

CURRICULUM VITAE

CHENG LI

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PERSONAL DATA

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 Dana-Farber Cancer Institute (DFCI)
 375 Longwood Ave. Boston, MA, 02215
Place of birth: Bole, Xinjiang, China

EDUCATION AND TRAINING

<i>Date</i>	<i>Degree/Title</i>	<i>Discipline</i>	<i>Institution</i>
2001 – 2002	Research Fellow	Computational Biology	Harvard School of Public Health/DFCI
1997 – 2001	Ph.D.	Statistics	University of California, Los Angeles
1991 – 1995	B.S.	Math/Computer Science	Beijing Normal University, China

ACADEMIC APPOINTMENTS

<i>Dates</i>	<i>Title</i>	<i>Department</i>	<i>Institution</i>
2002 –	Assistant Professor	Biostatistics	Harvard School of Public Health/DFCI
1995 – 1997	Asst. Administrator	Academic Office	Beijing Normal University

PROFESSIONAL SERVICES**External**

1. Associate editor, “IEEE/ACM Transactions on Computational Biology and Bioinformatics”, January 2006 –.
2. Member, Program Committee

- “Conference on Emerging Design and Analysis Issues in Genomic Studies in Population Sciences”, HSPH Biostatistics, October, 2007
- “Computational Systems Bioinformatics Conference (CSB2006)”, August, 2006.
- “The 2003 Affymetrix GeneChip Microarray Low-Level Workshop”, August 7-8, 2003, UC Berkeley.

3. Member, NIH review panel for RFA

- “Genomics of Transplantation Cooperative Research Program”, December 19-21, 2005.
- “Research Centers of Excellence in Pediatric Nephrology”, April 3, 2007 (remote review)

Internal

1. Member, Department committee of Biostatistics, HSPH

- Webpage committee, 2003-04, 06-08 (as chair)
- Diversity committee, 2005, 07
- Teaching effectiveness committee, 2004-05, 07

2. Member, Advisory Committee, HSPH Bioinformatics Core, 2004 –

3. Member, Biostatistics consulting group, DFCI microarray core facility, 2002 –

HONORS

1. Sino-American Pharmaceutical Professionals Association (New England) Contribution Award. December, 2003

MAJOR RESEARCH INTERESTS

I am interested in computational and statistical methods in microarray analysis of gene expression, genome alterations, and genetics, with the goal of contributing to understanding complex human diseases or traits such as cancer and aging.

I am also dedicated to developing and maintaining the user-friendly and free microarray software dChip, which provides many analysis and visualization methods for gene expression and SNP microarray data. New analysis methods are constantly developed and tested in dChip through collaborative projects and then provided for broader use.

RESEARCH SUPPORT

1. 2008 – 2011, NIH 1R01GM077122, PI, “*dChip: Analysis and Visualization of Oligonucleotide Expression and SNP Arrays*” (\$175K direct cost per year)
2. 2004 – 2006, Claudia Adams Barr Program in Cancer Research, PI, “*Developing analysis methods and software for oligonucleotide SNP microarrays*”, \$96K/year for two years.
3. 2003 – 2004, Friends of Dana-Farber Cancer Institute, PI, “*Developing analysis methods and software for SNP microarrays*”, \$44K for one year.

TEACHING EXPERIENCES

<i>Date</i>	<i>Course</i>	<i>Institution</i>	<i>Experience</i>
Fall 2007	Stat. Comp. Environ.	Dept. of Biostatistics, HSPH	Lecturer
Spring 2004	Computational Biology	Dept. of Biostatistics, HSPH	Lecturer
Spring 2003	Computational Biology	Dept. of Biostatistics, HSPH	Participant

<i>Date</i>	<i>Student/Postdoc</i>	<i>Institution</i>	<i>Experience</i>
2004 – 07	Patrick Loerch	Dept. of Biostatistics, HSPH	Ph.D. thesis advising
2002 – 06	Yu Guo	Dept. of Biostatistics, HSPH	Ph.D. thesis advising
2002 – 04	Ming Lin	Dept. of Biostatistics, HSPH	Ph.D. thesis co-advising
2001 – 04	Xuemin Fang	Dept. of Biostatistics, HSPH	Ph.D. thesis co-advising
2007 –	Jie Hu	Dept. of Biostatistics, HSPH	Research project advising
2005 – 06	Xi Deng	Dept. of Biostatistics, HSPH	Research project advising
2004 – 05	Evan Johnson	Dept. of Biostatistics, HSPH	Research project advising
2002 – 04	Ryung Kim	Dept. of Biostatistics, HSPH	Research project advising
2001 – 03	Sheng Zhong	Dept. of Biostatistics, HSPH	Research project advising
2004	Santhoshi Bandla	Northeastern University	Research project advising
2004 – 05	Yuhyun Park	Dept. of Biostatistics, HSPH	Postdoc co-advising
2003 – 04	Igor Leykin	Dept. of Biostatistics, HSPH	Postdoc co-advising
2004 – 05	Yunyu Zhang	DFCI/Harvard-MIT HST	M.S. thesis co-advising

