Walter Jessen

B.S., Ph.D.

– DIGITAL BIOLOGIST AND DATA SCIENTIST –

walter [at] walterjessen [dot] com – Indianapolis, IN

I am an entrepreneurial biologist and data scientist with **18 years of experience** in **drug development, diagnostics, and disease biology.** My expertise focuses on the analysis and modeling of large biomedical and clinical data to understand the molecular mechanisms that lead to disease development, progression, diagnostic detection, and response to treatment. I can use both existing approaches and innovate to solve major challenges in the R&D drug discovery process. I have **expertise in 'omics analysis, multivariate analysis, machine learning and data engineering**. I have expertise in building and analyzing disease biology models (knowledge graphs) that can be used to describe health and disease at the molecular level, and to **identify and prioritize candidate biomarkers and therapeutics**. I am knowledgeable with application development in a cloud-based environment and building and supporting expert systems, including artificial intelligence (AI), knowledge graphs, and user-generated platforms. I have a keen eye for improvement opportunities and a demonstrated ability to deliver computational biology solutions while working across different technologies and in a cross-functional environment.

– EXPERIENCE –

Associate Director for Biomarkers, Early & Exploratory Biostatistics, Data Science
Astellas Pharma US : February 2023 – Present

Biomarker statistical expert representing Data Science. Develops and executes project specific biomarker strategies for one or more multiple global projects. Participates in project teams for planning and development of early phase clinical trials in clinical development programs and/or lifecycle management of marketed products. Utilizes knowledge from clinical biomarkers in clinical trials with a variety of 'omics data and clinical trial endpoint data into the strategy for progressing development projects.

Key achievements:

- Provided strategic input and testing of high-performance scientific computing environments.
- Focused on generative AI capabilities, including synthetic data and large language models (LLMs).

Principal AI/ML Data Scientist & Systems Biologist
Laboratory Corporation of America (Labcorp) : July 2020 – February 2023

Leads development of diagnostic test recommendations using machine learning to provide insights based on real-world laboratory testing, augment clinical guidelines, and more accurately target early interventions for use in clinical decision support and clinical trial recruitment. Routinely runs experiments to determine evaluate model performance and parameter behaviour, improve feature selection, better explain model classification, and link to known disease biology and published results. **Leads new feature development** for Compass AI, consisting of an AI-driven biomarker-to-test and analyte-to-test recommendation system, a search engine for analytes, test & result codes, NGS panel genes, laboratories, and an ICD9/10 lookup and translation tool.

Key achievements:

- Leads development and implementation of test recommendations using machine learning.
- Develops disease biology models (disease-specific knowledge graphs) to identify biomarker candidates for client presentations and RFPs.
- Labcorp IT Innovation Days winner, 2021 Ambitious Idea: Clinical Decision Support with Artificial Intelligence.

Principal Data Scientist, Systems Biologist & Knowledge Engineer

Laboratory Corporation of America (Labcorp) : October 2019 – July 2020

Served as lead of knowledge engineering for a team of three focusing on an enterprise knowledge graph. Also a member of a larger team focused on machine learning to predict abnormal results for tests used in the diagnosis of a given disease. Interviewed medical subject matter experts to identify relevant testing. Built patient cohorts from Amazon Athena, Hadoop Hue, Datameer, and Oracle databases. Built, launched and administrated the Labcorp Knowledge Wiki, a platform to capture, archive and share biological, clinical, operational and institutional knowledge.

Key achievements:

- Lead development of an enterprise knowledge graph.
- Lead development of test recommendations using machine learning.
- Developed an internship project and managed a remote intern (2020).
- Labcorp IT Innovation Days winner, 2020 Most Innovative Idea: Cognitive MDSL on FHIR.

Senior Data Scientist, Systems Biologist & Knowledge Engineer

Laboratory Corporation of America (Labcorp) : November 2016 – October 2019

Leveraged existing methods and developed new analytical approaches for the discovery, integration, analysis, and modeling of molecular data from a wide variety of sources including patient data, literature and high-throughput 'omic platforms. Worked closely with scientists, software engineers and clinicians to support integrative data discovery and reporting (including biomarkers, alternative testing, etc.) in a clinical/diagnostic setting.

Key achievements:

- Launched the first production version of Compass AI, an internal company test search engine and biomarker recommendation system.
- Presented/promoted Compass AI across the enterprise on a monthly basis for over a year.
- Developed an internship project, managed an intern, and coordinated all site intern program activities (2017).

