

Anthony P. Fejes

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Summary

My background consists of strong programming skills as well as significant training in biochemistry and microbiology, which positions me well to contribute in multidisciplinary areas such as bioinformatics and computational biology. Additionally, I bring five years of hands-on experience in the development of software for Next-Generation DNA sequencing analysis and three years of leadership and organizational experience gained as the founder of a successful Canadian bioinformatics corporation.

Education

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| <i>2007–2012</i> | Ph.D. Bioinformatics
University of British Columbia , Vancouver, British Columbia, Canada
Thesis Supervisor: Dr. Steven J.M. Jones
Thesis: Algorithms and Applications of Next-Generation DNA Sequencing: Chip-Seq, database of human variations, and analysis of mammary ductal carcinomas |
| <i>2001–2004</i> | M.Sc. Microbiology & Immunology
University of British Columbia , Vancouver, British Columbia, Canada
Thesis Supervisor: Dr. J. Thomas Beatty
Thesis: Mass Spectrometry of <i>Rhodopseudomonas palustris</i> Chromatophores, Method for Displaying Proteomes |
| <i>1997–2001</i> | B.I.S. Independent Studies
University of Waterloo , Waterloo, Ontario, Canada
Thesis Supervisors: Dr. Paul Kearney, Dr. Patricia Schulte
Thesis: Selected Topics in Bioinformatics |
| <i>1995–2000</i> | B.Sc. Honours Co-op Biochemistry
University of Waterloo , Waterloo, Ontario, Canada
Thesis Supervisor: Dr. Elizabeth M. Meiering
Thesis: Computationally Modelled Properties of Beta-Trefoil Proteins |

Skills

Science	<ul style="list-style-type: none">• Extensive experience with molecular simulations and bioinformatics algorithms• Extensive experience with genomics and second generation (next-generation) sequencing platforms, PCR, electron microscopy, mass spectrometry analysis, microbial culture and molecular biology techniques
Computer	<ul style="list-style-type: none">• Expert knowledge with the Linux operating system, open source software and programming tool chain applications. Familiarity with Mac OSX and Windows.
Development	<ul style="list-style-type: none">• Significant experience with Java, C, C++, Pascal, HTML, ASP, SQL, Perl, BASIC, Cognos Suite Tools, Visual BASIC as well as numerous web development tools and languages

Professional Experience

2011-current	Bioinformatics Specialist CLC bio A/S , Århus, Denmark <ul style="list-style-type: none">• Develop algorithms for Next-Generation sequencing platform analysis• Develop work-flows and reporting for Clinical Diagnostic platform prototypes• Work with software engineering group to develop novel visualization platforms
2003-2006	Founder and Chief Scientific Officer ZymeWorks Inc. , Vancouver, British Columbia <ul style="list-style-type: none">• Responsible for intellectual property strategy and charting the company vision• Hired and managed a staff of engineers, scientists and interns• Oversaw the development and management of the company from founding• Responsible for identifying and meeting business opportunities
1999-2001	Software Consultant University of Waterloo , IST Department, Waterloo, Ontario <ul style="list-style-type: none">• Contracted to design and develop a comprehensive Cognos-based reporting system including web applications and catalogs• Planned and Implemented university-wide web deployment of Cognos suite tools• Managed co-op students and guided development on the Cognos platform
1998-1998	Programmer/Analyst (Co-op) University of Waterloo , IST Department, Waterloo, Ontario <ul style="list-style-type: none">• Y2k modifications and legacy programming in BASIC
1997-1998	Information Systems Programmer (Co-op) London Guarantee Insurance Company , IT Department, Toronto, Ontario <ul style="list-style-type: none">• Responsible for maintaining and coordinating changes for central reporting infrastructure based on core transaction data• Migration of company-wide transaction database to custom software package
1996-1996	Assistant Systems Analyst (Co-op) Human Resources Development Canada , LOAD Department, Hull, Quebec <ul style="list-style-type: none">• Change request management (CRM) application development

Academic Awards

- 2010 | Ph.D. Tuition Fee Award (University of British Columbia)
- 2010 | BIOTECanada TVG Student Bursary 2010 (BC)
- 2009 | Ph.D. Tuition Fee Award (University of British Columbia)
- 2009 | Award of Excellence (Silver category), Canadian Institutes of Health Research National Research Poster Competition.
- 2008 | Ph.D. Tuition Fee Award (University of British Columbia)
- 2008 | Michael Smith Foundation for Health Research, Research Trainee Award (3 years award)
- 2007 | Ph.D. Tuition Fee Award (University of British Columbia)
- 2007 | Genome BC Scientific Travel Award (3rd place poster at Research Exchange 2007)
- 2007 | Ph.D. Tuition Fee Award (University of British Columbia)
- 2000 | University of Waterloo Independent Studies Scholarship