Member of oral exam or thesis committees for other Ph.D. students: Elizabeth Whalen (2004 – 06), Natasa Rajjicic (2004 – 06), David Engler (2005), Beiying Ding (2004)

BIBLIOGRAPHY**Non-print Materials**

dChip Software for Gene Expression Microarray and SNP Microarray Analysis. (www.dchip.org); This software package has been continuously developed, maintained and supported since 2001. The main reference papers for the software have over 1000 citations).

Peer-reviewed Journals, Methods (* Corresponding authors)

1. **Li C.** Automating dChip: toward reproducible sharing of microarray data analysis. *BMC Bioinformatics*. 2008; In press.
2. Johnson WE, **Li C***, Rabinovic A. Adjusting batch effects in microarray expression data using Empirical Bayes methods. *Biostatistics*. 2007; 8(1): 118-127.
3. Beroukhim R, Lin M, Park Y, Hao K, Zhao X, Garraway LA, Fox EA, Hochberg EP, Mellinghoff IK, Hofer MD, Descoteaux A, Rubin MA, Meyerson M, Wong WH, Sellers WR*, **Li C***. Inferring Loss-of-Heterozygosity From Tumor-only Samples Using High-Density Oligonucleotide SNP Arrays. *PLoS Computational Biology*. 2006; 2(5): e41. 1-10.
4. Leykin I, Hao K, Cheng J, Meyer N, Pollak MR, Smith RJ, Wong WH, Rosenow C*, **Li C***. Comparative linkage analysis and visualization of high-density oligonucleotide SNP array data. *BMC Genetics*. 2005; 6:7. 1-16.
5. Lin M, Wei LJ, Sellers WR, Lieberfarb M, Wong WH*, **Li C***. dChipSNP: Significance Curve and Clustering of SNP-Array-Based Loss-of-Heterozygosity Data. *Bioinformatics*. 2004; 20: 1233-1240.
6. Zhong S, **Li C***, Wong WH*. (2003) ChipInfo: Software for Extracting Gene Annotation and Gene Ontology Information for Microarray Analysis. *Nucleic Acids Research*. 2003; 31:3483-3486.
7. **Li C**, Wong WH. Model-based analysis of oligonucleotide arrays: model validation, design issues and standard error application. *Genome Biology*. 2001; 2(8): research0032.1-0032.11
8. **Li C**, Wong WH. Model-based analysis of oligonucleotide arrays: Expression index computation and outlier detection. *Proc. Natl. Acad. Sci.* 2001; 98: 31-36.

Peer-reviewed Journals, Collaborative

9. Bae J, Mitsiades C, Tai YT, Bertheau R, Shamma M, Batchu RB, **Li C**, Catley L, Prabhala R, Anderson KC, Munshi NC. Phenotypic and functional effects of heat shock protein 90 inhibition on dendritic cell. *J Immunol*. 2007; 178(12):7730-7.
10. Park Y, Downing SR, Kim D, Hahn WC, **Li C**, Kantoff PW, Wei LJ. Simultaneous and exact interval estimates for the contrast of two groups based on an extremely high dimensional variable: Application to Mass Spec data. *Bioinformatics*. 2007; 23(12):1451-1458.

