Cancer Bioinformatics

Why we focus on Cancer Bioinformatics

Bioinformatics is a new interdisciplinary area involving biological, statistical and computational sciences. Bioinformatics will enable cancer researchers not only to manage, analyse, mine and understand the currently accumulated, valuable, high-throughput data, but also to integrate these in their current research programmes. The need for bioinformatics will become ever more important as new technologies increase the already exponential rate at which cancer data are generated.

What we do

• We work alongside clinical and basic scientists to support the cancer projects within the BCI. This is an ideal partnership between scientific experts, who know the research questions that will be relevant from a cancer biologist or clinician's perspective, and bioinformatics experts, who know how to develop the proposed methods to provide answers.

• We also conduct independent bioinformatics research, focussing on the development of computational and integrative methods, algorithms, databases and tools to tackle the analysis of the high volumes of cancer data.

• We are actively involved in the development of bioinformatics educational courses at the BCI. Our courses offer a unique opportunity for biologists to gain a basic understanding in the use of bioinformatics methods to access and harness large complicated high-throughput data and uncover meaningful information that could be used to understand molecular mechanisms and develop novel targeted therapeutics/diagnostic tools.

For more details, please visit: www.bci.qmul.ac.uk/study-with-us/bioinformatics.html

Cancer Bioinformatics

Key Publications

- Kadaba *et al.* Imbalance of desmoplastic stromal cell numbers drives aggressive cancer processes. *The Journal of pathology 2013;* 230(1):107-17.
- Ullah *et al.* SNPnexus: a web server for functional annotation of novel and publicly known genetic variants (2012 update). *Nucleic Acids Res* 2012; 40 (Web Server issue):W65-70.
- Cutts *et al.* O-miner: an integrative platform for automated analysis and mining of -omics data. *Nucleic Acids Res* 2012; 40 (Web Server issue):W560-8.
- Gadaleta *et al*. A global insight into a cancer transcriptional space using pancreatic data: importance, findings and flaws. *Nucleic Acids Res* 2011; 39: 7900-7.
- Cutts *et al.* The Pancreatic Expression database: 2011 update. *Nucleic Acids Res* 2011; 39 (Database issue): D1023-8.
- Gadaleta *et al*. Online resources of cancer data: barriers, benefits and lessons. *Briefings in Bioinformatics* 2011; 12: 52-63.
- Froeling *et al*. Retinoic Acid-Induced Pancreatic Stellate Cell Quiescence Reduces Paracrine Wnt-<beta>-Catenin Signaling to Slow Tumor Progression. *Gastroenterology* 2011; 141(4):1486-97.
- Wang Y *et al.* CEACAM6 attenuates the ability of adenovirus to infect cancer cells by blocking Src-mediated viral trafficking. *Journal of Clinical Investigation* 2009; 119:1604-15.

Who does the research

Dr. Claude Chelala   Senior Lecturer in Bioinformatics

Major Funders

- Barts and The London Charity
- Breast Cancer Campaign
- Cancer Research UK

http://www.bci.qmul.ac.uk/research/lab-facilities/bioinformatics

Barts and The London
School of Medicine and Dentistry

www.bci.qmul.ac.uk