

KA YEE YEUNG, PH.D.

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SCIENTIFIC RESEARCH EXPERIENCE

- Extensive independent research experience in computational biology.
- Experience as the Principal Investigator on NIH-funded research grants (R01 and K25).
- Proficient in the preparation, application and management of research grants.
- Diverse research expertise spanning multiple disciplines, including computational biology, computer science, statistics, and biology.
- Collaboration with biomedical and computational scientists to identify research problems, formulate the scientific framework and engineer practical solutions.
- Experience mentoring graduate students and working with software developers in research projects.
- Open-minded approach to problem solving.

RESEARCH INTERESTS

- Development of algorithms and tools for the inference of biological mechanisms by integrating heterogeneous high-throughput data sources.
- Design of practical algorithms and software tools to identify biologically meaningful biomarkers from high-throughput data.
- Customization and validation of data mining and pattern recognition methods applied to high-throughput biological data.
- Development of predictive network models from high-throughput data.
- Collaborative research work spanning both computational and biomedical disciplines.

EDUCATION

- 1998-2001 Ph.D. Computer Science, University of Washington, Seattle, WA
Advisor: Professor Walter L. Ruzzo.
- 1996-1998 M.S. Computer Science, University of Washington, Seattle, WA
Advisor: Professor Richard Karp.
- 1995-1996 M. Mathematics in Computer Science, University of Waterloo, Ontario, Canada
Advisor: Professor Ian Munro.
- 1992-1995 B. Mathematics in Computer Science and Actuarial Science from University of Waterloo, Ontario, Canada

RESEARCH POSITIONS

- 6/04-present **Research Assistant Professor**, Department of Microbiology, University of Washington, Seattle, WA
- 1/02-5/04 **Research Scientist/Senior Fellow**, Department of Microbiology, University of Washington, Seattle, WA
Mentor: Associate Professor Roger Bumgarner

PUBLICATIONS

Original Journal Publications

1. Oehler VG*, **Yeung KY***, Choi E, Bumgarner RE, Raftery AE and Radich. "The derivation of diagnostic markers of chronic myeloid leukemia progression from microarray data". *Blood* 2009. *Co-first authors.
2. Annest A., Bumgarner R.E., Raftery A.E., **Yeung K.Y.** Iterative Bayesian Model Averaging: a method for the application of survival analysis to high-dimensional microarray data. *BMC Bioinformatics*, 2009, 10: 72.
3. Chu VT, Gottardo R, Raftery AE, Bumgarner RE and **Yeung KY**. MeV+R: Using MEV as a GUI for Bioconductor applications. *Genome Biology* 2008, 9:R118.
4. Liu X, Sivaganesan S, **Yeung KY**, Guo J, Bumgarner RE and Medvedovic M. Bayesian Context-specific infinite mixture model for clustering of gene expression profiles across diverse microarray datasets. *Bioinformatics* 2006, 22: 1737-1744
5. Gottardo R, Raftery AE, **Yeung KY** and Bumgarner RE. Bayesian robust inference for differential gene expression in cDNA microarrays with multiple samples. *Biometrics* 2006, 62: 10-18.
6. Gottardo R, Raftery AE, **Yeung KY** and Bumgarner RE. Robust estimation of cDNA microarray intensities with replicates. *Journal of the American Statistical Association* 2006 101: 30-40.
7. Li Q, Fraley C, Bumgarner RE, **Yeung KY** and Raftery AE. Donuts, scratches and blanks: Robust model-based segmentation of microarray images. *Bioinformatics* 2005 21: 2875 - 2882.
8. **Yeung KY**, Bumgarner RE and Raftery AE. Bayesian model averaging: development of an improved multi-class, gene selection and classification tool for microarray data. *Bioinformatics* 2005 21: 2394-2402.
9. Vanasse GJ, Winn RK, Rodov S, Zieske AW, Li JT, Tupper JC, Peters MA, **Yeung KY**, and Harlan JM. Bcl-2 overexpression leads to increases in suppressor of cytokine signaling-3 expression in B cells and de novo follicular lymphoma. *Molecular Cancer Research* 2004, 2: 620-631.
10. **Yeung KY**, Medvedovic M, Bumgarner RE. From co-expression to co-regulation: how many microarray experiments do we need? *Genome Biology* 2004, 5:R48.
11. Medvedovic M, **Yeung KY**, Bumgarner RE. Bayesian mixture model based clustering of replicated microarray data. *Bioinformatics* 2004, 20:1222-1232.
12. **Yeung KY**, Bumgarner RE. Multi-class classification of microarray data with repeated measurements: application to cancer. *Genome Biology* 2003, 4:R83.
13. **Yeung KY**, Medvedovic M, Bumgarner RE. Clustering Gene-Expression Data with Repeated Measurements. *Genome Biology* 2003, 4:R34.
14. Barrett MT, **Yeung KY**, Ruzzo WL, Hsu L, Blount PL, Sullivan R, Zarbl H, Delrow J, Rabinovitch PS, Reid BJ. Transcriptional Analyses of Barrett's Metaplasia and Normal Upper GI Mucosae. *Neoplasia* 2002, 4(2):121-128.
15. **Yeung KY**, Fraley C, Murua A, Raftery AE, Ruzzo WL. Model-based Clustering and Data Transformations for Gene Expression Data. *Bioinformatics* 2001, 17:977-987.
16. **Yeung KY**, Ruzzo WL. Principal Component Analysis for Clustering Gene Expression Data. *Bioinformatics* 2001, 17:763-774.
17. **Yeung KY**, Haynor DR, Ruzzo WL. Validating Clustering for Gene Expression Data. *Bioinformatics* 2001, 17:309-318.

