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Kuan-Liang Liu

kuanliang.github.io
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Technical Skills

Programming languages: Python*, Perl*, R, visual basic, HTML*, Javascript
Framework/Libraries: Spark*, SparkSQL*, SparkML/lib*, 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   *June 2016*

- Developed algorithms for return product prediction and prescription analysis with scikit-learn and Pandas
- 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   *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   *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