Genomic and Phenotypic Data Exploration and Interpretation

Manuel X. Duval, Bioinformatics Scientist

Serve the Biotech and AgroTech industries.

- Address biotech industry needs by sourcing relevant data sets and analysis methods.
- Adopt reproducible research principles.
- Apply predictive modeling methods to identify genomic quantity(ies) contributing to the identification of novel therapeutic targets, target validation, disease selection/expansion, and identification of translational biomarkers.
- Build and validate models with genomics' features aimed at predicting endpoints.
- Extensive user of biological data, including nucleic-acid sequencing data.
- Familiar with current molecular biology, nextgen sequencing technologies and genome editing technologies.

Applied technologies:

- R Project for Statistical Computing
- Genomics
- Bioinformatics
- Linux/Cloud Computing
- NGS - RNA-Seq
- Machine learning

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About

Biotech opportunities

Biological systems operate under well-described rules. With this understanding, the green (agro) and red (human health) biotech industries can address critical needs. In **agro-tech**, the focus is on designing crops capable of producing biomass that can be efficiently converted into hydrocarbons. In **molecular medicine**, developing sensitive and specific tests for monitoring the actual therapeutic effect of interventions could improve patient outcomes. These are challenging problems that require data from well-designed studies and the application of advanced data analysis methods. My primary concern is to determine, with high confidence, which **molecular elements** (e.g., germline variations or steady-state levels of RNA molecules) contribute to, or are associated with, **specific endpoints of interest**.

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Professional Experience

Bioinformatics Scientist May 2023 – Current
amplifiDx Inc, Waltham, MA

- Build and deploy bioinformatics workflows for the design of specific and sensitive Nucleic Acid Amplification Test based assays. Analyze, manage and report experimental data.

Business Analyst II (IT) contractor Feb 2023 – May 2023
mindlance/Sanofi Pharmaceuticals, Cambridge, MA

- Captured user requirements and translated them into features' requests passed to developers. Applied the Agile scrum methodology.

Data Scientist contractor Feb 2022 – Dec 2022
InfoJini/EMD Serono, Billerica, MA

- Delivered Pharmaco-genomics and RNA-Seq data analyses in the context of a clinical trial for auto-immune indications (small-molecule candidate therapy): delivered germline candidate markers of drug exposure inter-individual variability.

Senior Data Scientist Jun 2019 – July 2021
Clear Gene Inc.,San Carlos, CA

- Applied statistical machine learning methods to RNA-Seq derived features for the discovery of a predictive model of tumor residual in solid biopsy. Delivered data analyses for the prospective studies and FDA submission.
- Developed the software environment (R package) for the current development of a diagnostic test.

Senior Data Analyst Apr 2018 – Jun 2019
Scipher Medicine Inc., Waltham, MA

- Developed an RNA-Seq based predictive test for precision medicine application.
- Applied statistical machine learning to RNA-Seq data sets in observational studies in the scope of discovering and developing a diagnostic test pertaining to patients' response to current therapies.

Senior Scientist III Bioinformatics Mar 2016 – Dec 2017
AbbVie Inc., Worcester, MA

- Delivered multi-omics data analyses for Translational Medicine projects, and RNA-Seq exosome technology deployment.
- Relying on peripheral blood metabonomics and proteomics data sets, inferred candidates subgroups of patients with a given autoimmune indication.
- Developed and deployed R shiny applications in the scope of enabling scientist to perform simple queries on large RNA-Seq data sets.

Bioinformatician contractor Aug 2015 – Mar 2016
Commonwealth Sciences, Inc./Agios, Cambridge, MA

- Somatic variants detection and analyses from DNA re-sequencing data, inferred clonality and normal cell content from tumor biopsies molecular data.

Staff Bioinformatician May 2014 – May 2015
Beckman Coulter Genomics, Danvers, MA

- Managed and analyzed Bioinformatics, NextGen DNA sequence data. Maintained whole DNA-Seq

(WGS) and RNA-Seq workflows from Illumina HiSeq instruments to data packages delivery to customers.

Senior Principal Bioinformatics Jul 2013 – May 2014
Boehringer Ingelheim, Ridgefield, CT

- Knowledge management bioinformatics, cardiovascular and metabolic disease drug discovery.
- Delivered RNA-Seq data analyses in the scope of comparing the molecular effects of standard of care with candidate therapies.

Bioinformatics Scientist Feb 2012 – May 2013
Enumeral Biomedical, Cambridge, MA

- Designed and implemented in-house antibody DNA sequence analyses workflow.
- Deployed solutions for cell cytometry data analyses for the development of novel antibody based biotherapeutics.

