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I am a bioinformatician with strong computational, mathematical and statistical backgrounds and rich experience in research as well as scientific software development. I believe that the progress of any modern scientific domain includes multidisciplinary and biology with statistics and computer science, which are now permanently bound together, are perfect examples of multidisciplinary scientific progress and the future of healthcare. One of my strongest points is my focus and my passion for perfectionism regarding my work and the success of any project I am involved in.

Key achievements

Research

- Bioinformatics insights in the elucidation of Kmt5a as a major controller in hepatic metabolic pathways through mediating H4K20 monomethylation (PMID: 28746875)
- Bioinformatics insights in the elucidation of Smyd3 as a key player among multiple cancer-promoting genes required for liver and colon cancer development (PMID: 26908355, 27245698)
- Integrative bioinformatics analysis, including handling of big datasets (TCGA consortium), assisting in the discovery of a positive regulatory loop between a Wnt-Regulated, with potential therapeutic properties, non-coding RNA and the ASCL2 gene which controls intestinal stem cell fate (PMID: 27292638)
- Gene expression analysis during the investigation of Set8 as a potential player in the development of hepatocellular carcinoma (PMID: 25515659)
- Bioinformatics transcriptome analysis of UUO mouse models in renal fibrosis (PMID: 27189340)
- PANDORA algorithm for systematic integration of RNA-Seq statistical algorithms for accurate detection of differential gene expression patterns (PMID: 25452340)
- A novel method and web application for the identification of internal standards for the normalization of CE/MS data (PMID: 27694997)

Software

- *SeqCVIBE*: an R Shiny application for the analysis, exploration, curation and visualization of big RNA-Seq datasets (manuscript in preparation, <https://github.com/pmoulos/seqcvibe>)
- *recoup*: an R/Bioconductor package for flexible and reusable visualizations of genomic profiles from Next Generation Sequencing data (manuscript in preparation, <https://github.com/pmoulos/recoup>)
- *metaseqR*: an R/Bioconductor package for the systematic integration of RNA-Seq statistical algorithms and interactive result reporting (PMID: 25452340)
- The Kidney and Urinary Pathway Knowledge Base (*KUPKB*) and the *KUPNetViz* applications for knowledge mining and gene network visualization in kidney disease (www.kupkb.org, PMID: 23883183, 22345404)
- *cinnamoned*: a web application for the CE/MS data processing and normalization based on internal standards (PMID: 27694997, <https://github.com/pmoulos/cinnamoned>)
- *StRAnGER*: Hybrid parametric and non-parametric prioritization and enrichment analysis of Gene Ontology annotations (<http://grissom.gr/stranger/>, PMID: 21293737)
- *Gene ARMADA*: software for the analysis of gene expression microarray data (<https://github.com/pmoulos/gene-armada>, PMID: 19860866)

Education

3/2007 – 3/2011: PhD in Bioinformatics, School of Chemical Engineering, National Technical University of Athens, Thesis Title: Development of Bioinformatics Methodologies for the Study of Highly Complex Biological Systems

9/2004 – 7/2005: DEA (MSc) Bioinformatique, Université Libre de Bruxelles, Thesis Title: Feature Selection and Stability Analysis for Classification using Microarray Data

9/1999 – 7/2004: School of Applied Mathematics and Physics, National Technical University of Athens, Majors: Computer Science Mathematics, Statistics, Thesis Title: Models of Cellular Control and Emergent Phenomena in Muticellular Systems

Positions

8/2017 – Present: “Stavros Niarchos” Foundation Researcher in Bioinformatics, Biomedical Sciences Research Center ‘Alexander Fleming’, Vari, Greece.

4/2014 – Present: Co-founder at HybridStat Predictive Analytics (www.hybridstat.gr): Bioinformatics consulting and services, software development for the analysis of big biological data.

6/2012 – Present: Post-doctoral researcher at the Biomedical Sciences Research Center ‘Alexander Fleming’, Vari, Greece, working on the analysis of Next Generation Sequencing data and the development of new analytical approaches for deep sequencing data.

