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EDUCATION

Graduate:	Joint CMU-Pitt Ph.D. Program in Computational Biology	08/2012- 04/2017
B.S. Major:	B.S. in Biotechnology, Shanghai Jiao Tong University (SJTU)	09/2008 - 06/2012
Minor:	Computer Technology and Application, SJTU	01/2010 - 06/2012

RESEARCH INTERESTS & PROFICIENT SKILLS

[1] High throughput **genomic data** analysis by **machine learning** and **statistical** methods
Clustering, classification, bi-clustering, meta-analysis, omics data analysis, linear models, regression, probability theory, gene regulation, data preprocessing, feature selection, dimension reduction, biomarker detection, pathway analysis, differential expression analysis, microarray (mRNA, SNP, etc) data analysis, clinical/survival data analysis

[2] Next Generation Sequencing (NGS) and **Long-read Sequencing** data analysis
transcriptome sequencing (RNA-Seq), whole genome sequencing (WGS), whole exome sequencing (WES), Chip-Seq, Oxford Nanopore sequencing
quality control (QC), trimming, alignment, fusion gene detection, gene expression, structural variation (SV) detection, copy number variation (CNV) analysis, SNP calling, peak calling, long-read sequencing (third-generation) analysis

[3] Coding and System: R, Unix/Linux bash script command, C++, MATLAB

[4] Software and Tools: Affymatrix software, Partek, NGS tools (fastqc, TopHat, Hisat, BWA, samtools, bedtools, GATK, htseq, cufflinks etc), fusion gene tools (SOAPfuse, FusionCatcher, TophatFusion, etc), structure variation tools (Delly, CNVnator, BreakDancer, Manta, etc), Nanopore tools (MinKNOW, NanoPlot, Porechop, Minimap2, etc), UCSC genome browser, Latex, GitHub

PROFESSIONAL EXPERIENCE

- **Structure variation and SNP calling**, *Post-doc* at The Jackson Laboratory, 06/2017 – 06/2018
  - Developed and implemented tools to detect structure variation via WGS read alignment signals and machine learning methods
  - Population evolution analysis to compare Tibetan and Han Chinese samples based on WGS data
- **Thesis Topic 1**: **Comprehensive evaluation of fusion transcript detection algorithms and a meta-caller to combine top performing methods in RNA-Seq data** (published by *NAR*)
  - Comprehensively evaluated 15 fusion transcript detection tools on RAN-Seq data
  - Recommended top performing tools and developed MetaCaller tool to combine their results
- **Thesis Topic 2: Meta-analytic framework for liquid association** (published by *Bioinformatics*)
  - Extended a three-way gene regulation algorithm into meta-analysis framework
  - Developed filtering criteria to allow whole genome scale calculation (O^3 searching space)
- **Thesis Topic 3: Meta-analysis to detect biclusters by plaid model**
  - Detected subset of genes and samples from gene expression profile among multiple cohorts
  - Maximized the objective function and applied gap statistics for pruning parameter selection
- **Machine learning and Meta-analysis on Genomics data**
  - Developed a sparse k-means clustering method to detect disease subtypes from multiple cohorts
  - MetaOmics: developed a GUI tool for multiple genomics data machine learning analysis
- **Collaboration works on NGS data and Array data**
  - Fusion transcript detection from RNA-Seq and WGS, Chip-seq data to predict cancer status
  - Copy Number Variation (CNV) detection from SNP array to associate with cancer status
  - Gene expression clustering, DE analysis and pathway enrichment analysis to detect biomarker

- **Summer intern** at PNC Marketing Department for data analysis, Summer 2016
  - Developed an R Shiny GUI and implemented survival analysis on cross sell data
  - Machine learning and data visualization on Customer cohort data and transaction data

PUBLICATIONS

Note: ^ represents co-first authors; * represents corresponding authors.

[1] **Silvia Liu^**, Wei-Hsiang Tsai^, Ying Ding^, ..., George C. Tseng*. Comprehensive evaluation of fusion transcript detection algorithms and a meta-caller to combine top performing methods in paired-end RNA-seq data. *Nucleic Acids Research* 44, no. 5 (2016): e47-e47.

[2] Zhiguang Huo, Ying Ding, **Silvia Liu**, Steffi Oesterreich*, George C. Tseng*. Meta-analytic framework for sparse K-means to identify disease subtypes in multiple transcriptomic studies. *Journal of the American Statistical Association*. (2015)

[3] Yan P. Yu^, **Silvia Liu^**, Zhigang Huo, ..., George C. Tseng and Jian-Hua Luo*. Genomic copy number variations in the genomes of leukocytes predict prostate cancer clinical outcomes. *PLoS ONE.* 2015 Aug 21; 10(8): e0135982. (PubMed ID: 26295840)

[4] Jian-Hua Luo*, **Silvia Liu**, Ze-Hua Zuo, Rui Chen, George C. Tseng*, Yan P. Yu*. Discovery and Classification of Fusion Transcripts in Prostate Cancer and Normal Prostate Tissue. *The American Journal of Pathology* 185, no. 7 (2015): 1834-1845. (PubMed ID: 25963990)

[5] Lin Wang^, **Silvia Liu^,** Ying Ding, Shin-sheng Yuan , Yen-Yi Ho*, and George C. Tseng*. Meta-analytic framework for liquid association. *Bioinformatics* (2017).