Senior Principal Scientist Jan 2001 – Aug -2011
Pfizer Inc. Groton/New London, CT

- Managed Pharmacogenomics data in a clinical development lab. Provided and delivered statistical data analyses services for clinical and translational research programs. Conducted OMICs' technologies evaluation in the scope of promoting the most relevant assays in terms of Drug Discovery and Development.
- Deployed an enterprise information system for the storage and analysis of transcriptomics data associated with their cognate co-variates' attributes. Supplied Computational Biology analyses and supported the preclinical models business needs with Bioinformatics services.

Research Scientist Jan 1996 – Dec -2000
Texas A&M University, College Station, TX

- Conducted high-throughput DNA sequence data capture and data analyses.
- Set-up and applied a bioinformatics data pipeline that delivered an annotated database of more than 10,000 non-redundant Expressed Sequence Tags (EST) from raw Sanger-based DNA sequence data. Developed and deployed a DNA micro array platform.
- Contributed to the establishment of the Texas A&M Laboratory for Functional Genomics with the set-up of DNA micro array production (printed arrays).

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Education

- [Academic degrees](#)
- [Certifications](#)
- [Professional Trainings](#)

Academic degrees

- **Post-baccalaureate Non-degree, Computer Science** (June 2020)
  [Texas A&M University, College Station, TX](#)
  (C and Java Programming. Data Modeling and Relational Databases)

- **PhD, Molecular and Microbiology** (October 1995)
  [Université Grenoble Alpes, Grenoble, France](#)

- **MS, Biochemistry** (June 1990)
  [Aix-Marseille University, Faculté des Sciences, Marseille, France](#)

- **BS, Math and Life Sciences** (June 1988)
  [Aix-Marseille University, Faculté des Sciences, Marseille, France](#)

Certifications

- **Linux Essentials** (Oct 2019)
  Linux Professional Institute
  [LPI000435511](#)

Professional Trainings

- Data and Models in Engineering, Science and Business [12.156s], MIT, Cambridge, MA, July 2012

- Umetrics Academy, Multivariate Data Analysis, MKS Instruments, Andover, MA, July 2010

- Intensive Courses in Computational Molecular Biology, Washington University Institute for Biomedical Computing, St Louis, MO, July 2000

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Publications

- Peer-reviewed journal articles
- Book chapters
- Patents
- White Papers
- Blogs

Peer-reviewed journal articles

- de Leeuw, MA and Duval, M. (2020), The Presence of Periodontal Pathogens in Gastric Cancer. Explor Res Hypothesis Med. 2020;5(3):87-96

- Srinivasan, S., Duval, M, Kaimal, V., Cuff, C., & Clarke, S. H. (2019), Assessment of methods for serum extracellular vesicle small RNA sequencing to support biomarker development. Journal of Extracellular Vesicles, 8(1)

- Duval, M. (2018), The inadequacy of the reductionist approach in discovering new therapeutic agents against complex diseases. Experimental Biology and Medicine. 2018;243(12):1004-1013

- Wong, V. and Duval, M. (2013), Inter-laboratory variability in array-based RNA quantification methods. Genomics Insights 2013:6 13–24

- Rajjou, L., Duval, M., Gallardo, K., Catusse, J., Bally, J., Job, C., and Job., D. (2011), Seed Germination and Vigor. Annual Review of Plant Biology 2011 May 4.

- Matteson S, Paulauskis J, Foisy S, Hall S, Duval M. (2010), Opening the gate for genomics data into clinical research: a use case in managing patients' DNA samples from the bench to drug development. Pharmacogenomics. 2010 Nov;11(11):1603-12.

- Pettit, S., des Etages, S.A., Mylecraine, L., Snyder, R., Fostel, J., Dunn, II, R.T., Haymes, K., Duval, M., Stevens, J., Afshari, C., and Vickers, A., (2009), Current and Future Applications of Toxicogenomics: Results Summary of a Survey from the HESI Genomics State of Science Subcommittee. Environmental Health Perspectives

- Csanky, E., Olivova, P., Rajnavolgyi, E., Hempel, W., Tardieu, N., Toth, Katalin, E., Jullien, A., Malderes-Bloes, C., Kuras, M., Duval, M., Nagy, L., Scholtz, B., Hancock, W., Karger, B., Guttman, A., and Takacs, L., (2007), Monoclonal antibody proteomics: Discovery and prevalidation of chronic obstructive pulmonary disease biomarkers in a single step. Electrophoresis 28(23), 4401 – 4406

- Duval, M., (2004), Intellectual property and genetic sequences: moving toward an integrated information system. Journal of International Biotechnology Law, 01(04), 156 – 160

- Dufresne, G. and Duval, M., (2004), Genetic sequences: how are they patented. Nature Biotechnology, 22(2) 231-232

- Anderle, P., Duval, M., Draghici, S., Kuklin, A., Littlejohn, T., Medrano, J.F., Vilanova, D., Roberts, M.A., (2003), Gene expression databases and data mining. Biotechniques. Mar; Suppl: 36 – 44

