**Kuan-Liang Liu**

[kuanliang.github.io](http://kuanliang.github.io)

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**Technical Skills**

**Programming languages:** Python\*, Perl\*, R, visual basic, HTML\*, Javascript

**Framework/Libraries:** Spark\*, SparkSQL\*, SparkMLlib\*, Numpy\*, Pandas\*, scikit-learn\*, Matplotlib\*, Bokeh, D3, sickit-flow, Tensorflow, HIVE\*, MapReduce, HDFS, Flask\*

**Databases:** mysql\*, sqlite\*, mongodb, Hbase

**Others:** Git/Github, deep learning, genomic analysis\* \*denotes expert level

**Projects**

**Return Product Prediction –** [github.com/kuanliang/return-board](http://github.com/kuanliang/return-board) *June 2016*

* + - * Developed algorithms for return product prediction and prescription analysis with scikit-learn
      * Designed and implement modeling and deployment pipeline with Spark, Flask, Sqlite
      * Optimized data pipeline efficiency via SparkSQL, SparkMLlib and python comprehension
      * Improved prediction precision to 90% and stability via ensemble learning algorithms

**Multinomial rRNA Bayesian classifier –** [sourceforge.net/p/gdrrnaclassifie/wiki/Home](https://sourceforge.net/p/gdrrnaclassifie/wiki/Home)*December 2014*

* Improved accuracy of naïve Bayesian classifier with multinomial model and Dirichlet priors for microbial and fungal rRNA taxonomic assignment

**Fungal LSU/ITS classifier -** [rdp.cme.msu.edu/classifier/classifier.jsp](https://rdp.cme.msu.edu/classifier/classifier.jsp) *December 2013*

* Designed and implement classification algorithms for fungal rRNA taxonomic assignment
* Built-up rRNA sequence analysis, classification and evaluation pipeline with Django, Json and Flot

**Professional Experience**

**Foxconn Precision –** Data Scientist China | *August 2015~Now*

* + - * Designed and implement machine learning predictive models for return products
      * Designed and conducted Big Data, machine learning training courses for engineers

**Georgia International –** Technical Director Taiwan **|** *September 2010~August 2015*

* + - Built the audit process information system.
    - Audited customers according to ISO 9001, TS 16949 and customer requirements
    - Create new CE marking service and signed 10 newly developed consulting deals

**TokyoTech University** – Visiting Scholar Tokyo **|** *July 2010~September 2010*

* + - Developed visualization tools for 16S rRNA taxonomy assignment results comparison

**Los Alamos National Laboratory** – Graduate Research Assistant/internship USA | *October 2008~December 2010*

* + - Designed machine learning algorithms for metagenomic read assignment
    - Designed classifier for fungal ITS/LSU rRNA sequence taxonomic assignment
    - Performed and built-up data analysis pipeline for human oral microbiome projects

**Education**

**Udacity** - Machine Learning Engineer Nanodegree *in progress*

**Coursera** - Processing mining – Data Science in action / Machine Learning Specialist *May 2015 / in progress*

**Edx** - Big Data / Data Science and Engineering with Apache Spark XSeries *August 2015 / in progress*

**MIT Professional Education -** Tackling the Challenge of Big Data *August 2015*

**National Cheng Kung University** - Information Management, M.S., Ph.D. *December 2014*

**National Cheng Kung University** - Industrial and Information Management, B.S. *June 2005*

**Awards, Honors, Scholarship**

* + - * Acceptance for STAMPS workshop at Marine Biology Laboratory USA *December 2014*
      * The winner of ISME (International Symposium of Microbial Ecology) travel grant *June 2010*
      * The winner of HMRC (Human Microbiome Research Conference) travel grant *May 2010*
      * Scholarship for Pittsburgh Science of Learning Center summer school *July 2010*

**Selected Publication**

A. P. Alfaro, **K. L. Liu**, C. R. Kuske and G. Xie, “From Genus to Phylum: LSU and ITS rRNA operon regions showed similar classification accuracy influenced by database composition”, Applied and Environmental Microbiology, 2014, 80(3), 829-40

**K. L. Liu**, T. T. Wong, “Naïve Bayesian Classifiers with Multinomial Models for rRNA Taxonomic Assignment”, IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10(5), 1334-9.

**K. L. Liu**, C. R. Kuske, A. P. Alfaro, S. Eichorst and G. Xie, “Accurate, rapid classification of fungi using the large subunit

rRNA gene”, Applied and Environmental Microbiology, March 2012, 78(5) 1523-33.

F. Yang, X, Zeng, K. Ning, **K. L. Liu**, C. C. Lo, W. Wang, J. Chen, D. Wang, R. Huang, X. Chang, P. S. Chain, G. Xie, J. Ling and J. Xu, “Saliva microbiomes distinguish caries-active from healthy human populations”, The ISME Journal, 2012, 6, 1-10