BIOGRAPHICAL SKETCH

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NAME: Shun, Tongying

eRA COMMONS USER NAME (agency login): tyshun

POSITION TITLE: Statistician

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
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 2 areas that are highly related to this project. First, 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. 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 have 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 have been responsible for transferring all data, protocols, and analysis information for the NCI Next-CBC projects to the NCI. I have an extensive background in statistics, with many years of informatics experience working in the biotechnology sector and in academia. I have been extensively involved in UPDDI multidisciplinary HTS/HCS project teams, including being an NIH MLSCN Informatics Working Group member.

1. 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.
2. 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.
3. 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.
4. Dudgeon DD, Shinde SN, Shun TY, Lazo JS, Strock CJ, Giuliano KA, Taylor DL, Johnston PA, Johnston PA. Characterization and optimization of a novel protein-protein interaction biosensor high-content screening assay to identify disruptors of the interactions between p53 and hDM2. Assay Drug Dev Technol. 2010 Aug;8(4):437-58. PubMed PMID: 20662736; PubMed Central PMCID: PMC2929144.

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 -	Statistician, 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. 1. I have developed multiple statistic methodologies for analyzing a wide range of High-Throughput and High-Content screening data for fixed and live cell-based, as well as whole organism-based fluorescence assays, for which I have authored and co-authored multiple scientific publications. In particular, my paper on “Identifying actives from HTS data sets…” was well received, leading to several invitations and presentations at national meetings. I built and managed the entire informatics infrastructure to support the UPDDI as a Molecular Libraries Screening Center Network (MLSCN) site. Furthermore, I have collaborated to provide processing, analysis, management and presentation of data on many assay and screening projects.
   a. 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.
   b. 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.
   c. 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.

d. Dudgeon DD, Shinde SN, Shun TY, Lazo JS, Strock CJ, Giuliano KA, Taylor DL, Johnston PA, Johnston PA. Characterization and optimization of a novel protein-protein interaction biosensor high-content screening assay to identify disruptors of the interactions between p53 and hDM2. Assay Drug Dev Technol. 2010 Aug;8(4):437-58. PubMed PMID: 20662736; PubMed Central PMCID: PMC2929144.

2. 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, 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.

b. 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.

D. Research Support

Ongoing Research Support

P30 CA047904 , NIH Davidson (PI) 08/01/10-07/31/20
Cancer Center Support Grant
The major goal of this grant is to enable UPCI laboratory and clinical investigators to work closely together to identify improved approaches for cancer prevention, diagnosis and treatment with the common goal of reducing the burden of cancer and improving cancer care for patients who are diagnosed with this disease.
Role: Co-Investigator

STAR 83573601, EPA Hutson (PI) 01/14/14-11/30/18
Vanderbilt-Pittsburgh Resource for Organotypic Models for Predictive Toxicology - VPROMPT - an EPA STAR Center
Our human-on-a-chip will be integrated into the Vanderbilt moderate throughput screening platform as a microfluidic device to allow use of the secreted media for: (a) assaying the secretome in near real-time for targeted high content metabolomics; (b) provide liver conditioned media to feed chemical metabolites to the 3 developmental organoids, and (c); track mechanisms of toxicity in the liver.
Role: Co-Investigator

5UH3TR000503-04, NIH Taylor (PI) 07/01/14-06/30/17
A 3D biomimetic liver sinusoid construct for predicting physiology and toxicity
Integration of microfluidic devices linking the gut, liver and kidney to create a platform for adsorption, metabolism and excretion and the starting point of distribution.
Role: Co-Investigator

3UH3TR000503-04S1 (UH3), NIH Taylor (PI) 09/01/15-06/30/16
Measuring the Temporal=Spatial Responses of Dormancy and Drug Resistance in a Human Breast Cancer Metastatic Niche within a Liver-on-a-Chip Microphysiological Platform
We will create a metastatic niche for breast cancer in a human, 3D, 4 cell liver microphysiology system (MPS) in order to investigate dormancy and drug resistance in vitro. This will lead to insights into the progression of the disease including epigenetic changes in the cancer cells induced by the microenvironment
Role: Co-Investigator

SAP#4100068731, PA Department of Health Stern (PI) 01/01/15-12/31/18
Determining mechanisms of disease progression using Quantitative Systems Pharmacology (QSP)
A major goal is to demonstrate the broad applicability of QSP; accordingly, we aim to determine the value of QSP to enable the development of novel therapeutic strategies in a set of diverse diseases.
Role: Co-Investigator

STAR 83573601, EPA Hutson (PI) 01/14/14-11/30/18
Vanderbilt-Pittsburgh Resource for Organotypic Models for Predictive Toxicology - VPROMPT - an EPA STAR Center
Our human-on-a-chip will be integrated into the Vanderbilt moderate throughput screening platform as a microfluidic device to allow use of the secreted media for: (a) assaying the secretome in near real-time for targeted high content metabolomics; (b) provide liver conditioned media to feed chemical metabolites to the 3 developmental organoids, and (c); track mechanisms of toxicity in the liver.
Role: Co-Investigator