[6] Ze-Hua Zuo, Yan P. Yu, Ying Ding, **Silvia Liu**, Amantha Martin, George Tseng*, Jian-Hua Luo*. Oncogenic Activity of miRNA 650 in Prostate Cancer Is Mediated by Suppression of CSR1 Expression. *The American Journal of Pathology* 185, no. 7 (2015): 1991-1999 (PubMed ID: 25956032)

[7] Yan P. Yu^*, Ying Ding^, Zhanghui Chen^, **Silvia Liu**, ..., George K. Michalopoulos, George C. Tseng*, Jian-Hua Luo*. Novel Fusion Transcripts Associate with Progressive Prostate Cancer. *The American Journal of Pathology*. Volume 184, Issue 10, October 2014, Pages 2840-2849 (PubMed ID: 25238935)

[8] Shirish Paranjpe, ..., **Silvia Liu**, ... , George K. Michalopoulos. Combined systemic elimination of MET and EGFR signaling completely abolishes liver regeneration and leads to liver decompensation. *Hepatology.* (2016)

[9] Zhang-hui Chen, ..., **Silvia Liu**, ..., Jian-Hua Luo*. MAN2A1–FER Fusion Gene Is Expressed by Human Liver and Other Tumor Types and Has Oncogenic Activity in Mice. *Gastroenterology,* 153.4 (2016) (PubMed ID: 28245430)

[10] Yan-Bing Qi, Xiao-Lei Wang, Ting Shi, **Shuchang Liu**, ..., Yi-Lei Zhao*. Multicomponent kinetic analysis and theoretical studies on the phenolic intermediates in the oxidation of eugenol and isoeugenol catalyzed by laccase. *Physical Chemistry Chemical Physics* 17, no. 44 (2015): 29597-29607. (PubMed ID: 26477512)

[11] D-M He, B-G Ren, **S Liu**, ..., J-H Luo*. Oncogenic Activity of Amplified Miniature Chromosome Maintenance 8 in Human Malignancies. *Oncogene*, 36 (2017) 3629-3639. (PubMed ID: 28481876)

[12] Zhang-Hui Chen, ..., **Silvia Liu,** ..., Jian-Hua Luo*. Targeting genomic rearrangements in tumor cells using Cas9-mediated insertion of a suicide gene. *Nature biotechnology*, 35.6 (2017) 543-550. (PubMed ID: 28459452)

[13] Timothy Becker, ..., **Silvia Liu**, ..., Charles Lee*, Ankit Malhotra*. FusorSV: An algorithm for optimally combining data from multiple structural variation detection methods. *Genome Biology*, 19:38 (2018).

[14] Anne Orr, ..., **Silvia Liu**, ..., George Michalopoulos*. Combined systemic disruption of MET and EGFR signaling causes liver failure in normal mice. Accepted by *The American Journal of Pathology*. (2018)

Paper in Preparation or Submitted:
[1] **Silvia Liu**, George Tseng*. Meta-analysis of biclustering in high throughput genomics data studies.
[2] **Silvia Liu**, Wan-Ping Lee*. SVlearning: A flexible platform for integrating structure variation callsets from multiple callers by machine learning algorithms.

[3] Wan-Ping Lee, Qihui Zhu, **Silvia Liu**, … , CZ Zhang*, Charles Lee*. Development of a Next Generation Sequencing (NGS)-Based Platform for Detection of Copy Number Variations (CNVs) Associated with Constitutional Disorders.
[4] Tianzhou Ma, …, **Silvia Liu**, …, George Tseng*. MetaOmics: a tool for meta-analysis on omics data. *Submitted*.
[5] Jian-Hua Luo*, **Silvia Liu**, …, Yan-Ping Yu*. Fusion Pten-NOLC1 Promotes C-Met and EGFR Signals in Human Cancers. *Submitted*.

TEACHING AND PRESENTATIONS

- **Oral presentation** at **ENAR conference** 2013 for Meta Liquid Association project
- **Poster present** for BGSA Symposium, School of Medicine, University of Pittsburgh, 10/2014
- **TA and Guest lecture** for course High throughput genomics data analysis, Computational Genomics and Bioinformatics in Human Genetics, 2014-2016

AWARD AND SOCIAL ACTIVITIES

- **Graduation with honor:** Excellent graduate in Shanghai, Jun 2012
- **Chinese national scholarship** (top 1%), *triple times*, 2008-2012
- Member of program **student association**, 2008-2011 for undergraduates, 2014-2016 for graduates
- **Shanghai World EXPO**, *starts of volunteer*, 10/2010