5/2011 – 5/2012: Post-doctoral researcher at Inserm (U1048, I2MC), Toulouse, France, working on the development of a pipeline for the analysis of CE/MS data with focus on the statistical identification of internal normalization standards and of a visualization interface for visualizing Semantic Web relationships stored in the Kidney and Urinary Pathway Knowledge Base (KUPKB).

9/2006 – 3/2011: Bioinformatics research assistant with focus on the analysis and meta-analysis of high-throughput functional genomics data, Metabolic Engineering and Bioinformatics Group, Institute of Biological Research and Biotechnology, National Hellenic Research Foundation.

4/2008 – 12/2008: Visiting researcher/bioinformatician in the laboratory of Prof. Henk G. Stunnenberg (NCMLS, Radboud University, Nijmegen, Netherlands), working on standardization, normalization, statistical analysis and analysis workflow organization for Next Generation Sequencing (ChIP-Seq) data.

1/2002 – 12/2009: Other activities: Statistical analysis of questionnaires and technical report writings, private courses in Statistics to students (university level), IT training of SME employees and IT support, teaching assistance during PhD.

Languages

English (excellent), French (excellent), Greek (mother tongue)

Skills

- Excellence with the use of various bioinformatics analysis tools and methodologies with focus on genome bioinformatics/genomics. Indicatively:
 - Next Generation Sequencing data analysis (computational pipelines setup for a variety of -Seq protocols, sequence alignment, data preprocessing, normalization, analysis and visualization)
 - DNA microarray data analysis (data preprocessing, normalization, statistical analysis, data mining, pathway and network analysis)
 - Biological sequence and DNA motif analysis
- Familiarity with a variety of biological databases with focus on genomic and small molecule data:
 - Biological sequences and DNA motifs (RefSeq, GenBank, TRANSFAC, JASPAR etc.).
 - High-throughput genomic data (GEO, SRA, ArrayExpress, SMD, ArrayTrack etc.).
 - Biological small molecules (KEGG Compound, ChEBI, HMDB, METLIN).
- Metabolomic MS data analysis (preprocessing, peak detection, normalization, statistics, database search).
- Excellent operation of engineering and statistical packages R, MatLab, Minitab, SPSS.
- Application programming/development
 - Programming languages: Perl, Python, MatLab, R
 - Web development: PHP, HTML, JavaScript, jQuery, Meteor.js, R Shiny
 - Database systems: MongoDB, MySQL
- Excellent familiarity with data mining techniques (feature selection, classification and regression algorithms)
- Elementary usage of Business Intelligence tools such as Microsoft PowerBI

Journal publications

- Nikolaou, K.C., **Moulos, P.**, Harokopos, V., Chalepakis, G., Talianidis, I.: *Kmt5a Controls Hepatic Metabolic Pathways by Facilitating RNA Pol II Release from Promoter-Proximal Regions*. Cell Rep. 2017, 20(4):909-922.
- Apostolou, G., Apostolou, N., **Moulos, P.**, Chatzipantelis, P.: *Endometrial cytopathology. An image analysis approach using the Ki-67 biomarker*. Cytopathology 2017, 28(5):385-390.
- Papadopoulou, T., Casemayou, A., Neau, E., Breuil, B., Caubet, C., Calise, D., Thornhill, B.A., Bachvarova, M., Belliere, J., Chevalier, R.L., **Moulos, P.**, Bachvarov, D., Buffin-Meyer, B., Decramer, S., Auriol, F.C., Bascands, J.L., Schanstra, J.P., Klein, J.: *Systems biology combining human- and animal-data miRNA and mRNA data identifies new targets in ureteropelvic junction obstruction*. BMC Syst Biol. 2017, 11(1):31.
- Boizard, F., Brunchault, V., **Moulos, P.**, Breuil, B., Klein, J., Lounis, N., Caubet, C., Tellier, S., Bascands, J.L., Decramer, S., Schanstra, J.P., Buffin-Meyer, B.: *A capillary electrophoresis coupled to mass spectrometry pipeline for long term comparable assessment of the urinary metabolome*. Sci Rep. 2016, 6:34453.