11. George RE, Attiyeh EF, Li S, Moreau LA, Neuberg D, **Li C**, Fox EA, Meyerson M, Diller L, Fortina P, Look AT, Maris JM. Genome-Wide Analysis of Neuroblastomas using High-Density Single Nucleotide Polymorphism Arrays. *PLoS ONE*. 2007; 2(2): e255.
12. Vallat LD, Park Y, **Li C**, Gribben JG. Temporal genetic program following B-cell receptor cross-linking: altered balance between proliferation and death in healthy and malignant B cells. *Blood*. 2007; 109(9):3989-97.
13. Juszczynski P, Kutok JL, **Li C**, Mitra J, Aguiar RC, Shipp MA. BAL1 and BBAP are regulated by a gamma interferon-responsive bidirectional promoter and are overexpressed in diffuse large B-cell lymphomas with a prominent inflammatory infiltrate. *Mol Cell Biol*. 2006; 26(14):5348-59.
14. Walker BA, Leone PE, Jenner MW, **C Li**, Gonzalez D, Johnson DC, Ross FM, Davies FE, Morgan GJ. Integration of global SNP-based mapping and expression arrays reveals key regions, mechanisms, and genes important in the pathogenesis of multiple myeloma. *Blood*. 2006; 108: 1733-1743.
15. Moran JL, Bolton AD, Tran PV, Brown A, Dwyer ND, Manning DK, Bjork BC, **Li C**, Montgomery K, Siepka SM, Vitaterna MH, Takahashi JS, Wiltshire T, Kwiatkowski DJ, Kucherlapati R, Beier DR. Utilization of a whole genome SNP panel for efficient genetic mapping in the mouse. *Genome Res*. 2006; 16:436-440.
16. Garraway LA, Widlund HR, Rubin MA, Getz G, Berger AJ, Ramaswamy S, Beroukhim R, Milner DA, Granter SR, Du J, Lee C, Wagner SN, **Li C**, Golub TR, Rimm DL, Meyerson ML, Fisher DE, Sellers WR. Integrative genomic analyses identify MITF as a lineage survival oncogene amplified in malignant melanoma. *Nature*. 2005; 436(7047):117-22.
17. LaFramboise T, Weir BA, Zhao X, Beroukhim R, **Li C**, Harrington D, Sellers WR, Meyerson M. Allele-Specific Amplification in Cancer Revealed by SNP Array Analysis. *PLoS Comput Biol*. 2005; 1(6): e65.
18. Wang Z, Neuburg D, **Li C**, Su L, Kim JY, Chen JC, Christiani DC. Global gene expression profiling in whole-blood samples from individuals exposed to metal fumes. *Environ Health Perspect*. 2005; 113(2):233-41.
19. Dahia PL, Hao K, Rogus J, Colin C, Pujana MA, Ross K, Magoffin D, Aronin N, Cascon A, Hayashida CY, **Li C**, Toledo SP, Stiles CD; Familial Pheochromocytoma Consortium. Novel Pheochromocytoma Susceptibility Loci Identified by Integrative Genomics. *Cancer Res* 2005; 65: 9651-9658.
20. Goodison S, Yuan J, Sloan D, Kim R, **Li C**, Popescu NC, Urquidi V. The RhoGAP protein DLC-1 functions as a metastasis suppressor in breast cancer cells. *Cancer Res*. 2005; 65(14):6042-53.
21. Zhao X, Weir BA, LaFramboise T, Lin M, Beroukhim R, Garraway L, Beheshti J, Lee JC, Naoki K, Richards WG, Sugarbaker D, Chen F, Rubin MA, Janne PA, Girard L, Minna J, Christiani D, **Li C**, Sellers WR, Meyerson M. Homozygous Deletions and Chromosome

- Amplifications in Human Lung Carcinomas Revealed by Single Nucleotide Polymorphism Array Analysis. *Cancer Research*. 2005; 65: 5561-5570.
22. Lu T, Pan Y, Kao SY, **Li C**, Kohane I, Chan J, Yankner BA. Gene regulation and DNA damage in the ageing human brain. *Nature*. 2004; 429: 883–891.
 23. Zhao X, **Li C**, Paez JG, Chin K, Janne PA, Chen TH, Girard L, Minna J, Christiani D, Leo C, Gray JW, Sellers WR, Meyerson M. An integrated view of copy number and allelic alterations in the cancer genome using single nucleotide polymorphism arrays. *Cancer Research*. 2004; 64:3060-3071.
 24. Janne PA, **Li C**, Zhao X, Girard L, Chen TH, Minna J, Christiani DC, Johnson BE, Meyerson M. High-resolution single-nucleotide polymorphism array and clustering analysis of loss of heterozygosity in human lung cancer cell lines. *Oncogene*. 2004; 23(15):2716-26.
 25. Hao K, **Li C**, Rosenow C, Wong WH. Detect and adjust for population stratification in population-based association study using genomic control markers. *European Journal of Human Genetics*. 2004; 12:1001-1006.
 26. Hao K, **Li C**, Rosenow C, Wong WH. Estimation of Genotype Error Rate Using Samples with Pedigree Information -- An application on GeneChip Mapping 10K array. *Genomics*. 2004; 84: 623-630.
 27. Wang ZC, Lin M, Wei LJ, **Li C**, Miron A, Lodeiro G, Harris L, Ramaswamy S, Tanenbaum DM, Meyerson M, Iglehart JD, Richardson A. Loss of heterozygosity and its correlation with expression profiles in subclasses of invasive breast cancers. *Cancer Research*. 2004; 64(1): 64-71.
 28. Willis DJ, Kalish JA, **Li C**, Deutsch ER, Contreras MA, LoGerfo FW, Quist WC. Temporal gene expression following prosthetic arterial grafting. *Journal of Surgical Research*. 2004; 120(1):27-36
 29. Kalish JA, Willis DJ, **Li C**, Link JJ, Deutsch ER, Contreras MA, Quist WC, Logerfo FW. Temporal genomics of vein bypass grafting through oligonucleotide microarray analysis. *Journal of Vascular Surgery*. 2004; 39(3):645-54.
 30. Dring AM, Davies FE, Fenton JA, Roddam PL, Scott K, Gonzalez D, Rollinson S, Rawstron AC, Rees-Unwin KS, **Li C**, Munshi NC, Anderson KC, Morgan GJ. A Global Expression-based Analysis of the Consequences of the t(4;14) Translocation in Myeloma. *Clin Cancer Res*. 2004; 10(17):5692-701.
 31. Paez JG, Lin M, Beroukhir R, Lee JC, Zhao X, Richter DJ, Gabriel S, Herman P, Sasaki H, Altshuler D, **Li C**, Meyerson M, Sellers WR. Genome coverage and sequence fidelity of phi29 polymerase-based multiple strand displacement whole genome amplification. *Nucleic Acids Research*. 2004; 32(9):e71.
 32. Bachoo RM, Kim RS, Ligon KL, Maher EA, Brennan C, Billings N, Chan S, **Li C**, Rowitch DH, Wong WH, DePinho RA. Molecular diversity of astrocytes with implications for neurological disorders. *Proc. Natl. Acad. Sci*. 2004; 101(22):8384-9.

