Xin Wang

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Summary

Computational biology scientist and bioinformatician with 10+ experience (both study and work experience) of statistics and computational biology. As leader of our Bioinformatics team, I play an extremely crucial role in advancing projects related to pyelonephritis, diabetic nephropathy, acute kidney injury, bladder dysfunction, and urinary tract infections – I am leading the bioinformatic projects integral to the success of 7 principal investigators. Professional in bioinformatics software/pipeline developments, large-scale data system analysis and manuscript/grant writing. Gain a wide experience in the majority analyses of genomic/epigenetic/transcriptome/proteomic sequences under different Platforms. And strong background in DNA damage repair, cancer genome instability, comparative and evolutionary genomics.

Skills

Excellent knowledge in statistics, sequencing pipeline or software development.
Proficient in Perl, R, and Shell, and extremely familiar with UNIX and Windows environments.
A wide experience in the majority analyses of genomic/epigenetic/transcriptome/proteomic sequences, i.e., WGS, WES, RNA-seq, ChiP-seq, MNase-seq, EU RNA-seq, Single-Cell RNA-seq, ATAC-seq, PacBio-seq.
Ability to handle multiple projects simultaneously and accurately.

Work Experience

11/23- now	Bioinformatic Director, Kidney and Urinary Tract Center	
		Nationwide children's hospital
11/22- now	Senior Bioinformatic Scientist,	
		Nationwide children's hospital
11/20- 11/22	Postdoctoral fellow	Bioinformatics (PI: Kaifu Chen)
		Boston Children's Hospital, Harvard Medical School
12/18 – 10/20	Postdoctoral fellow	Bioinformatics (PI: Kaifu Chen)
		Houston Methodist Hospital, Weill Cornell Medical College

Education

01/15 -- 10/18	Ph.D.	Bioscience (PI: Manuel Aranda)
		King Abdullah University of Science and Technology (KAUST)
09/11 – 07/14	Master	Genomics (PI: Songnian Hu)
		Beijing Institute of genomics, Chinese Academy of Science
09/07 – 06/11	BSc.	Agricultural Facility of Science & Engineering
		China Agricultural University

Editorial Activities

2022- 2023 Guest associate editor: *Genes* (DNA damage and repair in microorganism and mammalian systems)

2022- 2023 Guest associate editor: *Total Environment Research Themes* (Environmental exposome and biomarker monitoring)
2021 -2024 Review editor: *Frontiers in Cancer Genetics*

Reviewer of research articles (> 20): *Frontiers in Oncology Cancer Genetics，Frontiers in Genetics Bioinformatics and Computational Biology, Frontiers in medicine, Genes, Nutrients, Antioxidants, Metabolites, IJMS, Cancers, Hindawi, etc.*

Work Experience

2022-now:

- Leading bioinformatic team at KUTC and extensively working with all our Center principal investigators.
- Consulting pre- or post experiment to determine proper sequencing approaches, design, and integration.
- Customizing advanced analysis of in-depth investigations and developing new methods or pipelines.
- Contributing to grants and manuscripts, including developing the bioinformatic components, generating high quality figures, finding potential storyboards, and drafting manuscripts.
- Managing data storage and providing data analysis suggestions for the integration of large multi-omics data sets.
- Supervising and training postdocs or students for basic bioinformatic approaches.
- Performing bioinformatics analysis to interpret high throughput genomic data, including spatial transcriptome, scRNAseq, ChIP-seq, ATAC-seq, RNA-seq, whole genome and exome sequencing in the Kidney and Urinary Tract center.

2018- 2022:

- Developed DSBins software toolkits to identify and functionally profile large insertion events and other repair products at DNA double stand break.
- Understood the mechanisms of large insertions at DSB sites in various DNA damage repair gene deficiency, mitochondrion gene defects and aging, illustrating the genomic features, i.e., R-loops, G-quadruplex, Rad52 break site, ARS, TSS.
- Developed MutaGene to systematically decoded mutation driver of cancer genomic instability to elucidate potential biomarkers for immunotherapy outcomes by integrating loads of cancer resources.
- Developed novel pipelines, including detecting nucleosome distribution in forward and reverse strand at DSBs and tracing the nascent RNA changes after irradiation using ERCC normalization.

