SIQI TIAN

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SUMMARY OF SKILLS

- ❖ **Web Design & Development:**
  - _Back-end_: proficient with Python, Django | Node.js | MySQL | Apache, Nginx, uwsgi | OAuth, 3rd-party API.
  - _Front-end_: fluent in Javascript (jQuery, D3.js, DataTables, GSAP) | HTML5, CSS, Jinja | Photoshop, Illustrator.
  - _Misc_: fluent in Linux Shell | git | MATLAB, R | NumPy, Matplotlib | 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

10/2014 – present

Academic Data Sharing & Tool Server
Full-Stack Web Developer

@ Stanford University

- ❖ **Primer Design Server** (https://primerize.stanford.edu/);
- ❖ **RNA Mapping Database** (https://rmdb.stanford.edu/);
- ❖ **Eterna Data Browser** (http://medicine.eternadev.org/, _prototype_: http://data.t47.io/):
  - Implemented server back-end framework with Python + Django + Apache, equipped with job queue management, cloud data API, user account system, and prediction services.
  - Designed server front-end with Javascript (jQuery, Bootstrap, D3.js, DataTables) and HTML templates (Jinja). Delivered interactive data visualizer/browser and detailed tutorials for 30,000-user scientific community (EteRNA cloud lab).
- ❖ **Das Lab Website** (https://daslab.stanford.edu/, _demo:_ http://demo.t47.io/):
  - Deployed server at AWS (EC2 + ELB), with SSL + MySQL + cron configuration, integrated WebAuth + Kerberos access control.
  - Implemented server back-end with Python + Django + Apache, built internal platform + dashboard using 3rd-party APIs (AWS + GA + Slack + GitHub + Dropbox).
  - Created BOT for automating periodic tasks (scheduling, backup, update) and Slack notifications.
  - Designed server front-end with Javascript (jQuery, Fullcalendar), with server admin documentation.
- ❖ **Personal Portfolio** (http://t47.io/):
  - Built server back-end with Node.js + Express + Nginx, parallax scrolling front-end with Javascript (ScrollMagic + GSAP), Photoshop and Illustrator.

01/2013 – 12/2015

Academic Data Analysis & Software Automation
Graduate Research

@ Stanford University

- ❖ **HiTRACE** (https://github.com/hitrace/HiTRACE/, _server:_ http://hitrace.org/):
- ❖ **SpindleUtil** (https://github.com/t47io/SpindleUtil/):
  - Programmed massive parallel synthesis code, high-throughput data processing pipeline, fluorescence image quantitation and tracking in MATLAB, improved productivity by 10x.
  - Developed graphical output and GUI for RNA visualization in MATLAB and Python + Matplotlib. Automated simulation with cross-platform interface.
- ❖ **Primerize Algorithm** (https://github.com/DasLab/Primerize/):
- ❖ **RNA Dataset Kit** (https://github.com/hitrace/RDATKit/):
  - Rewrote dynamic-programming algorithm in Python + NumPy + Numba + Matplotlib. Published repositories as Python packages with dependencies and curated documentations.

06/2015 – 09/2015

Product Intelligence & Big Data Pipeline
Intern Analyst Data Scientist

@ Autodesk, Inc.

- Piloted data aggregation pipeline with Splunk / Datameer + S3 + Tableau Server / GBQ. Solved big data bottleneck, accelerated data validation, and ensured data integrity.
- Communicated with both architects/engineers and product managers to provide general aggregation schema solutions. Promoted data literacy by teaching and sharing data-driven insights with teams.

| 09/2014 – 04/2015 | **Translational Bioinformatics & Computational Biology** | @ Stanford University |
| | *Graduate Coursework* | |

- Performed GWAS and mined clinical records in R and MySQL.
- Implemented NW-align, K-means, KNN, MD simulation, and FEATURE network in Python + NumPy.

| 02/2012 – present | **High-Throughput RNA Biochemistry & Structure Prediction** | @ Stanford University |
| | *Graduate Research* | |

- Co-pioneered NGS-based high-throughput RNA mapping technique. Established quantitative data normalization. Developed robust structural validation with compensatory mutation.
- Characterized 1st mammalian IRES regulator RNA and 1st RNA element attenuates influenza virulence.

EDUCATION

| 09/2011 – present | **Stanford University**, *Ph.D in Biochemistry* (expected 2016) | GPA: <u>3.82</u> / 4.0 | *Stanford, CA* |

- *09/2011 – 08/2014* Stanford Graduate Fellow

| 09/2007 – 07/2011 | **China Agricultural University**, *B.S in Molecular Biology* | GPA: <u>3.88</u> / 4.0 | *Beijing, China* |

- *11/2010* Chancellor Scholarship, National Scholarship for *summa cum laude*
- *12/2009* "Triple Excellent" Student of University, Scholarship for *magna cum laude*

PUBLICATIONS

- Hagey, R.J., <u>Tian, S.</u>, 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.

- <u>Tian, S.</u>, and Das, R. (2016)
  "RNA structure through multidimensional chemical mapping."
  Quarterly Review of Biophysics in press.

- Cheng, C.Y., Chou, F.-C., Kladwang, W., <u>Tian, S.</u>, Cordero, P., and Das, R. (2015)
  "Consistent global structures of complex RNA states through multidimensional chemical mapping."
  eLife **4**: e07600.

- <u>Tian, S.</u>, 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., <u>Tian, S.</u>, 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., Popenda, M., Purzycka, K.J., Serganov, A., Stasiewicz, J., Szachniuk, M., Tandon, A., <u>Tian, S.</u>, 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., <u>Tian, S.</u>, 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.

- <u>Tian, S.</u>, 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., <u>Tian, S.</u>, 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., <u>Tian, S.</u>, 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.