

MINGWEI TANG

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Github: <https://github.com/MingweiWilliamTang>

EDUCATION

Ph.D in Statistics, Machine Learning track	<i>2013.9-2019.6 (expected)</i>
University of Washington	<i>Seattle, US</i>
M.S in Statistics	<i>2013.9-2017.12</i>
University of Washington	<i>Seattle, US</i>
B.S. in Mathematics and Statistics	<i>2009.9-2013.6</i>
Nanjing University	<i>Nanjing, China</i>

EXPERIENCE

Data Science Intern	<i>2017.6-2017.9</i>
<i>Microsoft</i>	<i>Redmond, U.S</i>
· Applied machine learning and text mining methods to identify bug prone files.	
Research Intern	<i>2016.6-2016.9</i>
<i>U.S Food and Drug Administration (FDA)</i>	<i>Silver Spring, U.S</i>
· Applied machine learning (random forest, boosting tree) methods for clinical site fraudulence detection.	
Graduate Research Assistant	<i>2013.9-now</i>
<i>University of Washington</i>	<i>University of Washington, US</i>
· Inference and prediction of infectious disease using time series stochastic modeling.	

SKILL

Machine learning, Deep learning, Data mining, Database, MapReduce, Experimental Design, A/B testing, Regression analysis, Statistical consulting, Stochastic modeling, Time series analysis, Optimization, Statistical inference

SOFTWARE

Proficient in	C++, Python, R, SQL, Java, Matlab, L ^A T _E X,
With working experience	Hadoop, Spark, C#, Unix Shell script, Javascript

PAPERS

1. **Tang, M.**, Dudas, G., Bedford, T. and Minin, V. Fitting stochastic epidemic models to gene genealogies using Linear Noise Approximation. Section on Bayesian Statistical Science (SBSS) of the American Statistical Association (2019). **Winner of Student Paper Award**
2. **Tang, M.** and Minin V. Stochastic epidemic models using the integration of incidence and gene genealogies

PATENT

Time-weighted risky code prediction	<i>MS 403893-US-NP (pending)</i>
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