

## Hae Kyung Im, Ph.D.

The University of Chicago  
Department of Medicine  
Section of Genetic Medicine  
KCBD 3220  
900 East 57th Street  
Chicago, IL 60637-1234  
Office: (773)-702-3898  
Fax: (773)-702-2567  
Email: haky@uchicago.edu  
Web page: <http://imlab.uchicago.edu>

### ACADEMIC APPOINTMENTS

2009-2014     Research Associate (Assistant Professor), Department of Health Studies,  
                    Biostatistics Laboratory, University of Chicago  
2014            Research Associate (Assistant Professor), Department of Medicine,  
                    Section of Genetic Medicine, University of Chicago

### ACADEMIC TRAINING

1990-1993     Licenciada in Physics (B.S.+M.S equivalent) Instituto Balseiro, Argentina  
1999-2000     M.S., Financial Mathematics, University of Chicago, Chicago, IL  
2001-2005     PhD, Statistics, University of Chicago, Chicago, IL  
2005-2007     Research Associate, Center for Integrating Statistical and Environmental  
                    Sciences, University of Chicago, Chicago, IL

### SCHOLARSHIP

#### (a) Peer-reviewed publications in the primary literature, exclusive of abstracts:

1. Im, H. K., Jagla, E., and Balseiro, C. (1994). Proximity effect of thin films on superconducting substrates. *Physical Review B* 50, 10117.
2. Im, H. K., Stein, M., and Kotamarthi, V. (2005). A new approach to scenario analysis using simplified chemical transport models. *J. Geophys. Res.* 110, D24205. <http://dx.doi.org/10.1029/2005JD006417>.
3. Im, H. K., Stein, M. L., and Zhu, Z. (2007). Semiparametric Estimation of Spectral Density With Irregular Observations. *Journal of the American Statistical Association* 102, 726–735.  
<http://www.tandfonline.com/doi/abs/10.1198/016214507000000220>.
4. Im, H. K., Rathouz, P. J., and Frederick, J. E. (2009). Space–time modeling of 20 years of daily air temperature in the Chicago metropolitan region. *Environmetrics* 20, 494–511.  
<http://scholar.google.com.proxy.uchicago.edu/scholar?hl=en&r=q=info:eV3xDDGCQIEJ:scholar.google.c>
5. Forester, J. D., Im, H. K., and Rathouz, P. J. (2009). Accounting for animal movement in estimation of resource selection functions: sampling and data analysis. *Ecology* 90, 3554–3565.