Principal & Entrepreneur

Highlight Health Media : December 2006 – December 2018

New media lab, incubator and online publisher focusing on health and life sciences (sole proprietorship). Created and delivered content to attract and engage a defined target audience. Served as editor and lead writer, **directed a staff of four**, oversaw advertising and social media, managed a variety of new media projects, and evaluated new ways to engage audiences and to communicate and collaborate utilizing multimedia tools and internet technologies. Advised clients on key tactics, best practices, digital marketing approaches, and channel measurement plans.

Key achievements:

- Self-taught web development, HTML, CSS, PHP, JavaScript and Linux server administration.
- Developed customized business intelligence systems (automated data mining) to help organizations dealing with information overload.
- Company was profitable for ten years.

Adjunct Assistant Professor of Bioinformatics

Indiana University School of Informatics and Computing : January 2016 – January 2017

Participated in departmental bioinformatics faculty research, in particular the development and use of a visual exploratory tool for expression panel biomarkers organized by molecular interaction networks (knowledge graphs).

Key achievements:

- Mentored undergraduate and graduate students through the Indiana Center for Systems Biology and Personalized Medicine focused on developing systems biology techniques for advancing drug discovery.

Systems Biologist & Senior Data Scientist
Covance : August 2012 – November 2016

Primary responsibility was to liaise Informatics with Covance Early Development and drive new collaborations. Researched existing methods and developed new approaches for the statistical and computational analysis and modeling of drug development data. Leveraged feature selection procedures to distill large datasets and identify relevant pieces of information. Collaborated with key business groups to develop and execute processes to collect, perform data quality assurance, and to structure data. Responsible for the visualization of data for clinical metrics, operational analysis, clinical and financial forecasting. Executed recurring data mining activities providing for key analytical capabilities.

Key achievements:

- Conceived and started development of Compass AI, an internal company test search engine and biomarker recommendation system.
- Developed internship projects, managed interns, and coordinated all site intern program activities (2014 – 2016).
- Nominated for the Covance Way Award, 2015, which recognizes the top 1% of employees globally who demonstrate exemplary performance during a given year.

Affiliate Research Scientist
Center for Systems Biology & Personalized Medicine : November 2013 – December 2015

Mentored students in the Indiana University Purdue University Indianapolis (IUPUI) Multidisciplinary Undergraduate Research institute Systems Pharmacology project "Rapid development of clinical trial candidates using cancer systems pharmacology." Identified relationships among genes, diseases, drugs, protein targets and symptoms/phenotypes.

Key achievements:

- Developed an academic and business relationship with the Center for Systems Biology & Personalized Medicine at IUPUI to recruit Covance interns.

Computational Biologist
Covance Biomarker Center of Excellence : April 2010 – August 2012

Routinely mined, analyzed and interpreted complex biological and clinical data from various sources. Developed computational tools and interfaces to support biomarker data mining. Developed computational methods and algorithms. Worked closely with therapeutic area experts and marketing to define and implement a digital science marketing strategy for the Biomarker Center of Excellence. Routinely oversaw and coordinated the creation, organization, production and dissemination of scientist-generated media. Maintained a portfolio of projects for external communication of science-related activities.

Key achievements:

- Responsible for bringing in over $400,000 in client project revenue.
- Conceived and implemented a method to model disease biology and identify candidate biomarkers.
- Developed an internship project and managed an intern (2012).
- Nominated for the Covance Way Award, 2011, which recognizes the top 1% of employees globally who demonstrate exemplary performance during a given year.

Bioinformatics Research Associate

Cincinnati Children's Hospital Medical Center : January 2008 – April 2010

Responsible for developing data resources that allowed for the use of a variety of statistical and biological analysis approaches to evaluate microarray data, as well as additional data related to variations in disease severity, histological patterns and proteomic data being collected from mouse animal models of neurofibromatosis type 1 (NF1), human neurofibromas and malignant peripheral nerve sheath tumors. **Lead bioinformatician that collaborated with principle investigators of the Neurofibromatosis Microarray and Systems Biology Consortium** to develop bioinformatics analyses to understand the molecular mechanisms by which tumors form and progress with the ultimate goal of developing treatment strategies.

Key achievements:

- Developed integrative genomic approaches to identify NF1 biomarkers and therapeutic targets.
- Identified MEK as a therapeutic target to reduced aberrantly proliferating cells in neurofibroma and MPNST, prolong survival of mice implanted with human MPNST cells, and shrink neurofibroma tumor volume.
- Developed systems biology approaches to understand the mechanisms of NF1, NF2 and Schwannomatosis tumor development and progression.