- Dufresne, G., Takacs, L., Heus, H.C., Codani, J.J. and Duval, M., (2002), Patent searches for genetic sequences: How to retrieve relevant records from patented sequence databases. Nature Biotechnology, 20(12): 1269 – 71

- Duval, M., Hsieh, T.F., Kim, S.Y. and Thomas, T.L., (2002), Molecular characterization of AtNAM: a member of the Arabidopsis NAC domain superfamily Plant Mol Biol., 50, 237 – 248

- Job, C., Laugel, S., Duval, M., Gallardo, K. and Job, D., (2001), Biochemical characterization of atypical biotinylation domains in seed proteins. Seed Science Research, 11, 149 – 162

- Dehaye, L., Duval, M., Viguier, D., Yaxley, J. and Job, D., (1997), Cloning and expression of the pea gene encoding SBP65, a seed-specific biotinylated protein. Plant Mol Biol., 35, 605 – 621

- Duval, M., Loiseau, J., Dehaye, L., Pépin, R., LeDeunff, Y., Wang, T., and Job, D., (1996), SBP65, a seed-specific biotinylated protein, behaves as a LEA protein in developing pea embryos. C.R. Acad. Sci. Paris., 319: 585 – 94

- Duval, M., Pépin, R., Job, C., Derpierre, C., Douce, R. and Job, D., (1995), Ultrastructural localization of the major biotinylated protein from Pisum sativum seeds. J. Exp. Bot. 46: 1783 – 1786

- Duval, M., DeRose, R.T., Job, C., Faucher, D., Douce, R. and Job, D., (1994), The major biotinyl protein from Pisum sativum seeds covalently binds biotin at a novel site. Plant Mol Biol., 26, 265 – 273

- Duval, M., Job, C., Alban, C., Douce, R. and Job, D., (1994), Developmental patterns of free and protein-bound biotin during maturation and germination of Pisum sativum: characterization of a novel seed-specific biotinylated protein. Biochem, J., 299, 141 – 150

- Duval, M., Job, C., Alban, C., Sparace, S., Douce, R. and Job, D., (1993), Synthesis and degradation of a novel biotinyl protein in developing and germinating pea seeds. C.R. Acad. Sci. Paris., 316, 1463 – 70

- Duval, M., Job, C. and Job, D., (1993), An immunoenzymatic study of the large subunits of wheat germ RNA polymerase II. Application to the study of an immobilized eukaryotic RNA polymerase. C.R. Acad. Sci. Paris., 316, Série III, 59 – 65

Book chapters

- Duval, M. and Hsieh, T.F., (2006), Patenting applied to Genetic Sequence Information. In Biotechnology and Genetic Engineering Review. Intercept Ltd., ISSN: 0264 – 8725. 23, 317 – 330
- Duval, M., (2002), DNA array information workflow and data management. In DNA Array Image Analysis: Nuts & Bolts. (2002). United States: DNA Press. (eds S. Sha and G. Kamberova), DNA Press ISBN 0-9664027-5-8

- Chuang, H.W., Hsieh, T.F., Duval, M. and Thomas, T.L., (2002), Genomic analysis of Arabidopsis gene expression in response to a systemic fungicide. In Genomics of Plants and Fungi, (eds. R.A. Prade and H.J.Bohnert), CRC Press pp 237-253. ISBN 13: 9780824741259

Patents

- Sequence Conversion Reaction (Filing Date: 2022), Schoenbrunner, N. and Duval, M., Assigned to BONADEA DIAGNOSTICS, LLC WO/2023/107713

- Monoclonal antibody based biomarker discovery and development platform. (Filing Date: 2005), Takacs, L., Guttman, A., Hancock, W., Karger, B., Duval, M. and Berna, P., Assigned to Northwestern University WO2005077106A3

- Systems and methods for sequence comparison (Filing Date: 2003), Duval, M., Codani, J.J., Takacs, L. and Glemet, E., Assigned to Gene it. WO2004051561A3

- Patent: Seed specific biotinylated protein, SBP65, from leguminous plants (Filing Date: 1998), De Rose, R., Douce, R., Duval, M., Job, C. and Job, D. Assigned to RHONE-POULENC AGROCHIMIE US5837820A

White Papers

- Reducing the odds — how to prepare for the impact of big data (2018), European Pharmaceutical manufacturer

Blogs

- Accessing the NCI Genomic Data Commons resource with Bioconductor R packages RPubs

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Teaching Experience

Graduate Professional Studies Instructor Mar 2014 – Jun 2015
[Brandeis University, Waltham, MA USA](#)
Whole-genome Gene Expression Analysis class.

Adjunct Professor Sep 2011 – Jul 2015
[University of New Haven, West Haven, CT, USA](#)
Bioinformatics, Database systems for biological research and Bioinformatics courses.
Introduction to NextGen DNA sequence analyses.

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