33. Davies FE, Dring AM, **Li C**, Rawstron AC, Shammas MA, O'Connor SM, Fenton JA, Hideshima T, Chauhan D, Tai IT, Robinson E, Auclair D, Rees K, Gonzalez D, Ashcroft AJ, Dasgupta R, Mitsiades C, Mitsiades N, Chen LB, Wong WH, Munshi NC, Morgan GJ, Anderson KC. Insights into the multistep transformation of MGUS to myeloma using microarray expression analysis. *Blood*. 2003; 102(13):4504-11.
34. Lieberfarb ME, Lin M, Lechpammer M, **Li C**, Tanenbaum DM, Febbo PG, Wright RL, Shim J, Kantoff PW, Loda M, Meyerson M, Sellers WR. Genome-wide Loss of Heterozygosity Analysis from Laser Capture Microdissected Prostate Cancer Using Single Nucleotide Polymorphic Allele (SNP) Arrays and a Novel Bioinformatics Platform dChipSNP. *Cancer Research*. 2003; 63(16): 4781-4785.
35. Schoenberg FP, Ferguson T, **Li C**. Inverting Dirichlet tessellations. *The Computer Journal*. 2003; 46(1): 76-83.
36. Schadt EE, **Li C**, Ellis B, Wong WH. Feature extraction and normalization algorithms for high-density oligonucleotide gene expression array data. *Journal of Cellular Biochemistry*. 2001; Supplement 37, 120-125.
37. Hakak Y, Walker JR, **Li C**, Wong WH, Davis KL, Buxbaum JD, Haroutunian V and Fienberg AA. Genome-wide expression analysis reveals dysregulation of myelination-related genes in chronic schizophrenia. *Proc. Natl. Acad. Sci*. 2001; 98:4746-4751.
38. Bhattacharjee A, Richards WG, Staunton J, **Li C**, Monti S, Vasa P, Ladd C, Beheshti J, Bueno R, Gillette M, Loda M, Weber G, Mark EJ, Lander ES, Wong W, Johnson BE, Golub TR, Sugarbaker DJ and Meyerson M. Classification of human lung carcinomas by mRNA expression profiling reveals distinct adenocarcinoma subclasses *Proc. Natl. Acad. Sci*. 2001; 98:13790-13795.
39. Schoenberg F, Berk R, Fovell R, **Li C**, Lu R, Weiss R. Approximation and inversion of a complex meteorological system via local linear filters. *Journal of Applied Meteorology*, 2001; 40(3), 446--458.
40. Schadt EE, **Li C**, Su C, Wong WH. Analyzing high-density oligonucleotide gene expression array data, *Journal of Cellular Biochemistry*. 2000; 80:192-202.
41. Irizarry K, Kustanovich V, **Li C**, Brown N, Nelson S, Wong W and Lee CJ. Genome-wide analysis of single-nucleotide polymorphisms in human expressed sequences, *Nature Genetics*. 2000; 26:233-236.

