CV and publications of Alexey Larionov

PhD in Molecular Oncology, MSc in Bioinformatics, MBChB in Medicine

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Employment

2013-present: Research Associate (Bioinformatics)

Acad. Lab. of Med. Genetics, School of Clinical Medicine, Cambridge University

Main tasks and responsibilities:

- Evaluate and select tools and algorithms for the bioinformatics tasks required within the group
- Evaluate and recommend IT infrastructure for the group (departmental servers, CRUK and University HPC clusters, AWS), provide recommendations for the additional IT equipment required for the group.
- Design and maintain the pipeline for primary WES data analysis (from fastq to annotated vcf).
 - The pipeline is written in shell, following the GATK best practices. Briefly: source data QC, alignment (BWA MEM), bam-files clean-up, sorting and marking PCR duplicates (samtools, picard and GATK tools), bam files pre-processing (GATK: local realignment and base quality recalibration), variant calling (GATK HC in gVCF mode) followed by joined variant calling from gVCFs to VCFs, variant filtering by a combination of VQSR and hard-filters, annotation with VEP.
 - The pipeline was implemented in several versions (on the University cluster, in CRUK CI cluster and on a departmental server) for flexibility and to speed-up data processing.
- Design and support project-specific data analyses down-stream of VCF files: variants prioritization based on NGS and clinical annotations data, rare variants association analyses, selection of variants based on biological functions, etc. The statistical analyses are mainly implemented in R (or PLINK); functional interpretation includes elements of interactive network analyses (e.g. using Cytoscape plugins).
- Support and teach non-bioinformaticians using my pipelines and third-party bioinformatics tools
- Contribute to preparation of manuscripts and grants applications, present bioinformatics results on international conferences.

My WES pipeline has been used to process many hundreds of samples over the last 5 years, for different projects within the group. It is being constantly updated. Currently I explore transition of the pipeline elements to AWS and work on implementing the recent resources and tools (e.g. adopting the new GATK-4 version, somatic varaints calling, alignment against GRCh38 etc).

Along with the bioinformatics tasks carried for the present employment, I continue publishing and teaching about endocrine and targeted treatments and endocrine resistance in breast cancer (carrying over from the previous employment in Edinburgh University). Also, I do occasional teaching: supervising students projects, lecturing and exam marking for Genomic Medicine, Molecular Medicine and Pharmacology courses in Cambridge, Cranfield and Edinburgh Universities; and I am a Fellow of The Higher Education Academy (UK).

2008-2013: Research Fellow

Edinburgh Cancer Research Centre, The University of Edinburgh, UK

My main task was to study molecular profiles of clinical biopsies of breast cancer to predict response and understand mechanisms of resistance to aromatase inhibitors (a modality of endocrine treatment in breast cancer). Most of the work was based on transcriptional profiling of tumours before and early on-treatment:

- 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).
- Low level microarray data analysis (mainly R-libraries for illumina microarray data processing)
- Extraction of RNA from frozen biopsies and submitting for micro-array analyses in local genomics facilities
- Supervision and support for PhD, MSc and MD students in the research group
- Preparation of publications, grant applications and presenting results on international meetings

The results were reported in multiple well cited papers and scientific meetings (see list of publications). Along with bioinformatics and wet-lab tasks during that employment I completed MSc in Applied Bioinformatics (Cranefield University) and PgCert in Academic Practices (Edinburgh University).

2002 - 2007: Research Fellow

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

Tasks and responsibilities: Study mechanisms and markers of endocrine resistance in breast cancer, validate micro-array gene expression data with qPCR:

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

During that employment I performed qPCR analysis on 200+ samples for tens of genes pre-selected using micro-array results. Also, I wrote a paper about standard-curve based method for qPCR data analysis, which has already been cited 500+ times (Larioniov et al, BMC bioinformatics, 2006).

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.

2000

Postdoctoral Research Fellow (fellowship awarded by the Royal Society)

Breast Research Unit, The University of Edinburgh, UK

Study local estrogen production in breast cancer tissues and in other peripheral tissues. Resulted into two well-cited 1-st author publications.

1992 - 1999

Postgraduate student (Medical oncology) then **PhD student** (Molecular oncology) then **Researcher** N.N.Petrov Institute of Oncology, St. Petersburg, Russia

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	Postgraduate specialization in medical oncology N.N.Petrov Institute of Oncology, St. Petersburg, Russia
1984-1992	MBChB in 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 Project supervision and marking for MSt Genomic Medicine course,
Cambridge University, 2017-2018

Invited lecturer and marking for BSc Clin. Pharmacology course,
Edinburgh University, 2012-2017

Project supervision for MSc Molecular Medicine course,
Cranfield University, 2011

Refereeing & Refereed papers for Genome Medicine, Breast Cancer Research, BMC Cancer,

editing BMC Bioinformatics, Breast Cancer Research & Treatment and for other journals (see more at https://publons.com/author/1373942/alexey-larionov#profile);

<u>Edited a book</u> for Springer about endocrine resistance in breast cancer (http://www.springer.com/gb/book/9783319179711).

