BIOGRAPHICAL SKETCH

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NAME: Whaley, Ryan

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: Technical Lead

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable.)*

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
University of Iowa, Iowa City, IA	BS	12/2001	Computer Science & Mathematics

A. Personal Statement

I am a software developer in the Department of Genetics and a co-technical lead of the PharmGKB. I have been with the PharmGKB since 2007. I am an application developer with a background in database administration, web application development, and project management. I received my B.S. in Computer Science and Mathematics at the University of Iowa. I then went on to become the DBA and senior software developer for the Department of Internal Medicine at the University of Iowa Hospitals & Clinics.

1. Hernandez-Boussard T, Whirl-Carrillo M, Hebert JM, Gong L, Owen R, Gong M, Gor W, Liu F, Truong C, Whaley R, Woon M, Zhou T, Altman RB, Klein TE. The pharmacogenetics and pharmacogenomics knowledge base: accentuating the knowledge. Nucleic Acids Res. 2008 Jan;36(Database issue):D913-8. PubMed PMID: 18032438; PubMed Central PMCID: PMC2238877.
2. Ashley EA, Butte AJ, Wheeler MT, Chen R, Klein TE, Dewey FE, Dudley JT, Ormond KE, Pavlovic A, Morgan AA, Pushkarev D, Neff NF, Hudgins L, Gong L, Hodges LM, Berlin DS, Thorn CF, Sangkuhl K, Hebert JM, Woon M, Sagreiya H, Whaley R, Knowles JW, Chou MF, Thakuria JV, Rosenbaum AM, Zaranek AW, Church GM, Greely HT, Quake SR, Altman RB. Clinical assessment incorporating a personal genome. Lancet. 2010 May 1;375(9725):1525-35. PubMed PMID: 20435227; PubMed Central PMCID: PMC2937184.

B. Positions and Honors

Positions and Employment

1999 - 2003 Application Developer, University of Iowa Hospitals & Clinics, Iowa City, IA
2003 - 2007 Database Administrator, University of Iowa Hospitals & Clinics, Iowa City, IA
2007 - 2013 Software Developer, Stanford University, Stanford, CA
2013 - Technical Lead, Stanford University, Stanford, CA

Other Experience and Professional Memberships

Honors

C. Contribution to Science

1. My contribution to science has been the development of software tool for the management of pharmcacogenetic data. All of these contributions has been with the PharmGKB organization. PharmGKB started as a resource for cataloging genotypic and phenotypic data from pharmacogenetic and pharmacogenomic (PGx) studies but has evolved into a knowledgebase that curates PGx literature. I have created, improved, and maintained the software tools necessary for

supporting the PharmGKB mission. These tools include data entry forms for curators, data import/export modules, and interactive web sites for visualizing knowledge.

a. Hernandez-Boussard T, Whirl-Carrillo M, Hebert JM, Gong L, Owen R, Gong M, Gor W, Liu F, Truong C, Whaley R, Woon M, Zhou T, Altman RB, Klein TE. The pharmacogenetics and pharmacogenomics knowledge base: accentuating the knowledge. Nucleic Acids Res. 2008 Jan;36(Database issue):D913-8. PubMed PMID: 18032438; PubMed Central PMCID: PMC2238877.

b. Ashley EA, Butte AJ, Wheeler MT, Chen R, Klein TE, Dewey FE, Dudley JT, Ormond KE, Pavlovic A, Morgan AA, Pushkarev D, Neff NF, Hudgins L, Gong L, Hodges LM, Berlin DS, Thorn CF, Sangkuhl K, Hebert JM, Woon M, Sagreiya H, Whaley R, Knowles JW, Chou MF, Thakuria JV, Rosenbaum AM, Zaranek AW, Church GM, Greely HT, Quake SR, Altman RB. Clinical assessment incorporating a personal genome. Lancet. 2010 May 1;375(9725):1525-35. PubMed PMID: 20435227; PubMed Central PMCID: PMC2937184.

2. I have also contributed software design and data analysis to pharmacogenetic consortia projects like the International Tamoxifen Pharmacogenomics Consortium (ITPC) and the International Clopidogrel Pharmacogenomics Consortium (ICPC).

a. Province MA, Goetz MP, Brauch H, Flockhart DA, Hebert JM, Whaley R, Suman VJ, Schroth W, Winter S, Zembutsu H, Mushiroda T, Newman WG, Lee MT, Ambrosone CB, Beckmann MW, Choi JY, Dieudonné AS, Fasching PA, Ferraldeschi R, Gong L, Haschke-Becher E, Howell A, Jordan LB, Hamann U, Kiyotani K, Krippl P, Lambrechts D, Latif A, Langsenlehner U, Lorizio W, Neven P, Nguyen AT, Park BW, Purdie CA, Quinlan P, Renner W, Schmidt M, Schwab M, Shin JG, Stingl JC, Wegman P, Wingren S, Wu AH, Ziv E, Zirpoli G, Thompson AM, Jordan VC, Nakamura Y, Altman RB, Ames MM, Weinshilboum RM, Eichelbaum M, Ingle JN, Klein TE. CYP2D6 genotype and adjuvant tamoxifen: meta-analysis of heterogeneous study populations. Clin Pharmacol Ther. 2014 Feb;95(2):216-27. PubMed PMID: 24060820; PubMed Central PMCID: PMC3904554.

b. Whaley R. ICPC Analysis Code. In: International Clopidogrel Pharmacogenomics Consortium [Internet]. Version 1.0. Stanford, CA: PharmGKB; 2014 September 26. This is a GitHub repo of the source code for running ICPC data analysis.. Available from: https://github.com/PharmGKB/ICPC. DOI: 10.5281/zenodo.11859.

c. Biernacka JM, Sangkuhl K, Jenkins G, Whaley RM, Barman P, Batzler A, Altman RB, Arolt V, Brockmöller J, Chen CH, Domschke K, Hall-Flavin DK, Hong CJ, Illi A, Ji Y, Kampman O, Kinoshita T, Leinonen E, Liou YJ, Mushiroda T, Nonen S, Skime MK, Wang L, Baune BT, Kato M, Liu YL, Praphanphoj V, Stingl JC, Tsai SJ, Kubo M, Klein TE, Weinshilboum R. The International SSRI Pharmacogenomics Consortium (ISPC): a genome-wide association study of antidepressant treatment response. Transl Psychiatry. 2015 Apr 21;5:e553. PubMed PMID: 25897834; PubMed Central PMCID: PMC4462610.

D. Additional Information: Research Support and/or Scholastic Performance

Completed Research Support

R24 GM061374, NIH / NIGMS Russ Altman and Teri Klein (PI) 04/01/00-06/30/15
PharmGKB: From Association to Mechanism
The Stanford Pharmacogenomics Knowledge Base (PharmGKB, http://www.pharmgkb.org/), an integrated data resource to support the NIGMS Pharmacogenetic Research Network and Database Initiative focuses on how genetic variation contributes to variation in the response to drugs, and will produce data from a wide range of sources, therefore interlinking genomic, molecular, cellular and clinical information about gene systems important for modulating.
Role: KP