

## CV and publications of Alexey Larionov

*BSc in Medicine, MSc in Bioinformatics, PhD in Molecular Oncology*

### Employment

#### **2013-present: Research Associate (Bioinformatics)**

*Acad. Lab. of Med. Genetics, School of Clinical Medicine, Cambridge University & Statistics and Computation Biology Group, CRUK Cambridge Institute*

#### Overall responsibilities:

- Design and implement pipelines for bioinformatics analyses required within the research group
- Support and teach non-bioinformatics using this pipelines

#### Examples of specific tasks:

- Design and implement pipeline for WES data analysis from fastq to annotated vcf.
  - Briefly: the current pipeline is written in shell, following the GATK best practices: source data QC; BWA MEM (GRCh37); bam-files QC, clean-up, sorting, marking PCR duplicates (samtools, picard, GATK tools); bam files pre-processing (local realignment and base quality recalibration); variant calling (GATK HC in g.VCF mode); variants filtering (a combination of VQSR and hard-filters); annotation with VEP; export to plain text files for downstream analyses in R.
  - The pipeline has been deployed in 3 versions: in the University cluster, in CRUK CI cluster and on a departmental server (for flexibility and to speed-up data processing).
- Continuously evaluate new tools, resources and algorithms relevant to the bioinformatics tasks within the group, suggest and implement changes to the pipelines (e.g. moving analyses to GRCh38)
- Continuously evaluate IT infrastructure available for the group (departmental servers, CRUK and University HPC clusters), provide recommendations for purchases of IT equipment for the group (e.g. NAS boxes, storage blades to install within the shared departmental racks etc); explore external computational facilities (e.g. deploying the pipeline elements on AWS).
- Perform down-stream analyses after generating VCF files: e.g. rare variants association analyses, selection of variants based on biological functions, etc (stat analyses are implemented in R; others – depending on the specific project objectives).
- Contribute to preparation of manuscripts and grants applications, present bioinformatics results on international conferences.
- Setup WES library preparation in the lab and teach the research assistant employed for the library preparations thereafter (this was a one-off wet-lab task; however, I was doing it because I had the skills and this was needed for the group at the time).

#### Main results:

During this employment I have processed many hundreds (1000+) of WES samples for different projects within the group, which have been presented on scientific conferences (publications in preparation) and used for successful grant applications. Along with the bioinformatics tasks carried for this employment, I continued publishing and teaching about endocrine treatment and resistance in breast cancer, gradually completing the commitments from my previous employment in Edinburgh University.

### **2008-2013: Research Fellow**

*Edinburgh Cancer Research Centre, The University of Edinburgh, UK*

#### Overall responsibility:

Study molecular mechanisms and markers of endocrine resistance and response in breast cancer.

#### Examples of specific tasks:

- Selection of optimal sets of informative genes (based on differential gene expression between responders and non-responders in training datasets)
- Design and validation of classification algorithms based on the selected genes (comparing logit regression models, SVM and decision tree- based algorithms).
- Collection and processing clinical annotations for available specimens
- Microarray data analysis (mainly R-libraries for Illumina microarray data processing)
- Extraction of RNA from frozen biopsies and submitting for micro-array analyses to local genomics facilities
- Supervision and support for PhD, MSc and MD students
- Preparation of publications, grant applications and presenting results on international meetings

#### Main results:

The results were reported in a number of well cited papers and scientific meetings (see list of publications). Along with the bioinformatics and wet-lab tasks during this employment I completed MSc in Applied Bioinformatics (Cranfield University, 2012) and PgCert in Academic Practices (Edinburgh University, 2013).

### **2002 – 2007: Research Fellow**

*Breast Research Unit, Edinburgh Western General Hospital, HNS Lothian, UK*

#### Overall responsibility:

Validate micro-array gene expression data with qPCR for a series of clinical biopsies of endocrine-treated breast cancer (before and after treatment):

#### Examples of specific tasks:

- Development of real-time PCR methodology for gene expression measurements in clinical samples of breast cancer
- Extraction of RNA, design and validation of primers, qPCR data analysis
- Collecting and organizing clinical annotations for data analysis
- Organizing clinical samples collection and storage

#### Main results:

Analyzed 200+ clinical biopsies for expression of tens of genes pre-selected from micro-array results. Summarized my experience in qPCR data analysis in a first-author paper that has been cited 500+ times (Larionov *et al*, BMC bioinformatics, 2005).

### **2001 – 2002: Clinical Research Associate**

*PSI Pharma Support Inc., St. Petersburg, Russia*

- Monitoring patients' well-being and regulatory compliance in a breast cancer clinical trial.

### **Jan-Dec 2000: Postdoctoral Research Fellow** (fellowship awarded by the RS)

*Breast Research Unit, The University of Edinburgh, UK*

- Study local estrogen production in breast cancer tissues and in other peripheral tissues. Resulted into several well-cited publications (see publications prior 2004).

