

## SUMMARY OF SKILLS

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### ❖ Web Design & Development:

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

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

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

## EXPERIENCE

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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.

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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	<b>Product Intelligence</b>	@ Autodesk, Inc.
–	<i>Intern Analyst Data Scientist</i>	
09/2015	<ul style="list-style-type: none"> <li>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.</li> <li>Communicated with both architects/engineers and product managers to understand *everything to provide general aggregation schema solutions (e.g. Lithium community forum).</li> <li>Cleaned up data models and reduced complexity. Improvised alternative data export route with Splunk enabling data validation 4 weeks in advance.</li> <li>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.</li> <li>Empowered the crowd by sharing data aggregation experience. Identified data literacy insufficiency.</li> </ul>	
09/2014	<b>Translational Bioinformatics and Computational Biology</b>	@ Stanford University
–	<i>Graduate Coursework</i>	
04/2015	<ul style="list-style-type: none"> <li>Performed genome-wide association study (GWAS) on microarray datasets for Parkinson's disease searching for significant SNP hits and GO term enrichment using R.</li> <li>Mined clinical records for integrative drug-lab measurement relations using R and MySQL.</li> <li>Implemented sequence alignment algorithm with affine gaps using dynamic programming, K-means clustering and KNN classification for machine learning of leukemia patient data.</li> <li>Implemented molecular dynamic (MD) simulation of protein folding dynamic in Python. Built chemoinformatics network of ligand similarity and drug FEATURE of diabetes targets.</li> </ul>	
02/2012	<b>High-Throughput RNA Biochemistry and Structure</b>	@ Stanford University
–	<i>Graduate Research</i>	
present	<ul style="list-style-type: none"> <li>Co-pioneered deep sequencing based high-throughput RNA mapping technique involving ligation and amplification. Reduced workload by 100-fold compared to conventional gel methods.</li> <li>Established quantitative method for data normalization, which is adopted as standard in field.</li> <li>Developed robust structural validation using systematic mutagenesis and multi-dimensional high-throughput RNA mapping technique with next-generation sequencing (NGS).</li> <li>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.</li> </ul>	

## EDUCATION

09/2011	<b>Stanford University, <i>Ph.D</i> in Biochemistry</b> (expected 2016)	Stanford, CA
–	09/2011 –	
present	08/2014	Stanford Graduate Fellow
09/2007	<b>China Agricultural University, <i>B.S</i> in Molecular Biology</b>	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.