Postdoctoral Research Fellow in Informatics: Genomics, Bioinformatics

Cincinnati Children's Hospital Medical Center : September 2004 – December 2007

Utilized transcriptional regulatory and gene interaction networks, cancer biology and embryonic and postnatal development in human and mouse models to inform and characterize biological states, disease processes and developmental disorders. Used functional and comparative genomics approaches, as well as the incorporation of histologic patterns and clinical information, to develop an integrative biology approach that could be applied to a range of genetic diseases.

Key achievements:

- Developed fluency with cancer biology and embryonic & postnatal development in human and mouse models.
- Developed a cross-species virtual microarray to analyze and visualize mouse-human gene ortholog expression.
- Developed bioinformatics, functional genomics, and statistical skills.

– EDUCATION –

Doctor of Philosophy (PhD): Molecular Biology and Biochemistry
Texas A&M University, College Station, TX : 2004

Developed a kinetic approach for analysis of chromatin remodeling in vivo, demonstrating that nucleosomes proximal to transactivator binding sites are remodeled earlier than those more distal. Developed an in vivo single molecule assay that identifies multiple promoter classes and supports a probabilistic model in which chromatin remodeling spreads from sites of transactivator binding and attenuates with distance. Bioengineered inducible DNA methyltransferase systems for the in vivo detection of chromatin structural changes, targeted methylation, and factor footprints.

Bachelor of Science (BS): Mathematical Physics
Purdue University, Hammond, IN : 1998

Physics research project involved the design, construction and use of a nitrogen laser for the study of dielectric breakdown and spark generation. Presented "Dielectric Breakdown and Spark Generation" at the Annual Argonne Undergraduate Research Symposium, Argonne National Lab.

- Teaching Assistant, Introductory Physics; Physics and Math Tutor
- Employed full-time while attending classes and maintained a GPA of 3.4
- President, Society of Physics Students
- "Best and Brightest" award, Department of Chemistry and Physics
- Nominated to Sigma Xi, the Scientific Research Honor Society

– SKILLS –

Creative / Critical thinking / Intellectual curiosity / Strong business acumen

Experienced in disease biology analysis

Providing actionable data / Producing testable hypotheses

Data analysis / Statistics / Data wrangling

Artificial Intelligence (AI) / Machine Learning (ML)

Python / R / SQL / Bash/shell scripting / HTML / CSS / JavaScript

AWS SageMaker / AWS Athena / AWS S3 / AWS QuickSight

Graph database management system Neo4j / Graph database query language Cypher

Git/ Jenkins / Jira (issue tracking) / Confluence (wiki) / Linux systems administration

Expert at communicating complex information to non-technical audiences

– PATENTS –

1. Predicting a Result for a Diagnostic Test from Patient Laboratory Testing History, pending, US 63/278,342.

2. Compositions and Methods for Detection of Diseases Related to Exposure to Inhaled Carcinogens, pending, US 20200332364 16/611628.

3. Compositions and Methods to Detect Kidney Fibrosis, pending, US20200087729A1 16/409520, EP3791190A2, CN112424605A, CA3098147A1, WO2019217899A2, JP2021523365A.

4. Compositions and Methods to Detect Non-Celiac Gluten Sensitivity, issued 9/2021, US 11,125,759. US20220074952A1, EP3622298A1, CN110622005A, CA3057421A1, WO2018209180A1, JP2020519877A.

5. Systems and Methods for Biomarker Identification, issued 12/2020, US 10,861,583. US20200332364A1, EP3622424A1, CN110892080A, CA3060364A1, WO2018209165A1, JP2020522045A.

– PUBLICATIONS –

1. Predicting Non-Alcoholic Steatohepatitis (NASH) Fibrosis from Patient Laboratory Testing History. **Jessen WJ**, Konzelman C, Robinson M, Connelly MA, Landschulz KT, Filozof C, Patrick R, Sullivan A, Letovsky S. In preparation.

2. Modeling COVID-19 disease biology to identify drug treatment candidates. **Jessen WJ**, Diaz Gaisenband S, Quintanilla M, Lula S, McLeroth P, Letovsky S. In preparation.