Non-peer Reviewed Publications

42. **Li C**, Amin S. Analysis of cancer genome alterations using single nucleotide polymorphism (SNP) microarrays. In *New developments in biostatistics and bioinformatics*. Edited by Jianqing Fan, Xihong Lin and Jun Liu. 2008; in press.
43. Zhong S, Tian L, **Li C**, Storch FK, Wong WH. Comparative Analysis of Gene Sets in the Gene Ontology Space under the Multiple Hypothesis Testing Framework. *Proc. IEEE Comp Systems Bioinformatics*. 2004; 425-435.

44. Han H, Giles CL, Zha H, **Li C**, and Tsioutsoulouklis K. Two Supervised Learning Approaches for Name Disambiguation in Author Citations. *Proceedings of ACM/IEEE Joint Conference on Digital Libraries (JCDL 2004)*. 2004; 296-305.
45. **Li C**, Wong WH. DNA-Chip Analyzer (dChip). In *The analysis of gene expression data: methods and software*. Edited by Parmigiani G, Garrett ES, Irizarry R and Zeger SL. Springer, New York. 2003; 120-141.
46. **Li C**, Tseng GC, Wong WH. Model-based analysis of oligonucleotide arrays and issues in cDNA microarray analysis. In *Statistical analysis of gene expression microarray data*. Edited by Terry Speed. CRC Press. 2003; 1-34.

PRESENTATIONS

Conferences, Workshops and Seminars

1. San Antonio Cancer Institute, University of Texas Health Science Center, March 27, 2008
2. Biogen Idec, Cambridge, MA, February 1, 2008
3. Department of Bioinformatics, M.D. Anderson Cancer Center, September 17, 2007
4. "International Conference on Bioinformatics", Zhejiang University, Hangzhou, China, June 11-14, 2007.
5. Center for Statistical Sciences, Brown University, March 19, 2007
6. Department of Biostatistics and Computational Biology, University of Rochester Medical Center, November 2, 2006.
7. Department of Biostatistics, University of Michigan School of Public Health, October 5, 2006.
8. The 4th International Bioinformatics Workshop. Central South University, Changsha, China. June 10-12, 2006.
9. Laboratory of Disease and Health Genomics, Chinese National Human Genome Center at Shanghai, China. June 9, 2006.
10. Department of Statistics, University of California, Riverside, May 9, 2006.
11. Hartwell Center for Bioinformatics and Biotechnology, St. Jude Hospital, Memphis, April, 2006.
12. The 7th Annual Affymetrix User Group Meeting, Chicago, May 19, 2004.
13. International Conference on Analysis of Genomic Data, Boston, May 10-11, 2004.

14. MSRI workshop on "Genetics of Complex Disease", UC Berkeley, February 12, 2004.
15. Feinstone Symposium on "Analysis and Integration of Microarray Data", University of Memphis, June 12, 2003.
16. Affymetrix Inc. Santa Clara, CA, March, 2003.
17. NCI Annual Director's Challenge Investigators Meeting, Bethesda, MD, November, 2002.
18. Joint Statistical Meeting, Invited session on "Analysis of Microarray Data", New York, August 11, 2002.
19. NCI "Applications of Bioinformatics in Cancer Detection" workshop, Bethesda, MD, August 6-7, 2002.
20. GeneLogic workshop on "low-level analysis of Affymetrix data". Bethesda, MD, November 19, 2001.
21. "DNA Microarray: Principals and Biotechnological Applications" Workshop, UCLA, September, 2001.
22. International Chinese Statistical Association, Applied Statistics Symposium, Chicago, June 7, 2001.
23. UCLA IPAM Functional Genomics program: "Mathematical and Statistical Challenges from Computational Biology", Lake Arrowhead, CA, December 11, 2000.
24. Joint Statistical Meeting, Invited session on "DNA Expression Arrays". Indianapolis, August 17, 2000.
25. Workshop on microarray technology, National Institute of Standards and Technology, Gaithersburg, MD, June 2000.

Courses

26. Affymetrix 500K SNP Array Data Analysis Workshop, The Broad Institute of MIT and Harvard, September 22, 2006.
27. Mini-Course on SNP analysis, HSPH Bioinformatics Core, Boston, May 26, 2006.
28. Course on "Advances in Genome Technology and Bioinformatics", Marine Biological Laboratory, Woods Hole, MA, October, 2005.
29. Microarray Short Course, University of Memphis, June 7-10, 2003
30. Short course on "Applications of Statistics to Genomics", Department of Biostatistics, HSPH, January, 2002.