Publications and Patents

- 2012 | D. Doherty, A. E. Chudley, G. Coghlan, G. E. Ishak, A. M. Innes, E. G. Lemire, R. C. Rogers, A. A. Mhanni, I. G. Phelps, S. J. M. Jones, S. H. Zhan, A. P. Fejes, H. Shahin, M. Kanaan, H. Akay, M. Tekin, B. Triggs-Raine, and T. Zelinski. "GPSM2 Mutations Cause the Brain Malformations and Hearing Loss in Chudley-McCullough Syndrome". In: *The American Journal of Human Genetics* (2012),
- 2012 | W. T. Gibson, R. L. Hood, S. H. Zhan, D. E. Bulman, A. P. Fejes, R. Moore, A. J. Mungall, P. Eydoux, R. Babul-Hirji, J. An, M. A. Marra, D. Chitayat, K. M. Boycott, D. D. Weaver, and S. J. Jones. "Mutations in EZH2 cause Weaver syndrome". In: *Am. J. Hum. Genet.* 90.1 (Jan. 2012), pp. 110–118
- 2011 | A. P. Fejes, A. Hadj Khodabakhshi, I. Birol, and S. J. Jones. "Human Variation Database: An open source database template for genomic discovery". In: *Bioinformatics* (Mar. 2011)
- 2011 | A. Heravi-Moussavi, M. S. Anglesio, S. W. Cheng, J. Senz, W. Yang, L. Prentice, A. P. Fejes, C. Chow, A. Tone, S. E. Kalloger, N. Hamel, A. Roth, G. Ha, A. N. Wan, S. Maines-Bandiera, C. Salamanca, B. Pasini, B. A. Clarke, A. F. Lee, C. H. Lee, C. Zhao, R. H. Young, S. A. Aparicio, P. H. Sorensen, M. M. Woo, N. Boyd, S. J. Jones, M. Hirst, M. A. Marra, B. Gilks, S. P. Shah, W. D. Foulkes, G. B. Morin, and D. G. Huntsman. "Recurrent Somatic DICER1 Mutations in Nonepithelial Ovarian Cancers". In: *N Engl J Med* (Dec. 2011)
- 2011 | A. P. Fejes, A. H. Khodabakhshi, I. Birol, and S. J. Jones. "Human variation database: an open-source database template for genomic discovery". In: *Bioinformatics* 27 (Apr. 2011), pp. 1155–1156

- 2011 H. Shin, H. Lee, A. P. Fejes, D. L. Baillie, H. S. Koo, and S. J. Jones. "Gene expression profiling of oxidative stress response of *C. elegans* aging defective AMPK mutants using massively parallel transcriptome sequencing". In: *BMC Res Notes* 4 (2011), p. 34
- 2010 V. Boeva, D. Surdez, N. Guillon, F. Tirode, A. P. Fejes, O. Delattre, and E. Barillot. "De novo motif identification improves the accuracy of predicting transcription factor binding sites in ChIP-Seq data analysis". In: *Nucleic Acids Res.* 38 (June 2010), e126
- 2010 S. J. Jones, J. Laskin, Y. Y. Li, O. L. Griffith, J. An, M. Bilenky, Y. S. Butterfield, T. Cezard, E. Chuah, R. Corbett, A. P. Fejes, M. Griffith, J. Yee, M. Martin, M. Mayo, N. Melnyk, R. D. Morin, T. J. Pugh, T. Severson, S. P. Shah, M. Sutcliffe, A. Tam, J. Terry, N. Thiessen, T. Thomson, R. Varhol, T. Zeng, Y. Zhao, R. A. Moore, D. G. Huntsman, I. Birol, M. Hirst, R. A. Holt, and M. A. Marra. "Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors". In: *Genome Biol.* 11 (2010), R82
- 2010 A. P. Fejes and J. S. Swaminathan G. and Vieceli. "System and method for modeling interactions." Patent 7769573 (US). Aug. 3, 2010
- 2008 A. P. Fejes, G. Robertson, M. Bilenky, R. Varhol, M. Bainbridge, and S. J. Jones. "FindPeaks 3.1: a tool for identifying areas of enrichment from massively parallel short-read sequencing technology". In: *Bioinformatics* 24 (Aug. 2008), pp. 1729–1730
- 2008 A. G. Robertson, M. Bilenky, A. Tam, Y. Zhao, T. Zeng, N. Thiessen, T. Cezard, A. P. Fejes, E. D. Wederell, R. Cullum, G. Euskirchen, M. Krzywinski, I. Birol, M. Snyder, P. A. Hoodless, M. Hirst, M. A. Marra, and S. J. Jones. "Genome-wide relationship between histone H3 lysine 4 mono- and tri-methylation and transcription factor binding". In: *Genome Res.* 18 (Dec. 2008), pp. 1906–1917
- 2008 R. Morin, M. Bainbridge, A. Fejes, M. Hirst, M. Krzywinski, T. Pugh, H. McDonald, R. Varhol, S. Jones, and M. Marra. "Profiling the HeLa S3 transcriptome using randomly primed cDNA and massively parallel short-read sequencing". In: *BioTechniques* 45 (July 2008), pp. 81–94
- 2008 A. P. Fejes and S. J. Jones. "Chip-Seq: Mapping of Protein-DNA Interactions". In: *Next-Generation Genome Sequencing: Towards Personalized Medicine*. Ed. by Michal Janitz. Wiley, John & Sons, November 2008
- 2004 M. Andronescu, A. P. Fejes, F. Hutter, H. H. Hoos, and A. Condon. "A new algorithm for RNA secondary structure design". In: *J. Mol. Biol.* 336.3 (Feb. 2004), pp. 607–624
- 2003 A. P. Fejes, E. C. Yi, D. R. Goodlett, and J. T. Beatty. "Shotgun proteomic analysis of a chromatophore-enriched preparation from the purple phototrophic bacterium *Rhodospseudomonas palustris*". In: *Photosyn. Res.* 78.3 (2003), pp. 195–203

