BIOGRAPHICAL SKETCH

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NAME: Shun, Tongying

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

POSITION TITLE: Lead Statistician/Director of HTS/HCS Informatics Core

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

INSTITUTION AND LOCATION	DEGREE (if applicable)	END DATE MM/YYYY	FIELD OF STUDY
China University of Geoscience, Wuhan, Hubei Provience	BS	06/1986	Applied Mathematics
New Mexico Institute of Technology, Socorro, New Mexico	MS	12/1995	Hydrology
Pennsylvania State University, University Park, Pennsylvania	PHD	06/1999	Applied Computer Science
Pennsylvania State University, University Park, Pennsylvania	MENG	06/1999	Computer Science and Engineering

A. Personal Statement

Presently my research focused in 3 areas. First area is the statistic and computational data analysis of High-Throughput and High-Content assays which include RNAi, biochemical, fixed and live cell-based fluorescence as well as whole organism assays. The second area is the application of statistics and machine-learning methodologies to characterize cellular/organism heterogeneity and exploring the relationships between cellular/organism heterogeneity, compound/drug mechanism(s) of action and cell signaling pathways. The third area is statistic application in evaluating reproducibility of temporal microphysiology data measured on NCAT Organ Tissue models. I received my PhD in 1999 from Pennsylvania State University, where I conducted multichannel singular spectrum analysis of precipitation, temperature and runoff time series and developed a dynamic model for rainfall-runoff using genetic algorithms. This experience enabled me to join Lexmark International, Inc., as a senior applied research scientist where I developed additional technical skills in computation and modeling. In 2001, I joined Automated Cell, Inc., as their statistician and data manager. For four years, I built and managed a High-Content Screening (HCS) database and developed customized software for image and data analysis, including automated measurement of cancer cell motility and proliferation. I was recruited to the Drug Discovery Institute at the University of Pittsburgh (UPDDI) in 2005, where I became the leader of the UPDDI HTS/HCS informatics team. I designed the UPDDI IT network; built a LIMS to manage compound registration and genealogy; performed data analysis of bioassays; generated SAR reports by matching the bioactivities with compound structures; implemented and deployed the HTS and HCS informatics software, and developed multiple statistical solutions for HTS and HCS data analysis. Since 2010, I had served as informatics core leader of the University of Pittsburgh Specialized Application Center (PSAC) to manage compound registration, compound inventory, sample tracking, quality control, and HTS/HCS data analysis. I had been responsible for transferring all data, protocols, and analysis information for the NCI Next-CBC projects to the NCI and extensively involved in UPDDI multidisciplinary HTS/HCS project teams, including being an NIH MLSCN Informatics Working Group member. I have contributed in the statistic and computational data analysis of High-Throughput and High-Content assays which include RNAi, biochemical, fixed and live cell-based fluorescence as well as whole organism assays. Under funded NCAT Tissue Chip programs at the UPDDI, I have involved to design and implement the Microphysiology Database which has been deployed to an on-line MPS database web server (https://mps.csb.pitt.edu/) for analyzing and modeling compound interactions with human and animal organ Models and established the methodology for evaluating reproducibility of the microphysiology experiment data.

1. Shun T, Gough AH, Sanker S, Hukriede NA, Vogt A. Exploiting Analysis of Heterogeneity to Increase the Information Content Extracted from Fluorescence Micrographs of Transgenic Zebrafish Embryos. Assay Drug Dev Technol. 2017 Aug/Sep;15(6):257-266. PubMed PMID: 28800244; PubMed Central PMCID: PMC5576098.
2. Gough A, Shun TY, Lansing Taylor D, Schurdak M. A metric and workflow for quality control in the analysis of heterogeneity in phenotypic profiles and screens. Methods. 2016 Mar 1;96:12-26. PubMed PMID: 26476369; PubMed Central PMCID: PMC5200891.
3. Shun TY, Lazo JS, Sharlow ER, Johnston PA. Identifying actives from HTS data sets: practical approaches for the selection of an appropriate HTS data-processing method and quality control review. J Biomol Screen. 2011 Jan;16(1):1-14. PubMed PMID: 21160066.
4. Gosai SJ, Kwak JH, Luke CJ, Long OS, King DE, Kovatch KJ, Johnston PA, Shun TY, Lazo JS, Perlmutter DH, Silverman GA, Pak SC. Automated high-content live animal drug screening using C. elegans expressing the aggregation prone serpin α1-antitrypsin Z. PLoS One. 2010 Nov 12;5(11):e15460. PubMed PMID: 21103396; PubMed Central PMCID: PMC2980495.