- <http://eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=pubmedid=20120822retmode=refcmd=p>
6. Gamazon, E. R., Im, H. K., Duan, S., Lussier, Y. A., Cox, N. J., Dolan, M. E., and Zhang, W. (2010). Exprtarget: an integrative approach to predicting human microRNA targets. *PLoS One* 5, e13534.  
<http://eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=pubmedid=20975837retmode=refcmd=p>
  7. Kenny, H. A., Leonhardt, P., Ladanyi, A., Yamada, S. D., Montag, A., Im, H. K., Jagadeeswaran, S., Shaw, D. E., Mazar, A. P., and Lengyel, E. (2011). Targeting the urokinase plasminogen activator receptor inhibits ovarian cancer metastasis. *Clinical Cancer Research* 17, 459–471.  
<http://clincancerres.aacrjournals.org/content/17/3/459.short>.
  8. Gamazon, E. R., Im, H. K., O'Donnell, P. H., Ziliak, D., Stark, A. L., Cox, N. J., Dolan, M. E., and Huang, R. S. (2011). Comprehensive evaluation of the contribution of X chromosome genes to platinum sensitivity. *Molecular cancer therapeutics* 10, 472–480.  
<http://eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=pubmedid=21252287retmode=refcmd=p>
  9. Ziliak, D., O'Donnell, P. H., Im, H. K., Gamazon, E. R., Chen, P., Delaney, S., Shukla, S., Das, S., Cox, N. J., Vokes, E. E., et al. (2011). Germline polymorphisms discovered via a cell-based, genome-wide approach predict platinum response in head and neck cancers. *Translational research : the journal of laboratory and clinical medicine* 157, 265–272.  
<http://eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=pubmedid=21497773retmode=refcmd=p>
  10. Huang, R. S., Gamazon, E. R., Ziliak, D., Wen, Y., Im, H. K., Zhang, W., Wing, C., Duan, S., Bleibel, W. K., Cox, N. J., et al. (2011). Population differences in microRNA expression and biological implications. *RNA Biology* 8, 692–701.  
<http://eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=pubmedid=21691150retmode=refcmd=p>
  11. Huang, R. S., Johnatty, S. E., Gamazon, E. R., Im, H. K., Ziliak, D., Duan, S., Zhang, W., Kistner, E. O., Chen, P., Beesley, J., et al. (2011). Platinum sensitivity-related germline polymorphism discovered via a cell-based approach and analysis of its association with outcome in ovarian cancer patients. *Clinical Cancer Research* 17, 5490–5500.  
<http://eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=pubmedid=21705454retmode=refcmd=p>
  12. Gamazon, E. R., Huang, R. S., Dolan, M. E., Cox, N. J., and Im, H. K. (2012). Integrative genomics: quantifying significance of phenotype-genotype relationships from multiple sources of high-throughput data. *Frontiers in genetics* 3, 202.  
<http://www.frontiersin.org/Journal/10.3389/fgene.2012.00202/full>.
  13. Im, H. K., Gamazon, E. R., Stark, A. L., Huang, R. S., Cox, N. J., and Dolan, M. E. (2012). Mixed effects modeling of proliferation rates in cell-based models: consequence for pharmacogenomics and cancer. *PLoS Genetics* 8, e1002525.  
<http://eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=pubmedid=22346769retmode=refcmd=p>
  14. Njiaju, U. O., Gamazon, E. R., Gorsic, L. K., Delaney, S. M., Wheeler, H. E., Im, H. K., and Dolan, M. E. (2012). Whole-genome studies identify solute carrier

transporters in cellular susceptibility to paclitaxel. *Pharmacogenetics and genomics*.

<http://eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=pubmedid=22437668retmode=refcmd=p>

15. Wen, Y., Gamazon, E. R., Bleibel, W. K., Wing, C., Mi, S., McIlwee, B. E., Delaney, S. M., Duan, S., Im, H. K., and Dolan, M. E. (2012). An eQTL-based method identifies CTTN and ZMAT3 as pemetrexed susceptibility markers. *Human Molecular Genetics* 21, 1470–1480.  
<http://eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=pubmedid=22171072retmode=refcmd=p>
16. Im, H. K., Gamazon, E. R., Nicolae, D. L., and Cox, N. J. (2012). On sharing quantitative trait GWAS results in an era of multiple-omics data and the limits of genomic privacy. *American Journal of Human Genetics* 90, 591–598.  
<http://eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=pubmedid=22463877retmode=refcmd=p>
17. Gamazon, E. R., Ziliak, D., Im, H. K., LaCroix, B., Park, D. S., Cox, N. J., and Huang, R. S. (2012). Genetic Architecture of MicroRNA Expression: Implications for the Transcriptome and Complex Traits. *American Journal of Human Genetics*.  
<http://eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=pubmedid=22658545retmode=refcmd=p>
18. Ziliak, D., Gamazon, E. R., LaCroix, B., Im, H. K., Wen, Y., and Huang, R. S. (2012). Genetic variation that predicts platinum sensitivity reveals the role of miR-193b\* in chemotherapeutic susceptibility. *Molecular cancer therapeutics*.  
<http://eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=pubmedid=22752226retmode=refcmd=p>
19. Stark, A. L., Delaney, S. M., Wheeler, H. E., Im, H. K., and Dolan, M. E. (2012). Functional consequences of PRPF39 on distant genes and cisplatin sensitivity. *Human Molecular Genetics*.  
<http://eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=pubmedid=22773733retmode=refcmd=p>
20. O'Donnell, P. H., Stark, A. L., Gamazon, E. R., Wheeler, H. E., McIlwee, B. E., Gorsic, L., Im, H. K., Huang, R. S., Cox, N. J., and Dolan, M. E. (2012). Identification of novel germline polymorphisms governing capecitabine sensitivity. *Cancer* 118, 4063–4073.  
<http://eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=pubmedid=22864933retmode=refcmd=p>
21. Im, H. K., Gamazon, E. R., Nicolae, D. L., and Cox, N. J. (2012). Response to Knoppers et al. *The American Journal of Human Genetics* 91, 579.  
<http://dx.doi.org/10.1016/j.ajhg.2012.07.025>.
22. Gamazon, E. R., Huang, R. S., Dolan, M. E., Cox, N. J., and Im, H. K. (2013). Integrative Genomics: Quantifying significance of phenotype-genotype relationships from multiple sources of high-throughput data. *Frontiers in genetics* 3, 202. <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3668276/>.
23. Gamazon, E. R., Pinto, N., Konkashbaev, A., Im, H. K., Diskin, S. J., London, W. B., Maris, J. M., Dolan, M. E., Cox, N. J., and Cohn, S. L. (2013). Trans-population analysis of genetic mechanisms of ethnic disparities in neuroblastoma survival. *JOURNAL OF THE NATIONAL CANCER INSTITUTE* 105, 302–309.