Invited Talks

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| 2011 | Invited Speaker, TGEN seminar series Translational Genomics Research Institute (TGEN), phoenix, AZ. |
| 2011 | Bioinformatics Careers Panellist, Vancouver Bioinformatics Users Group (VanBUG), Vancouver, BC. |
| 2011 | Guest Lecturer, Statistics 540 UBC, Vancouver, BC. |
| 2009 | Industry Panellist Fourth Canadian Student Conference on Biomedical Computing, Vancouver, BC. |

Conferences and Posters

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| Nov 2010 &
Feb 2011 | Fejes AP, An J, Li Y, Leach S, Zhao Y, Varhol R, Qian J, Jackman S, Chiu R, Mungall K, Robertson G, She W, Hirst M, Marra MA, BrooksWilson A, Jones SJM. Comparative Analysis of 4 Matched Normal Ductal Carcinoma in Situ Breast Cancer Celllines with 1600 NGS Sequenced Libraries.
Poster presented at the B.C. Cancer Agency Annual Cancer Conference 2010, Vancouver, BC and Advances in Genome Biology and Technology 2011, Marco Island, Florida. |
| Feb 2010 | Fejes AP, Leach S, Zhao Y, Varhol R, Hirst M, Marra MA, Brooks-Wilson A, Jones SJM. RNASeq Determination of Non-Synonymous Coding Mutations in 5 Breast Cancer Cell Lines and a Matched Normal Set.
Poster presented at Advances in Genome Biology and Technology 2010, Marco Island, Florida. |
| Jun 2009 | Fejes AP, Cezard T, Birol I, Jones SJM. Vancouver Short Read Analysis Package and FindPeaks 4.0: Tools for genome wide analysis of transcriptome expression, transcription factor binding and histone modification.
Poster presented at the Canadian Institutes of Health Research National Research Poster Competition, 2009, Winnipeg, Manitoba. |
| Feb 2009 | Fejes AP, Leach S, An J, Brooks-Wilson AR, Novik K, Jones SJM. Identifying cancer related changes in the protein coding genome.
Poster presented at Advances in Genome Biology and Technology 2009, Marco Island, Florida. |
| Apr 2008 | Fejes AP, Leach S, An J, Brooks-Wilson AR, Novik K, Jones SJM. The identification of mutation specific inhibitors through whole genome resequencing of breast cancer cell lines.
Poster presented at the Canadian Breast Cancer Research Alliance Reasons for Hope 2008, Vancouver, BC. |
| Feb 2008 | Fejes AP, Bilenky M, Robertson G, Hirst M, Marra MA, Jones SJM. FindPeaks 3.0.1: A Program for Binding Site Identification and Transcriptome Processing using Massively Parallel Sequencing.
Poster presented at Advances in Genome Biology and Technology 2008, Marco Island, Florida. |
| Dec 2007 | Fejes AP, Bilenky M, Robertson G, Jones SJM. First Generation Software Tools for Next-Generation Sequencing. |

- Poster presented at the B.C. Cancer Agency Annual Cancer Conference 2007, Vancouver, BC.
- May 2007 Robertson G, Hirst M, Bainbridge MN, Bilenky M, Zhao Y, Zeng T, Pandoh P, Fitcher K, Tam A, Prabhu AL, Moksa M, Lee S, Mah D, McDonald H, Delaney A, Thiessen N, Bernier B, Griffith OL, He A, Varhol R, Fejes AP, Euskirchen G, Snyder M, Marra MA, Jones SJM. Genome-wide Profiles of STAT1 DNA Association in HeLa S3 Cells Using Chromatin Immunoprecipitation and Massively Parallel Sequencing.
Poster presented at Cold Spring Harbor, The biology of Genomes Conference
- March 2007 Fejes AP, Bainbridge MN, Prabhu AL, Zhao Y, Magrini V, Mardis E, Hirst M, Relander T, Horsman DE, Gascoyne RD, Connors JM, Marra MA, Jones SJM. Protein Coding Sequence Changes in Follicular Lymphoma. Whole genome approach: untangling the web of cancer genes.
Poster presented at Genome BC Research Exchange 2007.
- Feb 2003 Fejes AP, Yi EC, Goodlett DR and Beatty JT, Mass Spectrometric and Proteomic Analysis of Chromatophores from *Rhodospseudomonas palustris*.
Poster presented at University of British Columbia, Department of Microbiology and Immunology poster session.

References

References available upon request.