

SUMMARY OF SKILLS

❖ Web Design & Development:

- *Back-end*: proficient with Python, Django | Node.js | MySQL | Apache, Nginx, uwsgi | OAuth, Slack, AWS API.
- *Front-end*: fluent in HTML5 | Javascript (jQuery, D3.js, DataTables, GSAP) | Photoshop, Illustrator.
- *Misc*: fluent in MATLAB | R | NumPy, Matplotlib | Linux Shell | git | pip, npm | LaTeX.

❖ Next-Generation Sequencing: Illumina NGS | RNA Biochemistry | High-Throughput Quantitation.

❖ Communication: efficient in writing documentations and time management; extremely detail-oriented.

EXPERIENCE

10/2014 – present **Web Design and Development, Data Sharing Platform** @ Stanford University
Project Leader, Full-Stack Web Developer

❖ Primer Design Server (<https://primerize.stanford.edu/>):

- Implemented server back-end from scratch: MATLAB process, CherryPy framework, and query management, which enables quantitative refinement and speeds up design by 10x.
- Designed server front-end interface and detailed tutorial page, which increases usage by 2x.

❖ RNA Mapping Database (<https://rmdb.stanford.edu/>):

- Redesigned server front-end completely with Bootstrap. Delivered interactive heatmap using D3.js, secondary structure visualization and structural prediction services.
- Created cross-platform interface for Eterna cloud lab, user dashboard and login system, which actively aided data sharing for a 30,000-user community with 100,000+ data points.

❖ Das Lab Website (<https://daslab.stanford.edu/>); Demo (<http://demo.t47.io/>):

- Deployed server at AWS using EC2 with ELB, and configuration of SSL, MySQL, Apache and cron. Integrated Stanford WebAuth with Kerberos for secure group access control.
- Reframed server back-end with Django, created easy-to-use publication management system. Implemented internal site organizing group resources.
- Created DasLab Bot for automating weekly meeting setup, notifications in Slack, configurable server backup scheduling and package version console.
- Integrated admin dashboard of Apache status, AWS CloudWatch, Google Analytics, GitHub, Slack, and Dropbox. Eliminated overhead of monitoring and visualization.
- Simplified HTML template script, optimized page loading, organized sitemap structure, restyled admin interface, and wrote detailed server admin manual.

❖ Eterna Data Browser (<http://medicine.eternadev.org/>); Prototype (<http://data.t47.io/>):

- Built interactive data browser using DataTables and jQuery with dynamic rendering and pagination. Delivered prototype with structured data query that is 20x faster than old browser.

01/2013 – 12/2015 **Academic Software Development, Automation** @ Stanford University
Graduate Research

❖ HiTRACE (<https://github.com/hitrace/hitrace/>); Server (<http://hitrace.org/>):

- Programmed massive parallel synthesis code and high-throughput data processing pipeline, which semi-automate high-dimensionality data for quantitative analysis.
- Developed graphical output codes in MATLAB, which are in daily use by entire lab. Built interface with other RNA modeling software, automated RNA diagram coloring.

❖ SpindleUtil (<https://github.com/t47io/SpindleUtil/>):

- Automated fluorescence intensity quantitation, image manipulation, spindle selector, tip-tracking visualizer in MATLAB, which improved productivity by 10x.

❖ Primerize (<https://github.com/DasLab/Primerize/>):

- Rewrote core algorithm in Python using NumPy and Numba @JIT compiler, improved speed by 5x.
- Simplified code structure, curated documentations, and published repository as Python package.

06/2015	Product Intelligence	@ Autodesk, Inc.
–	<i>Intern Analyst Data Scientist</i>	
09/2015	<ul style="list-style-type: none"> Piloted faster data aggregation pipeline with Datameer publishing to S3 buckets, Tableau Server and Google Big Query. Solved big data bottleneck, accelerated and reduced workload by 4x. Discovered and troubleshot 3 critical issues to ensure data integrity. Communicated with both architects/engineers and product managers to understand *everything to provide general aggregation schema solutions (e.g. Lithium community forum). Cleaned up data models and reduced complexity. Improvised alternative data export route with Splunk enabling data validation 4 weeks in advance. Test drove my own data aggregation by generating visualizations and insights. Promoted consumption and data-driven decision-making of other teams. Spoken highly of by stakeholders. Launched dashboard pages for desktop products and proposed future operation plans. Empowered the crowd by sharing data aggregation experience. Identified data literacy insufficiency. 	
09/2014	Translational Bioinformatics and Computational Biology	@ Stanford University
–	<i>Graduate Coursework</i>	
04/2015	<ul style="list-style-type: none"> Performed genome-wide association study (GWAS) on microarray datasets for Parkinson's disease searching for significant SNP hits and GO term enrichment using R. Mined clinical records for integrative drug-lab measurement relations using R and MySQL. Implemented sequence alignment algorithm with affine gaps using dynamic programming, K-means clustering and KNN classification for machine learning of leukemia patient data. Implemented molecular dynamic (MD) simulation of protein folding dynamic in Python. Built chemoinformatics network of ligand similarity and drug FEATURE of diabetes targets. 	
02/2012	High-Throughput RNA Biochemistry and Structure	@ Stanford University
–	<i>Graduate Research</i>	
present	<ul style="list-style-type: none"> Co-pioneered deep sequencing based high-throughput RNA mapping technique involving ligation and amplification. Reduced workload by 100-fold compared to conventional gel methods. Established quantitative method for data normalization, which is adopted as standard in field. Developed robust structural validation using systematic mutagenesis and multi-dimensional high-throughput RNA mapping technique with next-generation sequencing (NGS). Characterized first RNA translational regulatory elements on mammalian body-plan regulators; validated structure of first RNA element for flu virus packaging, and successfully attenuated virulence. 	