3. Cxcr3-expressing leukocytes are necessary for neurofibroma formation in mice. Fletcher JS, Wu J, **Jessen WJ**, Pundavela J, Miller JA, Dombi E, Kim MO, Rizvi TA, Chetal K, Salomonis N, Ratner N. JCI Insight. 2019 Feb 7;4(3):e98601. doi: 10.1172/jci.insight.98601. Online ahead of print. PMID: 30728335

4. Global methylation profiles in buccal cells of long-term smokers and moist snuff consumers. **Jessen WJ**, Borgerding MF, Prasad GL. Biomarkers. 2018 Nov;23(7):625-639. doi: 10.1080/1354750X.2018.1466367. Epub 2018 Jul 3. PMID: 29771158

5. Insertional Mutagenesis Identifies a STAT3/Arid1b/β-capelin Pathway Driving Neurofibroma Initiation. Wu J, Keng VW, Patmore DM, Kendall JJ, Patel AV, Jousma E, **Jessen WJ**, Choi K, Tschida BR, Silverstein KA, Fan D, Schwartz EB, Fuchs JR, Zou Y, Kim MO, Dombi E, Levy DE, Huang G, Cancelas JA, Stemmer-Rachamimov AO, Spinner RJ, Largaespada DA, Ratner N. Cell Rep. 2016 Mar 1;14(8):1979-90. doi: 10.1016/j.celrep.2016.01.074. Epub 2016 Feb 18. PMID: 26904939

6. Runx1 contributes to neurofibromatosis type 1 neurofibroma formation. Li H, Zhao X, Yan X, **Jessen WJ**, Kim MO, Dombi E, Liu PP, Huang G, Wu J. Oncogene. 2016 Mar 17;35(11):1468-74. doi: 10.1038/onc.2015.207. Epub 2015 Jun 15. PMID: 26073082

7. Therapeutic potential of HSP90 inhibition for neurofibromatosis type 2. Tanaka K, Eskin A, Chareyre F, **Jessen WJ**, Manent J, Niwa-Kawakita M, Chen R, White CH, Vitte J, Jaffer ZM, Nelson SF, Rubenstein AE, Giovannini M. Clin Cancer Res. 2013 Jul 15;19(14):3856-70. doi: 10.1158/1078-0432.CCR-12-3167. Epub 2013 May 28. PMID: 23714726

8. MEK inhibition exhibits efficacy in human and mouse neurofibromatosis tumors. Jessen WJ, Miller SJ, Jousma E, Wu J, Rizvi TA, Brundage ME, Eaves D, Widemann B, Kim MO, Dombi E, Sabo J, Hardiman Dudley A, Niwa-Kawakita M, Page GP, Giovannini M, Aronow BJ, Cripe TP, Ratner N. J Clin Invest. 2013 Jan;123(1):340-7. doi: 10.1172/JCI60578. Epub 2012 Dec 10. PMID: 23221341

9. Cyclin D1 is a selective modifier of androgen-dependent signaling and androgen receptor function. Comstock CE, Augello MA, Schiewer MJ, Karch J, Burd CJ, Ertel A, Knudsen ES, **Jessen WJ**, Aronow BJ, Knudsen KE. J Biol Chem. 2011 Mar 11;286(10):8117-27. doi: 10.1074/jbc.M110.170720. Epub 2011 Jan 5. PMID: 21212260

10. Ras-driven transcriptome analysis identifies aurora kinase A as a potential malignant peripheral nerve sheath tumor therapeutic target. Patel AV, Eaves D, **Jessen WJ**, Rizvi TA, Ecsedy JA, Qian MG, Aronow BJ, Perentesis JP, Serra E, Cripe TP, Miller SJ, Ratner N. Clin Cancer Res. 2012 Sep 15;18(18):5020-30. doi: 10.1158/1078-0432.CCR-12-1072. Epub 2012 Jul 18. PMID: 22811580

11. Gene expression analysis identifies potential biomarkers of neurofibromatosis type 1 including adrenomedullin. Hummel TR, **Jessen WJ**, Miller SJ, Kluwe L, Mautner VF, Wallace MR, Lázaro C, Page GP, Worley PF, Aronow BJ, Schorry EK, Ratner N. Clin Cancer Res. 2010 Oct 15;16(20):5048-57. doi: 10.1158/1078-0432.CCR-10-0613. Epub 2010 Aug 25. PMID: 20739432