18. Conference Proceeding

19. Karp RM, Stoughton R, **Yeung KY**. Algorithms for Choosing Informative Differential Gene Expression Experiments. *Proceedings of the 3rd annual international conference on computational biology (RECOMB)* 1999, pp. 208-217.

20. Review Article

21. **Yeung KY**, Bumgarner RE. Pattern recognition in expression data. *Recent Developments in Nucleic Acids Research* 2004, 1: 333-354.

22. Book Chapters

23. **Yeung KY**. "Clustering or automatic class discovery: non-hierarchical, non-SOM" in *A practical approach to microarray data analysis*. Kluwer Academic Publisher 2003, Chapter 16.
24. Bumgarner RE and **Yeung KY**. "Methods for the inference of biological pathways and networks" in *Computational Systems Biology*. Methods in Molecular Biology. 2009; 541:225-45.

PROFESSIONAL SKILLS & EXPERIENCE

Scientific Writing and Presentation Experience

- Proven track record of scientific manuscript publications (17 published peer-reviewed scientific articles and 1 submitted manuscript).
- Experience with research grant preparation and application.
- Extensive experience with scientific presentations. Presented at international scientific meetings and conferences.
- Excellent reviews from guest lectures, invited lectures and workshops.
- Excellent communication and presentation skills.

Technical Skills

- Programming experience in C, C++, Java, Perl, R, Splus, Matlab and Maple.
- Scientific writing using Latex, Bibtex, Microsoft Word and EndNote.
- Experience using both commercial and academic data analysis tools, including Bioconductor packages, R, Splus, Matlab, Maple, Rosetta Resolver, SpotFire, and GeneTraffic.
- Experience contributing to publicly available open-source software (including Bioconductor packages).
- Conversant with various operating systems, including Linux, Unix, Mac OS X, Windows; and standard software applications

Other Professional Experience

- Reviewer for various scientific journals, including Bioinformatics, BMC Bioinformatics, Genome Biology, Nucleic Acids Research, Applied Genomics and Proteomics, Biometrics, Biostatistics, the Computer Journal, Pattern Recognition Letters, Statistical Applications in Genetics and Molecular Biology, Journal of Bioinformatics and Computational Biology.
- Grant reviewer for NIH and the University of Washington Royalty Research Fund.
- Invited lectures at a bioinformatics summer school in 2004 (the Advanced School in Biomedicine and Bioinformatics, Lipari, Italy). <http://lipari.cs.unict.it/bio-info/index.htm>
- Experience with developing and managing research budget.
- Poster presentations at scientific meetings.

SPECIAL AWARDS & HONORS

- 2004 **Fast moving front in Computer Science**, Institute of Scientific Information (ISI) Essential Science Indicators. My first-authored publication titled "*Model-based clustering*

and data transformations for gene expression data" (Bioinformatics 2001) was selected to be one of the most highly cited recent papers in Computer Science (Jan 2004).
<http://www.esi-topics.com/fmf/2004/january04-KaYeeYeung.html>

- 2002 **Fast breaking paper in Computer Science**, Institute of Scientific Information (ISI) Essential Science Indicators. My first-authored publication titled "*Validating clustering for gene expression data*" (Bioinformatics 2001) was selected to be one of the most highly cited recent papers in Computer Science (Dec 2002).
<http://www.esi-topics.com/fbp/comments/december02-WalterLRuzzo.html>
- 1996 **Alan George Student Leadership Award**, University of Waterloo, Ontario, Canada
- 1995 **NSERC Scholarship**, National Sciences and Engineering Research Council, Canada. The Natural Sciences and Engineering Research Council of Canada (NSERC) provides financial support to high-calibre scholars who are engaged in postgraduate programs in the natural sciences or engineering.
- 1995 **Provost Scholarship**, University of Waterloo, Ontario, Canada
- 1995 **ITRC Scholarship**, University of Waterloo, Ontario, Canada
- 1995 Honorable Mention, **Outstanding Female Undergraduate Student Competition**, Computing Research Association (CRA). CRA's Outstanding Undergraduate Award program recognizes undergraduate students who show outstanding research potential in an area of computing research. <http://www.cra.org/Activities/awards/undergrad/>