B. Positions and Honors

Positions and Employment

1996 - 1999	Research Assistant, Earth Systems Science Center, Pennsylvania State University, University Park, PA
1999 - 2001	Senior Applied Research Scientist, Lexmark International Inc, Lexington, KY
2001 - 2005	Statistician/Data Manager, Automatic Cell Inc, Pittsburgh, PA
2006 - 2014	Statistician/Director of HTS/HCS Informatics Core, Drug Discovery Institute University of Pittsburgh, Pittsburgh, PA
2015 -	Lead Statistician/Director of HTS/HCS Informatics Core, Drug Discovery Institute University of Pittsburgh, Pittsburgh, PA

Other Experience and Professional Memberships

1996 - 1999	Member, American Geophysical Union
2006 -	Member, The Society for Laboratory Automation and Screening

Honors

C. Contribution to Science

1. I have contributed in the statistic and computational data analysis of High Throughput screening (HTS) and developed rigor reproducibility procedures to identify variability in the multi-level HTS data, detect systematic drift or decay in the HTS assay signal window, and to visualize systematic patterns.

   a. Svilar D, Dyavaiah M, Brown AR, Tang JB, Li J, McDonald PR, Shun TY, Braganza A, Wang XH, Maniar S, St Croix CM, Lazo JS, Pollack IF, Begley TJ, Sobol RW. Alkylation sensitivity screens reveal a conserved cross-species functionome. Mol Cancer Res. 2012 Dec;10(12):1580-96. PubMed PMID: 23038810; PubMed Central PMCID: PMC3877719.
   b. Zellefrow CD, Sharlow ER, Epperly MW, Reese CE, Shun T, Lira A, Greenberger JS, Lazo JS. Identification of druggable targets for radiation mitigation using a small interfering RNA screening assay. Radiat Res. 2012 Sep;178(3):150-9. PubMed PMID: 22747550; PubMed Central PMCID: PMC4528675.
   c. Kitchens CA, McDonald PR, Shun TY, Pollack IF, Lazo JS. Identification of chemosensitivity nodes for vinblastine through small interfering RNA high-throughput screens. J Pharmacol Exp Ther. 2011 Dec;339(3):851-8. PubMed PMID: 21880871; PubMed Central PMCID: PMC3226368.
   d. Shun TY, Lazo JS, Sharlow ER, Johnston PA. Identifying actives from HTS data sets: practical approaches for the selection of an appropriate HTS data-processing method and quality control review. J Biomol Screen. 2011 Jan;16(1):1-14. PubMed PMID: 21160066.

2. I have developed the statistical and machine learning methodologies for evaluating the reproducibility of various HCS assay data and built rigorous testing procedures to evaluate the robustness and reproducibility of HCS data. These statistic and machine learning methodologies were implemented by using R, SAS, MATLAB, etc. and shared with the academic community and industry collaborators, such as TIBCO (Palo Alto, CA 94304, USA).

    a. Shun T, Gough AH, Sanker S, Hukriede NA, Vogt A. Exploiting Analysis of Heterogeneity to Increase the Information Content Extracted from Fluorescence Micrographs of Transgenic Zebrafish Embryos. Assay Drug Dev Technol. 2017 Aug/Sep;15(6):257-266. PubMed PMID: 28800244; PubMed Central PMCID: PMC5576098.

