

### A. BCPL profile

#### 1. CURRENT RESEARCH

##### 1. Genome sequence analysis

Genome analysis, annotation & interpretation of genomics data ChIP-seq, RNA-seq, expression analysis of complex genomic sequences Comparative transcriptomics & proteomics Metabolic pathway inference from genomic annotation, large-scale methods

##### 2. Comparative genomics

Whole-genome comparison, metrics for species/strain taxonomy & classification Metabolic reconstruction, pathway detection & evolutionary history inference Metabolic innovation, synthetic design of metabolic reaction & pathway variants Horizontal gene transfer, detection, inference, the Last Universal Common Ancestor

##### 3. Algorithms & databases

Genome repository databases, pangenome/paleogenome analysis, ortholog detection Genome-aware algorithms for phylogenetic profiles, gene clusters, gene fusions Document clustering & concept discovery, ontology inference Compositional bias detection & masking, applications for database searches Sequence matching, network visualization, large-scale sequence comparison Ancestral state reconstructions: from protein families to genome content

##### 4. Systems biology

Biological network topology analysis & interpretation, functional module detection Protein interaction detection, multi-domain decomposition of protein families Translational bioinformatics, pathological versus physiological stress Translational bioinformatics, low-dose ionizing radiation exposure

##### 5. Science policy

Science communication: history of science, metaphors in science, ancient science Community actions for research & training: GEBA, GSC, Mikrobiokosmos, OHSCB, ISCB Historical development of a new field: computation in biology, and beyond

#### 2. FUTURE PROSPECTS

Synthetic biology: context-free module detection via evolutionary inference Ancestral state reconstructions: from genome content to genomic sequences Astrobiology (exobiology): life detection protocols, universal reaction inference

### B. BCPL history

#### 1. EBI (1996-2005)

Established the Computational Genomics Group at the European Bioinformatics Institute (EBI) Pioneered work in genome analysis-annotation, clustering, text mining, genome aware methods Overseen more than 50 research staff over a period of approximately 10 years

#### 2. INA-CERTH (2006-2007)

Established the Computational Genomics Unit at the Institute of Agrobiotechnology (INA) Attracted a number of EBI colleagues from Cambridge UK to Thessalonica GR, group of 10

Installed computational infrastructure, high-end servers & storage systems at INA, now INAB

### 3. KCL (2008-2010)

Established the Centre for Bioinformatics at King's College London (KCL) Overseen the management & activities of five research groups at KCL Founded & expanded the MSc & PhD courses in Bioinformatics at KCL

### 4. CERTH/AUTH/UofT (2011-2013)

Associate Researcher at CERTH, PI for the Microme project Associate Researcher at AUTH (Aristotle University), PI for the Cerebrad project Visiting Professor at the University of Toronto, research in RNAseq sequence analysis