- **Moulos, P.**, Samiotaki, M., Panayotou, G., Dedos, S.G.: *Combinatory annotation of cell membrane receptors and signalling pathways of Bombyx mori prothoracic glands*. Sci Data. 2016, 3:160073.
- Giakountis, A., **Moulos, P.**, Sarris, M.E., Hatzis, P., Talianidis, I.: *Smyd3-associated regulatory pathways in cancer*. Semin Cancer Biol. 2016, S1044-579X(16)30041-4.
- Papadodima, O., **Moulos, P.**, Koryllou, A., Piroti, G., Kolisis, F., Chatziioannou, A., Pletsas, V.: *Modulation of Pathways Underlying Distinct Cell Death Mechanisms in Two Human Lung Cancer Cell Lines in Response to SN1 Methylating Agents Treatment*. PLoS One. 2016, 11(7):e0160248.
- Giakountis, A., **Moulos, P.**, Zarkou, V., Oikonomou, C., Harokopos, V., Hatzigeorgiou, A.G., Reczko, M., Hatzis, P.: *A Positive Regulatory Loop between a Wnt-Regulated Non-coding RNA and ASCL2 Controls Intestinal Stem Cell Fate*. Cell Reports. 2016, S2211-1247(16)30621-0.
- **Moulos, P.**, Sarris, M.E., Talianidis, I.: *Mechanism of gene-specificity of oncogenic regulators*. Cell Cycle. 2016 May 31:0. [Epub ahead of print]
- Arvaniti, E., **Moulos, P.**, Vakrakou, A., Chatziantoniou, C., Chadjichristos, C., Kavvas, P., Charonis, A., Politis, P.K.: *Whole-transcriptome analysis of UUO mouse model of renal fibrosis reveals new molecular players in kidney diseases*. Sci Rep. 2016, 6:26235.
- Sarris, M.E., **Moulos, P.**, Haroniti, A., Giakountis, A., Talianidis, I.: *Smyd3 Is a Transcriptional Potentiator of Multiple Cancer-Promoting Genes and Required for Liver and Colon Cancer Development*. Cancer Cell. 2016, 29(3):354-66.
- Alexandratos, A., **Moulos, P.**, Nellas, I., Mavridis, K., Dedos, S.G.: *Reassessing ecdysteroidogenic cells from the cell membrane receptors' perspective*. Sci Rep. 2016, 6:2022.
- Milongo, D., Bascands, J.-L., Huart, A., Esposito, L., Breuil, B., **Moulos, P.**, Siwy, J., Ramírez-Torres, A., Ribes, D., Lavayssière, L., Del Bello, A., Muscari, F., Alric, L., Bureau, C., Rostaing, L., Schanstra, J.-P., Kamar, N.: *Pretransplant urinary proteome analysis does not predict development of chronic kidney disease after liver transplantation*. Liver Int. 2015, 35(7), 1893-901.
- Nikolaou, K.C., **Moulos, P.**, Chalepakis, G., Hatzis, P., Oda, H., Reinberg, D., Talianidis, I.: *Spontaneous development of hepatocellular carcinoma with cancer stem cell properties in PR-SET7-deficient livers*. EMBO J. 2015, 34(4), 430-47.
- **Moulos, P.**, Hatzis, P.: *Systematic integration of RNA-Seq statistical algorithms for accurate detection of differential gene expression patterns*. Nucleic Acids Res. 2015, 43(4), e25.
- **Moulos, P.**, Klein, J., Jupp, S., Stevens, R., Bascands, J.-L., Schanstra, J.P.: *The KUPNetViz: A biological network viewer for multiple -omics datasets in kidney diseases*. BMC Bioinformatics 2013, 14:235.
- Klein, J., Jupp, S., **Moulos, P.**, Fernandez, M., Buffin-Meyer, B., Chayaa, R., Charonis, A., Bascands, J.-L., Stevens, R., Schanstra, J.-P.: *The KUPKB: a novel Web application to access multiomics data on kidney disease*. FASEB J. 2012, 26(5), 2145-2153.
- Rao, N.A.S., McCalman, M.T., **Moulos, P.**, Francoijs, K.J., Chatziioannou, A., Kolisis, F.N., Alexis, M.N., Stunnenberg, H.G., Mitsiou, D.J.: *Coactivation of GR and NFKB alters the repertoire of their binding sites and target genes*. Genome Res. 2011, 21(9), 1404-1416¹.
- Chatziioannou, A., Kanaris, I., Doukas, C., **Moulos, P.**, Maglogiannis, I., Kolisis, F.N.: *The GRISSOM Platform: Enabling distributed Processing and Management of Biological Data through fusion of Grid and Web Technologies*. IEEE Transactions on Information Technology in Biomedicine 2011, 15(1), 83-92.
- Chatziioannou, A., **Moulos, P.**: *Exploiting statistical methodologies and controlled vocabularies for prioritized functional analysis of genomic experiments: The StrAnGER web application*. Front Neurosci. 2011, Jan 26, 5:8.
- **Moulos, P.**, Papadodima, O., Chatziioannou, A., Loutrari, H., Roussos, C., Kolisis, F.N.: *A transcriptomic computational analysis of mastic oil-treated Lewis lung carcinomas reveals molecular mechanisms targeting tumor cell growth and survival*. BMC Medical Genomics 2009, 2:68.
- Chatziioannou, A., **Moulos, P.**, Kolisis, F.N.: *Gene ARMADA: an integrated multi-analysis platform for microarray data implemented in MATLAB*. BMC Bioinformatics 2009 10:354.
- Nielsen, R., Pedersen, T.A., Hagenbeek, D., **Moulos, P.**, Siersbaek, R., Megens, E., Denissov, S., Borgesen, M., Francoijs, K.J., Mandrup, S., Stunnenberg, H.G.: *Genome-wide profiling of PPARgamma:RXR and RNA polymerase II occupancy reveals temporal activation of distinct metabolic pathways and changes in RXR dimer composition during adipogenesis*. Genes Dev 2008, 22(21):2953-2967.