Publications

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 <u>Personalized</u>
 <u>Treatment of Breast Cancer</u>. 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: <u>Resistance to Targeted Anti-Cancer Therapeutics</u>. 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

These are only papers published within the last 5 years or cited at least 50 times. Citation counts are given by Google Scholar 24Feb2018: https://scholar.google.co.uk/citations?hl=en&user=hGLjJ-kAAAAJ.

- Fewings E, **Larionov** A *et al* **(2018)** Whole exome sequencing to detect germline pathogenic variants in PALB2 and other cancer-predisposing genes in CDH1 mutation negative diffuse gastric cancer families. *The Lancet Gastroenterology & Hepatology*, doi:10.1016/S2468-1253(18)30079-7
- **Larionov** AA (**2018**) Current therapies for human hpidermal growth factor receptor 2-positive metastatic breast cancer patients. *Front. Oncol.* 8:89, doi:10.3389/fonc.2018.00089.
- Flageng MH, **Larionov** A, *et al* **(2017)** 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*. 165:228, PMID: 27343990.
- Toi M, ... **Larionov** A, *et al* **(2015)** Personalization of loco-regional care for primary breast cancer patients. *Future Oncol*. 11:1297, PMID: 25952777 and 25952778 (parts 1 and 2)
- Turnbull AK, ... **Larionov** AA, *et al* (**2015**) Accurate prediction and validation of response to endocrine therapy in breast cancer. *J Clin Oncol*. 33:2270, PMID: 26033813
- López-Knowles E ... **Larionov** A *et al* **(2015)** Integrative analyses identify modulators of response to neoadjuvant aromatase inhibitors in patients with early breast cancer. *Breast Cancer Res*. 17:35, PMID: 25888249
- Arthur LM, ... **Larionov** AA, et al (**2014**) Molecular changes in lobular breast cancers in response to endocrine therapy. *Cancer Res.* 74:5371, PMID: 25100562
- Sokolenko AP, ... **Larionov** AA, *et al* **(2014)** High prevalence of GPRC5A germline mutations in BRCA1-mutant breast cancer patients. *Int J Cancer*. 134:2352, PMID: 24470238
- Kuligina ESh, ... **Larionov** AA, *et al* (**2013**) Value of bilateral breast cancer for identification of rare recessive at-risk alleles: evidence for the role of homozygous GEN1 c.2515_2519delAAGTT mutation. *Fam Cancer*. 12:129, PMID: 23104382.
- Miller WR and **Larionov** AA (**2012**) Understanding the mechanisms of aromatase inhibitor resistance. <u>Breast</u> <u>Cancer Res</u> 14:201 PMID: 22277572, **cited by 55**

- 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 by 72
- 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. <u>Breast Cancer Res.</u> 12:R52 PMID: 20646288, **cited by 50**
- 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 by 960**
- 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 by 86**
- 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 PIMD: 17885619, **cited by 82**
- Mackay A, ... Larionov A et al (2007) Molecular response to aromatase inhibitor treatment in primary breast cancer. <u>Breast Cancer Research</u>. 9(3):14. PMID: 17555561, cited by 105
- **Larionov** A *et al* (**2005**) A standard curve based method for relative real time PCR data processing. <u>BMC</u> <u>Bioinformatics</u> 6:62 PMID: 15780134, **cited by 614**
- Tomlinson VAL, ... Larionov A et al (2005) Translation elongation factor eEF1A2 is a potential oncoprotein that is overexpressed in two-thirds of breast tumours. <u>Bmc Cancer</u>. 5:7. PMID: 16156888, cited by 143
- **Larionov** A *et al* (**2003**) Aromatase in skeletal muscle. *J Steroid Biochem Mol Biol* 84:485 PMID: 12732294, cited by 59
- Berstein L, ... Larionov A *et al* (2002) Neoadjuvant therapy of endometrial cancer with the aromatase inhibitor letrozole: endocrine and clinical effects. *Eur J Obstet Gynecol Reprod Biol*. 105:161, PMID: 12381480, cited by 71

Conference talks

- **Larionov** A **(2014)** Recent findings from translational research of neoadjuvant endocrine therapy. <u>Invited</u> <u>lecture</u>. Kyoto Breast Cancer Consensus Conference, 20-22 February 2014, **Kyoto, Japan**
- **Larionov** A **(2013)** An invited faculty member for biomarker discovery <u>panel discussion</u>. 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. <u>Oral presentation</u> in BIT Life Sciences' 3rd World Cancer Congress-Breast Cancer Conference: 25-27April 2010, **Shanghai, China**
- **Larionov** A *et al* (**2007**) Reproducibility and interpretation of quantitative gene expression measurements in breast cancer biopsies. <u>Oral presentation</u> in the 10th Nottingham International Breast Cancer Conference, 18 20 September, 2007, **Nottingham, UK**
- **Larionov** A *et al* (**2004**) Data processing in real time PCR. <u>Oral presentation</u> in the 1st International qPCR Symposium & Application Workshop Transcriptomics, Clinical Diagnostics & Gene Quantification, 3rd 6th March, 2004, **Freising-Weihenstephan**, **Germany**