CURRICULUM VITAE

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Personal Details

Full Name: Ali Oghabian
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Research positions

- *2022- :* PostDoc at Neuromuscular diseases research laboratory, Folkhälsan, Biomeidcum 1, Uni. of Helsinki.

Subject of research: bulk/single-cell RNAseq analysis, gene expression splicing analysis, Neuromuscular diseases.

- *2020-2021:* PostDoc at Obesity Research unit, Biomeidcum 1, Uni. of Helsinki.

Subject of research: bulk/single-cell RNAseq, Machine learning, Obesity & diet.

- *2011-2019:* Ph.D. student and PostDoc at RNA splicing laboratory, Institute of Biotechnology (HiLife), Viikinkaari 9, 00014 University of Helsinki, Finland

Subject of research: RNA splicing, intron retention & alternative splicing analysis.

- *2010-2011:* Department of Obstetrics and Gynecology, Helsinki University Central Hospital, Biomedicum Helsinki (B407b), Haartmaninkatu 8, 00029 HUS, Finland
  Subject of research: Expression Quantitative Trait Loci (eQTL) analysis.

- *2009-2010:* Computational Systems Biology Lab, Biomedicum I, Uni. of Helsinki.

Subject of research: Unsupervised machine learning, Biclustering algorithms, and automation of flow cytometry data analysis.

Degrees

- *Ph.D. in Biological and Environmental Sciences – genetics (2019):* Uni. of Helsinki.
- *M.Sc. Bioinformatics (2011):* Uni. of Helsinki, Helsinki, Finland.
- *B.Sc. in Computer Engineering (2007):* Uni. of Science and Culture, Tehran Iran.

Publications

A- Papers:

- Wolf, B. D., **Oghabian, A.**, *et al.* "Chromosomal instability by mutations in the novel minor spliceosome component CENATAC", EMBO J. 2021 Jul 15;40(14):e106536. DOI: 10.15252/embj.2020106536.

- Van der Kolk, B. W. , Saari S., *et al.,* "Molecular pathways behind acquired obesity: Adipose tissue and skeletal muscle multiomics in monozygotic twin pairs discordant for BMI", Cell Rep Med. 2021 Mar 30;2(4):100226. DOI:10.1016/j.xcrm.2021.100226.

- **Oghabian, A.**, Greco, D., *et al.*, "IntEREst: intron-exon retention estimator", BMC Bioinformatics, 2018, 19 (1), 130. DOI: 10.1186/s12859-018-2122-5.

- Sarkar, D., **Oghabian, A.**, *et al.*, "Multiple isoforms of ANRIL in melanoma cells: structural complexity suggests variations in processing", International journal of molecular sciences 06/2017; 18 (7), 1378. DOI:10.3390/ijms18071378.

- Niemelä, E. H.[*], **Oghabian, A.**[*], *et al.*, "Global analysis of the nuclear processing of transcripts with unspliced U12-type introns by the exosome", NAR 05/2014; 42(11). DOI:10.1093/nar/gku391.

* Joint first author

- **Oghabian, A.**, Kilpinen, S., *et al.*, "Biclustering Methods: Biological Relevance and Application in Gene Expression Analysis", PLoS ONE 03/2014; 9(3):e90801.
- Argente,J., *et al.*, "Defective minor spliceosome mRNA processing results in isolated familial growth hormone deficiency", EMBO Mol. Med. 03/2014; 6:299-306.
- Lahesmaa-Korpinen, A-M. K. , Jalkanen, S., *et al.*, (2011), "FlowAnd: Comprehensive Computational Framework for Flow Cytometry Data Analysis", Journal of Proteomics and Bioinformatics 11/2011, p. 245-249.

B- Thesis:

- *Ph.D. thesis:* Bioinformatics analysis of intron retention events associated with the minor spliceosome. *Supervisor:* Mikko Frilander, Docent.

Link: http://urn.fi/URN:ISBN:978-951-51-4699-1

- *M.Sc. thesis:* Biclustering methods and their application in microarray data analysis. *Supervisor:* S. Hautaniemi, DTech, Docent.

Scholarships

- 2022-: PostDoc scholarship (for 3 years) granted by Magnus Ehrnrooth foundation.
- *2012-2016:* Ministry of Education and Culture scholarship granted by Viikki Doctoral Programme in Molecular Biosciences (VGSB).
- *2018:* 2nd place prize (out of 45 teams), as member of the Cimorgh team, at the Next Generation Sequencing analysis challenge organized by http://iChallenge.ir .

Developed software

- **IntEREst:** Intron Exon Retention Estimator, bioconductor.org/packages/IntEREst/ .
- **FlowAnd:** Flow cytometry analysis module of Anduril, http://anduril.org/flowand/ .

Presentations

- *Poster presentations* at RNA meeting 2019, 2018, 2016, 2014, and 2013. Subjects: intron retention, alternative splicing analysis, IntEREst software, and minor spliceosomal diseases.
- *Poster presentations* at ISMB/ECCB 2015 and ECCB 2012. Subjects: Intron retention and alternative splicing analysis, and IntEREst software.
- Oral presentation: at NordForsk and NorFA RNA network meeting 2013. Subject: "Global Analysis of Exosome Knock-down by Intron Retention Level Estimation Using RNA-Seq".

Teaching and tutoring

- Teaching "Gene expression analysis" course at the Tarbiat Modares University (TMU) during Fall 2022.
- Invited speaker & tutoring at Next Generation Genomics (NGG) 2021, 2018 & 2016.
- Teaching & tutoring at CSC course: *Introduction to parallel computing 2014.*

Other academic merits

- *Reviewer:* Briefings in Bioinformatics, PeerJ Computer Science, International Journal of Machine Learning and Cybernetics, International Journal of Data Mining and Bioinformatics, and Imperial College Computing Student Workshop (ICCW13).