EDUCATION

09/2011	Stanford University, <i>Ph.D</i> in Biochemistry (expected 2016)	Stanford, CA
–	09/2011 –	
present	08/2014	Stanford Graduate Fellow
09/2007	China Agricultural University, <i>B.S</i> in Molecular Biology	Beijing, China
–	11/2010	Chancellor Scholarship, National Scholarship for <i>summa cum laude</i>
07/2011	12/2009	“Triple Excellent” Student of University, Scholarship for <i>magna cum laude</i>

PUBLICATIONS

- ❖ Hagey, R.J., **Tian, S.**, Elazar, M., Kladwang, W., Pham, E.A., Taubenberger, J.K., Das, R., and Glenn, J.S. (2016)
“A novel pan-genotypic RNA secondary structure mediates influenza A virus packaging and disease.”
Nature manuscript submitted.
- ❖ **Tian, S.**, and Das, R. (2016)
“RNA structure through multidimensional chemical mapping.”
Quarterly Review of Biophysics in press.
- ❖ Cheng, C.Y., Chou, F.-C., Kladwang, W., **Tian, S.**, Cordero, P., and Das, R. (2015)
“Consistent global structures of complex RNA states through multidimensional chemical mapping.”
eLife **4**: e07600.
- ❖ **Tian, S.**, Yesselman, J.D., Cordero, P., and Das, R. (2015)
“Primerize: Automated primer assembly for transcribing non-coding RNA domains.”
Nucleic Acid Research **43** (W1): W522 - W526.
- ❖ Lee, S., Kim, H., **Tian, S.**, Lee, T., Yoon, S., and Das, R. (2015)
“Automated band annotation for RNA structure probing experiments with numerous capillary electrophoresis profiles.”
Bioinformatics **31**(17): 2808 - 2815.
- ❖ Miao, Z., Adamiak, R.W., Blanchet, M-F., Boniecki, M., Bujnicki, J.M., Chen, S-J., Cheng, C.Y., Chojnowski, G., Chou, F-C., Cordero, P., Cruz, J.A., Ferré-D'Amaré, A, Das, R., Ding, F., Dokholyan, N.V., Dunin-Horkawicz, S., Kladwang, W., Krokhotin, A., Lach, G., Magnus, M., Major, F., Mann, T.H., Masquida, B., Matelska, D., Meyer, M., Peselis, A., Popena, M., Purzycka, K.J., Serganov, A., Stasiewicz, J., Szachniuk, M., Tandon, A., **Tian, S.**, Wang, J., Xiao, Y., Xu, X., Zhang, J, Zhao, P., Zok, T., and Westhof, E. (2015)
“RNA-Puzzles Round II: Assessment of RNA structure prediction programs applied to three large RNA structures.”
RNA **21** (6): 1066 - 1084.
- ❖ Xue, S., **Tian, S.**, Fujii, K., Kladwang, W., Das, R., and Barna, M. (2015)
“RNA regulons in *Hox* 5' UTRs confer ribosome specificity to gene regulation.”
Nature **517**: 33 - 38.
- ❖ **Tian, S.**, Cordero, P., Kladwang, W., and Das, R. (2014)
“High-throughput mutate-map-rescue evaluates SHAPE-directed RNA structure and uncovers excited states.”
RNA **20** (11): 1815 - 1826.
- ❖ Kladwang, W., Mann, T.H., Becka, A., **Tian, S.**, Kim, H., Yoon, S., and Das, R. (2014)
“Standardization of RNA chemical mapping experiments.”
Biochemistry **53** (19): 3063 - 3065.
- ❖ Shi, Y., Wang, Z., Meng, P., **Tian, S.**, Zhang, X., and Yang, S. (2013)
“The glutamate carboxypeptidase *AMP1* mediates abscisic acid and abiotic stress responses in *Arabidopsis*.”
New Phytologist **199** (1): 135 - 150.