### **1992 – 1999: Postgraduate student then PhD student then Research scientist**

*N.N.Petrov Institute of Oncology, St. Petersburg, Russia*

- Completed postgraduate specialization and PhD in clinical oncology
- Obtained a grant from the Russian Foundation for Fundamental Research for studying extra-gonadal estrogen production

## **Education**

### **2011-2013 Postgraduate Certificate in Academic Practices**

Edinburgh University, UK

### **2010-2012 MSc in Applied Bioinformatics** (bursary awarded by BBSRC)

Cranfield University, UK

### **2001-2002 Postgraduate Certificate in computer sciences**

State Polytechnical University, St. Petersburg, Russia

### **1994-1997 PhD in experimental oncology** - recognized by UK NARIC

N.N.Petrov Institute of Oncology, St. Petersburg, Russia

### **1992-1994 Specializing in clinical oncology**

N.N.Petrov Institute of Oncology, St. Petersburg, Russia

### **1984-1992 BSc in clinical medicine** (with distinction) - recognized by UK NARIC

I.P.Pavlov State Medical University, St. Petersburg, Russia

## **Additional bioinformatics trainings**

**2015** CRUK Bioinformatics Summer School: Best practices in the analysis of **RNA-Seq** and **ChIP-Seq** data (27-31 July, Cambridge)

**2015** Wellcome Trust Advanced Course in Human Genome Analysis: Genetic **Analysis of Multifactorial Diseases** (11-17 July, Hinxton)

**2015** Variant analysis with **GATK** (23-24 April 2015, Cambridge)

**2014** **ARCHER** Summer School: Introduction to **High Performance Computing & Programming with MPI** (30 June-4 July, Edinburgh)

## **Other academic activities**

**Teaching** Invited lecturer and marked exam papers: BSc course in Clin. Pharmacology, *Edinburgh University*, **2012-2016**

Projects supervision: MSc course in Molecular Medicine, *Cranfield University*, **2011**

**Refereeing & editing** Refereed papers for BMC Bioinformatics, J. Computational Sci, Breast Cancer Res, Breast Cancer Res and Treatment and other journals; edited book for Springer

## Publications

My hi-index is 20. The citation counts below were taken from Google Scholar on 23Nov 2016. These are only selected publications. See more publications on Google Scholar <https://scholar.google.co.uk/citations?hl=en&user=hGLjJ-kAAAAJ>

### Book edited

**A. Larionov** (editor) (2015) Resistance to aromatase inhibitors in breast cancer. Springer, ISBN: 978-3-319-17971-1

### Book chapters

**Larionov A** (2016) Novel translational research of neo-adjuvant endocrine therapy. Chapter in *Personalized Treatment of Breast Cancer*. Editors: Masakazu Toi, Eric Winer, John Benson, Suzanne Klimberg.

Springer, ISBN: 978-4-431-55551-3

**Larionov A & Miller WR** (2015) Prediction of Response to Aromatase Inhibitors in Breast Cancer. Chapter in *Resistance to Aromatase Inhibitors in Breast Cancer*. Editor: Alexey A Larionov, Series: *Resistance to Targeted Anti-Cancer Therapeutics*. Springer, ISBN: 978-3-319-17971-1

Sims A, **Larionov A**, et al. (2013) Use of microarray analysis to investigate EMT gene signatures. Chapter in *Adhesion Protein Protocols*. Editor Amanda S. Coutts, Springer ISBN 978-1-62703-538-5

### Articles

Flageng MH, **Larionov A**, et al. (2016) Treatment with aromatase inhibitors stimulates the expression of epidermal growth factor receptor-1 and neuregulin 1 in ER positive/HER-2/neu non-amplified primary breast cancers. *J Steroid Biochem Mol Biol*. Epub ahead of print. PMID: 27343990.

Turnbull A, ... **Larionov A et al** (2015) Accurate Prediction and Validation of Response to Endocrine Therapy in Breast Cancer. *J Clin Oncol*. 33:2270-2278. PMID: 26033813 **Cited: 20**

Turnbull A, ... **Larionov A, et al** (2012) Direct integration of intensity-level data from Affymetrix and Illumina microarrays improves statistical power for robust reanalysis. *BMC Med Genomics* 5:35 PMID: 22909195 **Cited: 21**

Miller WR and **Larionov AA** (2012) Understanding the mechanisms of aromatase inhibitor resistance. *Breast Cancer Res* 14:201 PMID: 22277572 **Cited: 43**

Sokolenko A ... **Larionov A et al** (2012) High prevalence and breast cancer predisposing role of the BLM c.1642 C > T (Q548X) mutation in Russia. *International Journal of Cancer*. 130(12):2867-2873. PMID: 21815139 **Cited: 34**

Miller WR, **Larionov A, et al.** (2012) Sequential changes in gene expression profiles in breast cancers during treatment with the aromatase inhibitor, letrozole. *Pharmacogenomics J* 12(1):10-21. PMID: 20697427 **Cited: 25**

**Larionov AA** and Miller WR (2010) Tailoring of endocrine treatment in breast cancer. *Treatment Strategies-Oncology* 1:61 (<http://www.cambridgeresearchcentre.co.uk/contents/breast-cancer/>)