Selected conference proceedings

- **Moulos, P.**, Kanaris, I., Bontempi, G.: *Stability of feature selection algorithms for classification in high-throughput genomics datasets*. Conf Proc 13th IEEE Bioinformatics and Bioengineering (BIBE), 2013.
- Valavanis, I., **Moulos, P.**, Maglogiannis, I., Klein, J., Schanstra, J.-P., Chatziioannou, A.: *Intelligent Selection of human miRNAs and mouse mRNAs related to Obstructive Nephropathy*. IEEE AIAB 2011.

¹ equal first authorship

- **Moulos, P.**, Valavanis, I., Klein, J., Maglogiannis, I., Schanstra, J.-P., Chatziioannou, A.: *Unifying the Integration, Analysis and Interpretation of multi-omic datasets: Exploration of the disease networks of Obstructive Nephropathy in children*. IEEE EMBC 2011.
- **Moulos, P.**, Maglogiannis, I., Chatziioannou, A.: *Applying gap statistic for automated unsupervised estimation of optimal number of clusters in microarray datasets*. CIBB 2010.
- Chatziioannou, A., **Moulos, P.**, Pilalis, E., Kolisis, F.N., Maglogiannis, I., Doukas, C.: *GRISSOM web based grid portal: Exploiting the power of grid infrastructure for the interpretation and storage of DNA microarray experiments*, ITAB 2009:1-5.
- Chatziioannou, A., **Moulos, P.**: *Extending the Interpretation of Gene Profiling Microarray Experiments to Pathway Analysis Through the Use of Gene Ontology Terms*. ICCS 2007: 55-61, 22-27/7/2007, Sheffield, England.
- Chatziioannou, A., **Moulos, P.**: *ANDROMEDA: A MATLAB Automated cDNA Microarray Data Analysis Platform*. AIAI 2007: 127-136, 19-21/9/2007, Athens, Greece.

Book Chapters

- Chatziioannou, A., **Moulos, P.**: *DNA Microarrays: Analysis and Interpretation*. In: Exarchos, T.P., Papadopoulos, A., Fotiadis, D.I.: *Handbook of Research on Advanced Techniques in Diagnostic Imaging and Biomedical Applications*, 2009.
- Chatziioannou, A., **Moulos, P.**: *Interpretation of Gene Expression Microarray Experiments*. In: Maglogiannis, I., Karpouzis, K., Wallace, B.A., Soldatos, J.: *Emerging Artificial Intelligence Applications in Computer Engineering*, 2007.