12. Transcriptional recapitulation and subversion of embryonic colon development by mouse colon tumor models and human colon cancer. Kaiser S, Park YK, Franklin JL, Halberg RB, Yu M, **Jessen WJ**, Freudenberg J, Chen X, Haigis K, Jegga AG, Kong S, Sakthivel B, Xu H, Reichling T, Azhar M, Boivin GP, Roberts RB, Bissahoyo AC, Gonzales F, Bloom GC, Eschrich S, Carter SL, Aronow JE, Kleimeyer J, Kleimeyer M, Ramaswamy V, Settle SH, Boone B, Levy S, Graff JM, Doetschman T, Groden J, Dove WF, Threadgill DW, Yeatman TJ, Coffey RJ Jr, Aronow BJ. Genome Biol. 2007;8(7):R131. doi: 10.1186/gb-2007-8-7-r131. PMID: 17615082

13. PTEN and NF1 inactivation in Schwann cells produces a severe phenotype in the peripheral nervous system that promotes the development and malignant progression of peripheral nerve sheath tumors. Keng VW, Rahrmann EP, Watson AL, Tschida BR, Moertel CL, **Jessen WJ**, Rizvi TA, Collins MH, Ratner N, Largaespada DA. Cancer Res. 2012 Jul 1;72(13):3405-13. doi: 10.1158/0008-5472.CAN-11-4092. Epub 2012 Jun 14. PMID: 22700876

14. Integrative genomic analyses of neurofibromatosis tumours identify SOX9 as a biomarker and survival gene. Miller SJ, **Jessen WJ**, Mehta T, Hardiman A, Sites E, Kaiser S, Jegga AG, Li H, Upadhyaya M, Giovannini M, Muir D, Wallace MR, Lopez E, Serra E, Nielsen GP, Lazaro C, Stemmer-Rachamimov A, Page G, Aronow BJ, Ratner N. EMBO Mol Med. 2009 Jul;1(4):236-48. doi: 10.1002/emmm.200900027. PMID: 20049725

15. Activator protein-1 transcription factors are associated with progression and recurrence of prostate cancer. Ouyang X, **Jessen WJ**, Al-Ahmadie H, Serio AM, Lin Y, Shih WJ, Reuter VE, Scardino PT, Shen MM, Aronow BJ, Vickers AJ, Gerald WL, Abate-Shen C. Cancer Res. 2008 Apr 1;68(7):2132-44. doi: 10.1158/0008-5472.CAN-07-6055. PMID: 18381418

16. Mapping chromatin structure in vivo using DNA methyltransferases. **Jessen WJ**, Dhasarathy A, Hoose SA, Carvin CD, Risinger AL, Kladde MP. Methods. 2004 May;33(1):68-80. doi: 10.1016/j.ymeth.2003.10.025. PMID: 15039089

17. The SWI/SNF ATPase Brm is a gatekeeper of proliferative control in prostate cancer. Shen H, Powers N, Saini N, Comstock CE, Sharma A, Weaver K, Revelo MP, Gerald W, Williams E, **Jessen WJ**, Aronow BJ, Rosson G, Weissman B, Muchardt C, Yaniv M, Knudsen KE. Cancer Res. 2008 Dec 15;68(24):10154-62. doi: 10.1158/0008-5472.CAN-08-1794. PMID: 19074882

18. Prolonged exposure to reduced levels of androgen accelerates prostate cancer progression in Nkx3.1; Pten mutant mice. Banach-Petrosky W, **Jessen WJ**, Ouyang X, Gao H, Rao J, Quinn J, Aronow BJ, Abate-Shen C. Cancer Res. 2007 Oct 1;67(19):9089-96. doi: 10.1158/0008-5472.CAN-07-2887. PMID: 17909013

19. Targeted cytosine methylation for in vivo detection of protein-DNA interactions. Carvin CD, Dhasarathy A, Friesenhahn LB, **Jessen WJ**, Kladde MP. Proc Natl Acad Sci U S A. 2003 Jun 24;100(13):7743-8. doi: 10.1073/pnas.1332672100. Epub 2003 Jun 13. PMID: 12808133

20. Bayesian hierarchical model for transcriptional module discovery by jointly modeling gene expression and ChIP-chip data. Liu X, **Jessen WJ**, Sivaganesan S, Aronow BJ, Medvedovic M. BMC Bioinformatics. 2007 Aug 3;8:283. doi: 10.1186/1471-2105-8-283. PMID: 17683565

21. Active PHO5 chromatin encompasses variable numbers of nucleosomes at individual promoters. **Jessen WJ**, Hoose SA, Kilgore JA, Kladde MP. Nat Struct Mol Biol. 2006 Mar;13(3):256-63. doi: 10.1038/nsmb1062. Epub 2006 Feb 19. PMID: 16491089