Miller WR and **Larionov A** (2010) Changes in expression of oestrogen regulated and proliferation genes with neoadjuvant treatment highlight heterogeneity of clinical resistance to the aromatase inhibitor, letrozole. *Breast Cancer Res*. 12:R52 PMID: 20646288 **Cited: 35**

Hrstka R, ... **Larionov A et al** (2010) The pro-metastatic protein anterior gradient-2 predicts poor prognosis in tamoxifen-treated breast cancers. *Oncogene*. 29(34):4838-4847. PMID 20531310 **Cited: 56**

Creighton CJ, ... **Larionov AA et al** (2009) Residual breast cancers after conventional therapy display mesenchymal as well as tumor-initiating features. *PNAS* 106(33):13820-13825 PMID: 19666588 **Cited: 790**

- Larionov AA and Miller WR (2009)** Challenges in defining predictive markers for response to endocrine therapy in breast cancer. *Future Oncol* 5:1415 PMID: 19903069 **Cited: 21**
- Miller WR, **Larionov A et al (2009)** Gene expression profiles differentiating between breast cancers clinically responsive or resistant to letrozole. *J Clin Oncol* 27:1382 PMID: 19224856 **Cited: 79**
- Miller WR, **Larionov A et al (2007)** Changes in breast cancer transcriptional profiles after treatment with the aromatase inhibitor, letrozole. *Pharmacogenetics and Genomics*. 17:813 PMID: 17885619 **Cited: 73**
- Mackay A, ... **Larionov A et al (2007)** Molecular response to aromatase inhibitor treatment in primary breast cancer. *Breast Cancer Research*. 9(3):14. PMID: 17555561 **Cited: 99**
- Larionov A et al (2005)** A standard curve based method for relative real time PCR data processing. *BMC Bioinformatics* 6:62 PMID: 15780134 **Cited: 509**
- Tomlinson VAL, ... **Larionov A et al (2005)** Translation elongation factor eEF1A2 is a potential oncoprotein that is overexpressed in two-thirds of breast tumours. *Bmc Cancer*. 5:7. PMID: 16156888 **Cited: 140**
- Larionov A et al (2003)** Aromatase in skeletal muscle. *J Steroid Biochem Mol Biol* 84:485 PMID: 12732294 **Cited: 56**
- Berstein L, ... **Larionov A et al (2002)** Neoadjuvant therapy of endometrial cancer with the aromatase inhibitor letrozole: endocrine and clinical effects. *European Journal of Obstetrics Gynecology and Reproductive Biology* 105(2):161-165. PMID: 12381480 **Cited: 60**
- Larionov A et al (2002)** Local uptake and synthesis of oestrone in normal and malignant postmenopausal breast tissues. *J Steroid Biochem Mol Biol* 81:57 PMID: 12127042 **Cited: 29**
- Berstein LM, **Larionov AA et al (1996)** Aromatase in breast cancer tissue--localization and relationship with reproductive status of patients. *J Cancer Res Clin Oncol*. 122(8):495-8. PMID: 8698750 **Cited: 29**

### Selected conference talks and posters

- Larionov A et al (2016)** Simple and effective variant filters to complement GATK-VQSR in WES data analysis. *Poster* in The European Human Genetics Conference. May 21-24, 2016. **Barcelona, Spain**
- Larionov A et al (2015)** Genetic predisposition to bilateral breast cancer: bioinformatics challenges in whole exome sequencing data analysis. *Poster* in The European Human Genetics Conference. June 6-9, 2015. **Glasgow, Scotland**
- Larionov A (2014)** Recent findings from translational research of neoadjuvant endocrine therapy. *Invited lecture*. Kyoto Breast Cancer Consensus Conference, 20-22 February 2014, **Kyoto, Japan**
- Larionov A (2013)** An invited faculty member for biomarker discovery *panel discussion*. Controversies in Breast Cancer conference, 9-10 February 2013, **Kolkata, India**
- Larionov A (2010)** Molecular heterogeneity of endocrine resistance in breast cancer: profiling of clinical specimens. *Oral presentation* in BIT Life Sciences' 3<sup>rd</sup> World Cancer Congress-Breast Cancer Conference: 25-27 April 2010, **Shanghai, China**
- Larionov A et al (2007)** Reproducibility and interpretation of quantitative gene expression measurements in breast cancer biopsies. *Oral presentation* in the 10th Nottingham International Breast Cancer Conference, 18 – 20 September, 2007, **Nottingham, UK**
- Larionov A et al (2005)** Repeatability and sources of uncertainty in relative real time PCR gene expression measurements in breast cancer biopsies. *Poster* in 28th Annual San Antonio Breast Symposium, 8-11 December, 2005, **San Antonio, USA**
- Larionov A et al (2004)** Data processing in real time PCR. *Oral presentation* in the 1st International qPCR Symposium & Application Workshop Transcriptomics, Clinical Diagnostics & Gene Quantification, 3rd - 6th March, 2004, **Freising-Weihenstephan, Germany**