

# KOSTAS LYKOSTRATIS

ROOM 3, FLAT 3F  
LANGTON CLOSE  
LONDON  
WC1X 0HD

NATIONALITY: GREEK • D.O.B: 29.01.1980

MOBILE 07966 294435 • E-MAIL [kostas@ludwig.ucl.ac.uk](mailto:kostas@ludwig.ucl.ac.uk)

## EDUCATION

---

### 2002 **PhD, Bioinformatics & Systems Biology**

#### University of London

*Thesis:* Computational Modelling of the Dynamics of Signalling Pathways

*Description:* In this project, computational models of signal transduction processes will be built, and predictions from the models will be compared to experimental results. The aim will be to develop an understanding of the importance of the different stages in the signal transduction processes involving Rho, to explore the effects of and sensitivity to changes at different stages, and, ultimately, to explore how cytoskeletal rearrangement and cell motility can be controlled. It is essential that the computational modelling is closely linked to experimental work, with the goal of developing an interaction between model and experiment. Effort will be focused on the design and implementation of a relational database, generation of computer models, complementary experimental tests and refinement and expansion of software tools.

*Techniques:* Systems Biology software; Database design; Java programming; Perl scripting.

### 2002 **MRes, Bioinformatics** (Awarded Distinction)

#### University of York

- Biological sequence analysis
- Programming in Perl
- Programming in JAVA
- Databases
- Machine learning
- Pattern recognition and Neural Networks
- Molecular aspects of disease
- Structural Bioinformatics

### 2001 **BSc, Human Genetics**

#### University of Leicester

2:1 Honours degree.

### 1998 **Panhellenics** (Greek A-Level Equivalent)

#### Skydra Senior College

Biology (85%), Chemistry (80%), Physics (70%), Modern Greek Literature (66.5%)

## AWARDS

---

Best Annual Poster Presentation, Biological Sciences Department, University of Leicester 2001

## RESEARCH EXPERIENCE

---

- May-Sep 2002**      **Astra Zeneca R&D (MRes External placement)**  
Design of an Automated SNP Viewer  
The project involved the design of a system for automated mining of SNP-information and the generation of new information previously unavailable. An interactive viewer was developed to aid visualisation of the gene of interest, the coding region, the SNP locations and the effects of the polymorphisms at the protein level. The developed system was used as a template for the identification of SNPs that might play key role in disease genes or genes with differential behaviour on drugs and medical treatments.  
*Techniques:* Perl programming, JAVA programming, CGI scripting, HTML editing, SRS.
- Feb-Apr 2002**      **MRes project II**  
Identification of conserved core structures and residues in kinesins  
Structural alignments of all the kinesin motor domain structures confirmed that these enzymes share a common core structure and revealed extensive similarity outside the conserved nucleotide binding site residues. A model structure composed of the structurally invariant core residues was constructed. This model was subsequently used to scan the entire RCSB PDB database for structurally similar proteins.  
*Techniques:* Molecular structure analysis, multiple structural alignments and Perl scripting.
- Nov-Dec 2001**      **MRes project I**  
Computational Analysis of Microarray Data  
*Techniques:* Examination of gene expression levels of 1611 genes using Hierarchical clustering, K-means clustering and Principal Component Analysis.
- Oct-Apr 2000-2001**      **BSc final year project**  
Investigation into the methylation state of Caspase 8 and E-cadherin in cancer cell lines and formalin fixed tissues from neuroblastomas.
- June-Sept 2000**      **Research assistant** (Leicester Royal Infirmary)  
Developing experimental protocols for the design and refinement of a new experimental technique: DNA bisulfite treatment and Methylation Specific PCR.

## SKILLS

---

- Computing**      Bioinformatics Software:  
Systems Biology Modelling (SBW, Jarnac, Jdesigner, E-Cell, Virtual-Cell, GEPASI, SBML, CellML and others), Molecular Modelling (Quanta, Rasmol, VMD, SwissPDB); Structural & Sequence Alignments (CAMINE, VAST, DALI, ClustalX, GCG package, BioEdit, HMMer, PSI-BLAST and others), Phylogenetic Analysis (Treeview, PAUP), Microarray Data Analysis (EisenLab Cluster-Treeview, Jexpress, TIGRMultipleExperimentViewer, AMANDA, GENESPRING);  
Other Software & Operating Systems:  
Microsoft Office, Reference Manager, Macromedia Dreamweaver - Flash, Corel Draw, Adobe Photoshop, Windows and Unix-Linux operating systems;
- Development**      Programming Languages and Database Systems  
JAVA (Applets, Applications, Servlets, JSPs, SWING-AWT, Graphics 2D); PERL (CGI, Tk); JavaScript; HTML; XML; SQL (ORACLE 8i, MySQL); Unix shell scripting (Bash, T-shell).