- <http://eutils.ncbi.nlm.nih.gov/entrez/eutils/elink.fcgi?dbfrom=pubmedid=23243203retmode=refcmd=p>
24. Gamazon, E. R., Lamba, J. K., Pounds, S., Stark, A. L., Wheeler, H. E., Cao, X., Im, H. K., Mitra, A. K., Rubnitz, J. E., Ribeiro, R. C., et al. (2013). Comprehensive genetic analysis of cytarabine sensitivity in a cell-based model identifies polymorphisms associated with outcome in AML patients. *Blood* 121, 4366–4376.  
<http://www.bloodjournal.org/cgi/doi/10.1182/blood-2012-10-464149>.
  25. Eadon, M. T., Wheeler, H. E., Stark, A. L., Zhang, X., Moen, E. L., Delaney, S. M., Im, H. K., Cunningham, P. N., Zhang, W., and Dolan, M. E. (2013). Genetic and epigenetic variants contributing to clofarabine cytotoxicity. *Human Molecular Genetics*.  
<http://www.hmg.oxfordjournals.org/cgi/doi/10.1093/hmg/ddt240>.
  26. Lonsdale, J., Thomas, J., Salvatore, M., Phillips, R., Lo, E., Shad, S., Hasz, R., Walters, G., Garcia, F., Young, N., et al. (2013). The Genotype-Tissue Expression (GTEx) project. *Nature Genetics* 45, 580–585.  
<http://dx.doi.org/10.1038/ng.2653>.
  27. Weng, L., Ziliak, D., Im, H. K., Gamazon, E. R., Philips, S., Nguyen, A. T., Desta, Z., Skaar, T. C., the Consortium on Breast Cancer Pharmacogenomics (COBRA), Flockhart, D. A., et al. (2013). Genome-wide discovery of genetic variants affecting tamoxifen sensitivity and their clinical and functional validation. *Annals of Oncology* 24, 1867– 1873.  
<http://annonc.oxfordjournals.org/cgi/doi/10.1093/annonc/mdt125>.
  28. Gorsic, L. K., Stark, A. L., Wheeler, H. E., Wong, S. S., Im, H. K., and Dolan, M. E. (2013). EPS8 Inhibition Increases Cisplatin Sensitivity in Lung Cancer Cells. *PLoS One* 8, e82220. <http://dx.doi.org/10.1371>
  29. Lee, S. M., Karrison, T. G., Cox, N. J., and Im, H. K. (2013). Quantitative allelic test-a fast test for very large association studies. *Genetic epidemiology* 37, 831–839.  
<http://onlinelibrary.wiley.com.proxy.uchicago.edu/doi/10.1002/gepi.21768/full>.
  30. LaCroix, B., Gamazon, E. R., Lenkala, D., Im, H. K., Geeleher, P., Ziliak, D., Cox, N. J., and Huang, R. S. (2014). Integrative analyses of genetic variation, epigenetic regulation, and the transcriptome to elucidate the biology of platinum sensitivity. *BMC genomics* 15, 292.  
<http://www.biomedcentral.com/1471-2164/15/292>.
  31. Ferguson, M. K., Im, H. K., Watson, S., Johnson, E., Wigfield, C. H., and Vigneswaran, W. T. (2014). Association of body mass index and outcomes after major lung resection. *European Journal of Cardio-Thoracic Surgery*.  
<http://ejcts.oxfordjournals.org/cgi/doi/10.1093/ejcts/ezu008>.
  32. Lenkala, D., LaCroix, B., Gamazon, E. R., Geeleher, P., Im, H. K., and Huang, R. S. (2014). The impact of microRNA expression on cellular proliferation. *Human Genetics* pp. 1–8. <http://link.springer.com/10.1007/s00439-014-1434-4>.
  33. Stark, A. L., Hause, R. J., Gorsic, L. K., Antao, N. N., Wong, S. S., Chung, S. H., Gill, D. F., Im, H. K., Myers, J. L., White, K. P., et al. (2014). Protein Quantitative Trait Loci Identify Novel Candidates Modulating Cellular Response to Chemotherapy. *PLoS Genetics* 10, e1004192.  
<http://dx.plos.org/10.1371/journal.pgen.1004192>.