- Worked as an expert and collaborated with cancer biologists to design WGS, WES, RNA-seq, ChiP-seq, MNase-seq, EU RNA-seq, Single-Cell RNA-seq, ATAC-seq, PacBio-seq data processing pipelines and provide statistical analysis for customized needs by biologist. Investigated the mechanisms of MECOM as a master regulator to determine endocardium differentiation in hypoplastic left heart syndrome using scRNA-seq, RNA-seq, ATAC-seq etc. Decoded biological mechanisms of Mitochondrial Tyrosine tiRNA on skeletal muscle using RNA-seq.
- Play major roles in grant application. The DSBins toolkits to illustrated large insertion events at DSB have been granted by NIH. Single Cell analyses of MECOM to determine endocardium differentiation in hypoplastic left heart syndrome has been granted by Additional Ventures SVRF Fund. The analyses of profiling the nucleosome at DSBs has been granted by NIH.
- Help to guide other postdoc with certain project advice, ranging from bioinformatic basic to manuscript updates.

Before postdoc research:
- Created two automatic pipelines to assemble 8 whole genomes and annotate them.
- Investigated the evolution of coral calcification and thermal resilience specification in corals, and understood the evolutionary processes that allowed the soft ancestor to become the ecosystem builder they are today.
- Understood the role of genetics/epigenetics in response to stress, and explore new strategies to increase the thermal resilience of corals in tropical areas.
- Helped with the maintenance and storage of High-performance computing (HPC) system.

GitHub packages:

MutaGene: Identify potential mutators that can drive the changes of tumor mutation burden.
https://github.com/gucascau/MutaGene.git
iDSBins: High-throughput identification of large and complex DNA insertions at DNA double strand breaks. https://github.com/gucascau/iDSBins.git
LargeInsertionFeature: Large Insertion Feature Analyses
https://github.com/gucascau/LargeInsertionFeature.git
iDSBindel: Detection of small insertions, small deletions, no changes at DNA double strand break sites.
https://github.com/gucascau/iDSBindel.git
iDSBInvert: Characterization of the inverted repeats from ssDNA transformation.
https://github.com/gucascau/iDSBInvert.git
iMMBIR: Detection of local short foldback inversions at DNA double strand break sites
https://github.com/gucascau/iMMBIR.git
NascentDiff: A pipeline to conduct a differential expression analysis in genome-wide and RNA expression levels using ERCC normalization.
https://github.com/gucascau/NascentDiff.git
Pyelonephritis: Spatial Map of Mouse Pyelonephritis
https://github.com/gucascau/Pyelonephritis.git