    b. Johnston PA, Nguyen MM, Dar JA, Ai J, Wang Y, Masoodi KZ, Shun T, Shinde S, Camarco DP, Hua Y, Huryn DM, Wilson GM, Lazo JS, Nelson JB, Wipf P, Wang Z. Development and Implementation of a High-Throughput High-Content Screening Assay to Identify Inhibitors of Androgen Receptor Nuclear Localization in Castration-Resistant Prostate Cancer Cells. Assay Drug Dev Technol. 2016 May;14(4):226-39. PubMed PMID: 27187604; PubMed Central PMCID: PMC4876501.

    c. Johnston PA, Sen M, Hua Y, Camarco D, Shun TY, Lazo JS, Grandis JR. High-content pSTAT3/1 imaging assays to screen for selective inhibitors of STAT3 pathway activation in head and neck cancer cell lines. Assay Drug Dev Technol. 2014 Jan-Feb;12(1):55-79. PubMed PMID: 24127660; PubMed Central PMCID: PMC3934522.

    d. Gosai SJ, Kwak JH, Luke CJ, Long OS, King DE, Kovatch KJ, Johnston PA, Shun TY, Lazo JS, Perlmutter DH, Silverman GA, Pak SC. Automated high-content live animal drug screening using C. elegans expressing the aggregation prone serpin α1-antitrypsin Z. PLoS One. 2010 Nov 12;5(11):e15460. PubMed PMID: 21103396; PubMed Central PMCID: PMC2980495.

3. I have applied statistic and machine-learning methodologies to develop data analysis methods for characterizing cellular/organism heterogeneity and exploring the relationships between cellular/organism heterogeneity, compound/drug mechanism(s) of action and cell signaling pathways, which are important to the understanding of complex drug perturbations in the development of disease treatments.

    a. Gough A, Shun TY, Taylor DL, Schurdak M. Integrating Analysis of Cellular Heterogeneity in High-Content Dose-Response Studies. Methods Mol Biol. 2018;1745:25-46. PubMed PMID: 29476461.

    b. Gough A, Stern AM, Maier J, Lezon T, Shun TY, Chennubhotla C, Schurdak ME, Haney SA, Taylor DL. Biologically Relevant Heterogeneity: Metrics and Practical Insights. SLAS Discov. 2017 Mar;22(3):213-237. PubMed PMID: 28231035; PubMed Central PMCID: PMC5464733.

    c. Gough A, Shun TY, Lansing Taylor D, Schurdak M. A metric and workflow for quality control in the analysis of heterogeneity in phenotypic profiles and screens. Methods. 2016 Mar 1;96:12-26. PubMed PMID: 26476369; PubMed Central PMCID: PMC5200891.

    d. Gough AH, Chen N, Shun TY, Lezon TR, Boltz RC, Reese CE, Wagner J, Vernetti LA, Grandis JR, Lee AV, Stern AM, Schurdak ME, Taylor DL. Identifying and quantifying heterogeneity in high content analysis: application of heterogeneity indices to drug discovery. PLoS One. 2014;9(7):e102678. PubMed PMID: 25036749; PubMed Central PMCID: PMC4103836.

4. I have developed a statistical methodology for evaluating the reproducibility of temporal microphysiology experiment data which has been integrated to an on-line MPS database web server (https://mps.csb.pitt.edu/).

    a. Gough A, Vernetti L, Bergenthal L, Shun TY, Taylor DL. The Microphysiology Systems Database for Analyzing and Modeling Compound Interactions with Human and Animal Organ Models. Appl In Vitro Toxicol. 2016 Jun 1;2(2):103-117. PubMed PMID: 28781990; PubMed Central PMCID: PMC5119471.

    b. Vernetti LA, Senutovitch N, Boltz R, DeBiasio R, Shun TY, Gough A, Taylor DL. A human liver microphysiology platform for investigating physiology, drug safety, and disease models. Exp Biol Med (Maywood). 2016 Jan;241(1):101-14. PubMed PMID: 26202373; PubMed Central PMCID: PMC4723301.