34. Kraja, A. T., Chasman, D. I., North, K. E., Reiner, A. P., Yanek, L. R., Kilpeläinen, T. O., Smith, J. A., Dehghan, A., Dupuis, J., Johnson, A. D., et al. (2014). Pleiotropic genes for metabolic syndrome and inflammation. *Molecular Genetics and Metabolism* pp. 1–54.  
<http://dx.doi.org/10.1016/j.ymgme.2014.04.007>.
35. Fang, H, X Liu, J Ramirez, N Choudhury, M Kubo, Hae Kyung Im, A Konkashbaev, et al. 2014. "Establishment of CYP2D6 Reference Samples by Multiple Validated Genotyping Platforms.." *The Pharmacogenomics Journal*, July. doi:10.1038/tpj.2014.27.
36. Wheeler, H. E., Aquino-Michaels, K., Gamazon, E. R., Trubetskoy, V. , Dolan, M. E., Huang, R. S., Cox, N. J., and Im, H. K. (2014). Poly-Omic Prediction of Complex Traits: OmicKriging. *Genetic epidemiology*.  
<http://eutils.ncbi.nlm.nih.gov/entrez/eutils/efetch.fcgi?dbfrom=pubmedid=24799323retmode=refcmd=p>

(b) Peer-reviewed works in 'non-traditional' outlets:

(c) Peer-reviewed works accepted or in press

(d) Non-peer-reviewed original articles

(e) Books:

(e) Book chapters:

(f) Other works that are publically available (websites, interviews, publications in the popular press, testimony, computer programs, protocols, reagents, inventions, patents not listed above, etc.)

OmicKriging. 2014. Software package for multiple omic prediction of complex traits in R.  
<http://cran.r-project.org/web/packages/OmicKriging/index.html>

(g) Clinical trials that are ongoing and unpublished

1. PI: R. Stephanie Huang, PhD and Richard Larson, MD. My role: Statistician.  
Title: "Monitoring Tyrosine Kinase Inhibitors (TKI) Response in Chronic Myeloid Leukemia (CML) Patients by Longitudinal Collection and Evaluation of 'Omics' Data"

2. Protocol Chair: Gini F Fleming, MD. My role: Statistician.  
Title: "Validation of a Polygenic Neurotoxicity Risk Score in Patients with Unusually Severe Paclitaxel-Induced Neuropathy"