Publications

- Chen Z[1], **Wang X[1],** Gao X, Arslanovic N, Chen KF and Tyler J. Bulk transcriptional inhibition after irradiation is mainly due to loss of nascent transcripts from the rDNA and histone genes. *Elife* (2024). (**Co-first author,** Package: NascentDiff)
- Yu Y[1], **Wang X[1]**, Fox J[1], Yu R, Thakre P, McCauley B, Nicoloutsos N, Li Q, Hastings PJ, Dang W, Chen KF and Ira G. Yeast EndoG prevents genome instability by degrading cytoplasmic DNA, *Nature Communication* (2024) (In press, **Co-first author,** Packages: iDSBins, iDSBindel, LargeInsertionFeature)
- Jun C[1], **Wang X[1]**, Advani V, Lu YW, Malizia A, Singh GB, Huang ZP, Liu J, Wang C, Oliveria E, Mably J, Chen KF, and Wang D. Mitochondrial Tyrosine 5′tiRNAs are important regulators for mitochondrial and cell health in skeletal muscle myoblast, *Cell Proliferation* (2023) (**Co-first author**)
- **Wang X**, Zoccola D, Liew YJ, Tambutte E, Cui G, Allemand D, Tambutte S, Aranda M, The evolution of calcification in reef-building corals, *Molecular Biology and Evolution* (2021).
- **Wang X**, Liew YJ, Li Y, Zoccola D, Tambutte S, Aranda M. Draft genomes of the corallimorpharians *Amplexidiscus fenestrafer* and *Discosoma* sp. *Molecular Ecology Resources* (2017).
- **Wang X**, Drillon G, Ryu T, Voolstra CR, Aranda M. Genome-based analyses of six hexacorallian species reject the "Naked coral" Hypothesis. *Genome Biology and Evolution* (2017).
- Liew YJ[1], Howells EJ[1], **Wang X**, Michell C, Burt JA, Idaghdour Y & Aranda M. Intergenerational epigenetic inheritance in reef-building corals, *Nature Climate Change* (2020)
- Lv J, Meng S, Gu QL, Zhu S, ..**Wang X**, ..Zhang LL. Epigenetic landscape reveals MECOM as an endothelial lineage regulator, *Nature Communication* (2023)
- Wang GY, Xia B, .. **Wang X**, Chen KF. MACMIC Reveals Dual Role of CTCF in Epigenetic Regulation of Cell Identity Genes, *Genomics, Proteomics & Bioinformatics* (2021).
- Xia B, Zhao DY, Wang GY, .. **Wang X**, Cao Q, Zhang LL, and Chen KF. Machine learning reveals cell identity regulator by histone codes, *Nature Communication* (2020).
- Wang GY, Meng QS, .. **Wang X**, Cao Q, Chen KF. TADsplimer reveals splits and mergers of topologically associating domains for epigenetic regulation of transcription. *Genome Biology*. (2020)
- Chen JE[1], Cui G[1], **Wang X**, Liew YJ, Aranda M. Recent expansion of heat- activated retrotransposons in the coral symbiont *Symbiodinium microadriaticum*. *The ISME* (2018).
- Joseph D, **Wang X**, Aranda M, Berumen, M. Draft genome of an iconic Red Sea reef fish, the blacktail butterflyfish (*Chaetodon austriacus*): current status and its characteristics. *Molecular Ecology Resources* (2016).

- Joseph D, Pablo S, Marek J, **Wang X**, Aranda M, Berumen, M. Using a butterflyfish genome as a general tool for RAD-Seq studies in specialized reef fish. *Molecular Ecology Resources* (2017).
- **Wang X** authored in IC4R Project Consortium. Information Commons for Rice (IC4R). *Nucleic Acids Research* (2015).
- Luo M, Hao, L, **Wang X**, Hu S. MicroRNA profiles and potential regulatory pattern during the early stage of spermatogenesis in mice. *Science China Life Sciences* (2015).

Under review

- **Wang X**, Yan Q, Wang GY, .., Chen KF. Mutators-derived genomic instability reveals new biomarkers for immunotherapy. (Under review in *npj Precision Oncology*) (Packages: MutaGene)
- Yu Y[1], **Wang X**[1], Fox J, Hastings PJ, Chen KF, Ira G. RPA and Rad27 limit templated and inverted insertions at DNA breaks (Under review in *Nucleic Acids Research*) (**Co-first author,** Packages: iDSBInvert and iMMBIR)
- Becknell B, El-Harakeh M, Rodriguez-Tirado F, Grounds K, Li B, **Wang X**, and Ashley Jackson. Keratin 5 Basal Cells are Temporally Regulated Developmental and Tissue Repair Progenitors in Bladder Urothelium (Under review in *American Journal of Physiology-Renal Physiology*)
- Schwartz L, Simoni A, Yan P, Salamon K, Turkoglu A, Martinez GV, Zepeda-Orozco D, Eichler T, **Wang X**, and Spencer JD. Insulin receptor orchestrates kidney antibacterial defenses (Under review in *Proceedings of the National Academy of Sciences*)