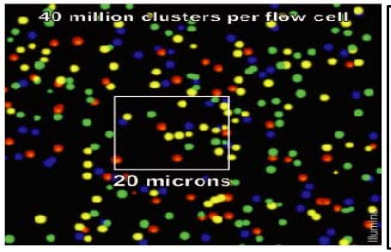

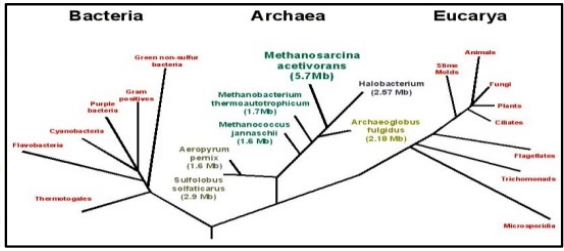

Unit 3: Annotations in Gene Ontology

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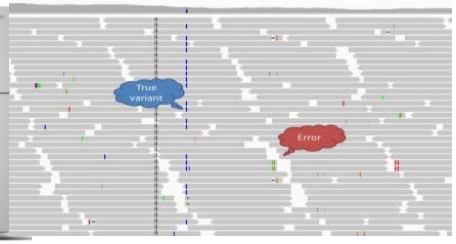

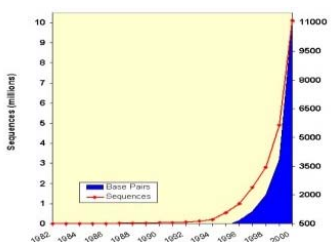

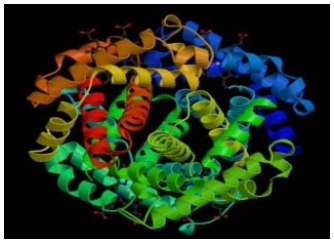

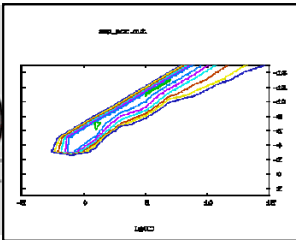

Three types of GO annotations

1. Annotation through manually-reviewed experimental evidence
2. Annotation through manually-reviewed computational analysis evidence
3. Annotation by electronically-generated computational analysis evidence

http://www.geneontology.org/

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Annotation through manually-reviewed experimental evidence

IDA	Inferred from Direct Assay
IPI	Inferred from Physical Interaction
IMP	Inferred from Mutant Phenotype
IGI	Inferred from Genetic Interaction
IEP	Inferred from Expression Pattern
EXP	Inferred from Experiment

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Annotation through manually-reviewed computational analysis

ISO	Inferred from Sequence Orthology
ISA	Inferred from Sequence Alignment
ISM	Inferred from Sequence Model
ISS	Inferred from Sequence or Structural Similarity
IGC	Inferred from Genomic Context
IBA	Inferred from Biological aspect of Ancestor
IBD	Inferred from Biological aspect of Descendant
RCA	Inferred from Reviewed Computational Analysis
IKR	Inferred from Key Residues
IRD	Inferred from Rapid Divergence

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Annotation by completely electronically generated computational analysis without manual review

IEA	Inferred from Electronic Annotation

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Misc other manual annotations

TAS	Traceable Author Statement
NAS	Non-traceable Author Statement
IC	Inferred by Curator
ND	No biological Data available
NR	

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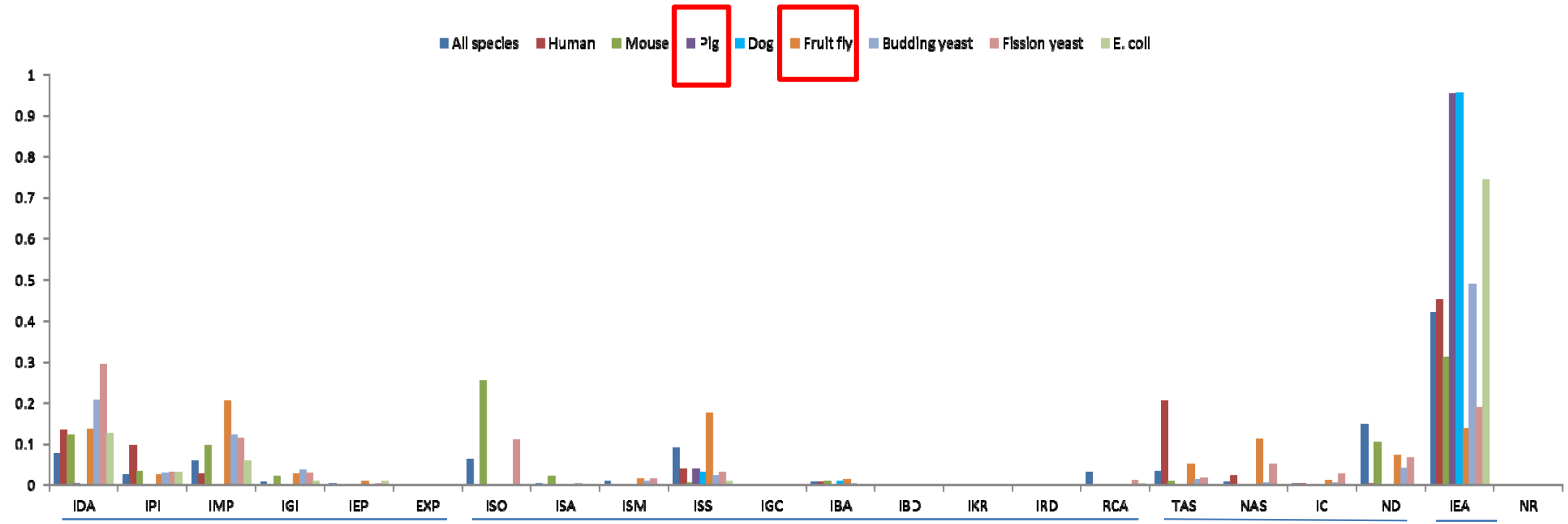

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生物信息学：导论与方法
Bioinformatics: Introduction and Methods

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