(j) Works in review, in preparation, etc. not yet publically available [list ONLY if available for BSD review]

## FUNDING

### (a) Past:

1. NIH R01 CA136765. PI: Dolan, E. My role: Co-Investigator. Title: "Genetic determinants associated with pemetrexed response and toxicity". Total direct costs: \$ Total direct costs: \$212,900. Annual salary recovery or effort: 10%. Project period: 5/1/09-5/31/14.
2. U01 GM61393 PI: Ratain, M. My role: Co-Investigator. Title: "Pharmacogeneticomics of Anticancer Agents Research Group". Total direct costs: \$1,927,268. Annual salary recovery or effort: 25%. Project period: 07/16/10-06/30/15.
3. NIH R01MH101820 PI: Cox, N., Nicolae, D. My role: Co-Investigator. Title: "Harnessing GTEx to Create Transcriptome Knowledge and Inform Disease Biology". Total direct costs: \$400,714. Annual salary recovery or effort: 25%. Project period: 8/1/13-6/30/16
4. NIH R01 MH090937 PI: Cox, N. My role: Co-Investigator. Title: "Using the Transcriptome for SNP and Gene Annotation". Total direct costs: \$415,462 Annual salary recovery or effort: 25%. Project period: 09/17/10-07/31/12
5. NIH/NCI P30 CA14599 PI: LeBeau, M. My role: Co-Investigator. Title: "UCCRC-Cancer Center Support Grant; Subproject: Biostatistics Facility". Total direct costs: \$14,113,613 Annual salary recovery or effort: 10%. Project period: 07/22/08-03/31/13
6. NIH U01 HG005773 PI: Cox, N. My role: Co-Investigator. Title: "Rare Variants and Complex Human Phenotypes". Total direct costs: \$737,290 Annual salary recovery or effort: 25%. Project period: 7/1/10-3/31/13
7. NIH R01 CA125541 PI: Salgia, R. My role: Co-Investigator. Title: "Studies of a novel therapeutic target in non-small cell lung cancer". Total direct costs: \$849,870 Annual salary recovery or effort: 10%. Project period: 01/15/07-11/30/11.
8. NIH/ NIA R01 OH009482 PI: Van Cauter E. My role: Co-Investigator. Title: "Cardiometabolic Risk of Shift Work: Sleep Loss vs. Circadian Disruption". Total direct costs: \$2,181,345 Annual salary recovery or effort: 10%. Project period: 09/01/09-08/31/14
9. R01 DK083553 NIH/ARRA/Johns Hopkins Subaward. PI: Im, HK. My role: PI Investigator. Title: "Identifying Disease Variants for Familial Crohn's Disease". Total direct costs: \$19,983 . Annual salary recovery or effort: 0.3%. Project period: 09/01/09-08/31/11
10. NIH R21 CA139278 PI: Dolan, E. My role: Co-Investigator. Title: "Incorporation of microRNA expression in pharmacogenetic prediction models". Total direct costs: \$242,000 Annual salary recovery or effort: 5%. Project period: 03/1/09-02/28/11
11. U01 DK062429 NIH/Yale University Subaward PI: Nicolae, D. My role: Co-Investigator. Title: "IBD Genetics Consortium Data Coordinating Center". Total direct costs: \$ 163,267. Annual salary recovery or effort: 25%. Project period: 09/01/08-08/31/11.
12. NIH/NCCAM U54 RR023560 PI: Solway, J. My role: Internal Scientific Advisory Panel, Statistical reviewer. Title: "Clinical Translational Science Award".

Total direct costs: \$38,185,326. Annual salary recovery or effort: 10%.  
Project period: 09/17/07-09/29/12.

(b) Current:

- 1.NIH K12 CA139160 PI: Olopade, O Program Director. My role: K-Awardee. Title: "Institute for Translational Medicine's Paul Calabresi Career Development in Clinical Oncology Award - Systems Approach to Complex Traits Prediction and Dissection". Total direct costs: \$212,900. Annual salary recovery or effort: 75%. Project period: 1/1/2014-12/31/2015/05.
- 2.NIH P30 DK020595 PI: Matthew Brady. My role: PI of pilot grant. Title: "Diabetes Research and Training Center Pilot and Feasibility Grant Program". Total direct costs: \$20,000. Annual Salary recovery or effort: 0%. Project period 2/1/2014-1/31/2015

(c) Pending:

**HONORS, PRIZES, AND AWARDS**

- |           |   |
|-----------|---|
| 1989      | Goethe Institute Merit Scholarship, Bremen, Germany |
| 1990-1994 | Instituto Balseiro Scholarship, Argentina           |

**INVITED SPEAKING**

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|------|--|
| 2006 | Invited talk, Multivariate Methods in Environmetric Conference, "Novel approach to scenario analysis using simplified chemical transport models", Chicago, IL.   |
| 2011 | Platform presentation, International Meetings in Human Genetics, "Quantifying significance of phenotype-genotype relationships when various sources of high throughput data on the same individuals are integrated". Montreal, Canada. |
| 2012 | Platform presentation in the Statistical Analysis Resource Workshop, "Polygenic Prediction of complex phenotypes and drug response", Austin, TX.   |
| 2013 | Research seminar, "Genetic Architecture and Poly-Omic Prediction of Complex Traits", Department of Biostatistics, University of Wisconsin, Madison, WI.  |
| 2013 | Research seminar, "Harnessing the Power of Statistics in Genomic Science", Department of Biostatistics, University of Michigan, Ann Arbor, MI  |
| 2013 | Research seminar, "Harnessing the Power of Statistics to Enable Biomedical Discovery", Department of Medicine, Genetic Medicine, University of Chicago, Chicago, IL.   |
| 2013 | Platform presentation, International Society of Genetic Epidemiology, "Poly-Omic Prediction of Complex Traits: OmicKriging", Chicago, IL.  |
| 2013 | Research seminar, "Genomic Tools to Predict and Dissect the Biology of Complex Disorders", Department of Medicine, Endocrinology, University of Chicago, Chicago, IL.  |
| 2013 | Plenary lecture, Alliance for Clinical Trials in Oncology, Pharmacogenomics and Population Pharmacology Core Committee   |

- Meeting, "Poly-Omic Prediction of Complex Traits: OmicKriging", Chicago, IL.
- 2014 Research seminar, "Systems Approach to Complex Traits Prediction and Dissection", Department of Health Studies, University of Chicago, Chicago, IL.
- 2014 Research seminar, "Large Scale Prediction and Dissection of Complex Traits", Predictive Analytics and Comparative Effectiveness Center, Tufts Medical Center, Boston, MA
- 2014 Invited Oral Presentation – Joint Statistical Meetings, "On Sharing Quantitative Trait GWAS Results in an Era of Multiple-Omics Data and the Limits of Genomic Privacy", Boston, MA.

### **INVITED, ELECTED, OR APPOINTED EXTRAMURAL SERVICE**

Various Manuscript reviewer for American Journal of Human Genetics, Annals of Applied Statistics, Journal of Agricultural, Biological, and Environmental Statistics.

### **OTHER EMPLOYMENTS**

- 1994-1996 Researcher at tire manufacturing company, FATE, Buenos Aires, Argentina.
- 1996-1999 Consultant Business Risk Management, Arthur Andersen, Buenos Aires, Argentina.
- 2007-2009 Statistician for Quantitative Trading, Fixed Income Research, Credit Suisse, NY, NY.

### **PROFESSIONAL SOCIETIES**

Elected or invited membership:

Other:

American Statistical Association  
 American Society of Human Genetics  
 International Genetic Epidemiology Society  
 American Association for Cancer Research

### **SERVICE**

**University of Chicago**

Committee membership:

- 2009-2011 Reviewer for Internal Scientific Advisory Panel – Institute of Translational Medicine
- 2010 Biostatistics Laboratory Search Committee

Other:

### **Extramural (not indicated above)**

Leadership roles:



Other: