Guangyu Shan

Curriculum Vitae

Education

2013–Present **Master of Science(M.S.), Bioinformatics(expected)**, *AMMS(Academy of Military Medical Sciences)*, Beijing, *GPA − 79.0/100.*

2009–2013 **Bachelor of Science(B.S.), Bioengineering**, *Wuhan Bioengineering Institute*, Wuhan, *GPA − 88.9/100.*

Interests

Research Machine Learning, Metagenomics, Complex Network Analysis, Text Mining

Sports Basketball, Badminton, Swimming, Running

Experience

Vocational

2012 **Summer Intern**, BGI, Shenzhen.
QC(Quality Control) technician of noninvasive prenatal testing team on performing real-time quantitative PCR experiments.

Miscellaneous

2014 **Volunteer**, *Beijing Society of Neuroscience*, Beijing.
Reception.

Honors & Awards

2010 **National Encouragement Scholarship**, Ministry of Education, Wuhan, China.

2011 **Rank 7th in Men's 1500-metre Race in the Sports-meeting**, Wuhan Bioengineering Institute, Wuhan, China.

2014 **Advanced Outstanding Student**, Institute of Radiation Medicine, AMMS, Beijing, China.

2015 **Top 30 in Ali Baichuan Startup Competition**, Alibaba, Hangzhou, China.

Technical Skills

Basic C

Intermediate Python = R > Ruby, Linux/Mac OS X = Vim > LaTeX> GitHub, MySQL > MongoDB

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| Advanced | Text Mining, Bioinformatics, Data Analysis, Complex Network Analysis |

Languages

Chinese	**Native proficiency**	
English	**Full professional proficiency**	*Conversationally fluent(CET-6)*
Japanese	**Elementary proficiency**	*Basic words and phrases only*

Comments

Teacher	**Good self-learning ability**	*Yiming Lu(Associate Professor in AMMS)*
Teacher	**Always accomplish work quickly**	*Wubin Qu(Associate Professor in AMMS)*
Advisor	**Have sufficient curiosity in science**	*Chenggang Zhang(Professor in AMMS, associate director of the State Key Laboratory of Proteomics of China)*

Projects

2013–2014   **Leader**, A MeSH-based Text Mining Method for Identifying Potential Prebiotics, Beijing, Under Review by *Plos One*.

Prebiotics contribute to the well-being of their host by altering the composition of organisms in the gut microbiome. Because finding new prebiotics was in a slow step, a substantial part of candidates are yet to be identified. However, relevant features of known prebiotics have been hidden in the well-documented literature. In this paper, we developed a medical subject headings (MeSH)-based text mining method for identifying potential prebiotics using structured text downloaded from PubMed. We defined an optimal feature set for prebiotics prediction using a systemic feature-ranking algorithm and showed that, using this feature set, a variety of carbohydrates can be well classified into different clusters with a high agreement to their chemical structures and functions. The features were assigned to weights based on their importance and carbohydrates for testing were scored and ranked based on their feature profiles. We used a cross-validation procedure to assess the accuracy of the prediction and found our method could predict potential prebiotics with a specificity of 0.838 and a sensitivity of 0.876. At last, we identified eleven potential prebiotics that were greatly supported by the literature analysis. Overall, our study presents both a novel framework for predicting potential prebiotics from knowledge and a set of promising potential prebiotics.

Detailed achievements:
- Developed a novel framework for predicting potential prebiotics.
- Provided a set of promising potential prebiotics.

2014–2015   **Leader**, A CUSTOMIZED LITERATURE SERVICE BASED ON WECHAT PUBLIC PLATFORM, Beijing, Published on *Chinese Journal of Bioinformatics*.

Literature study is a necessary way for tracking progress in a certain research field and conceiving the project development. In order to solve the onerous literature tracking problem in a mobile terminal, we developed a PubMed Customized Retrieving system (PCR) on WeChat Public Platform by means of immediacy, convenience, personalization features of mobile internet. The service provides several convenient features such as literature customization, literature querying and Impact Factor (IF) Querying by parsing input, matching built-in journals name-table dynamically and retrieving PubMed database. This work values a lot on improving literature learning efficiency and reducing time cost for researchers.

Detailed achievements:
- Literature Customization
- Literature Querying
- IF Querying

2015–Present   **Leader**, TOPOLOGICAL CHARACTERISTICS OF POSTOPERATIVE SURVIVAL RATE-RELATED MOLECULES IN HEPATOCELLULAR CARCINOMA-ASSOCIATED COMPLEX NETWORKS, Beijing, Published on *Military Medical Sciences*.

Objective To explore the network structure of genes and microRNAs(miRNAs) at the system level and to study topological characteristics of survival rate related molecules by means of survival analysis. **Methods** Regulatory networks were established with genes of hepatocellular carcinoma(HCC) and with the expression prifiling data of miRNA. Survival knowledge in nodes was studied.**Results** All the nodes in gene co-expression networks conformed to power-law distribution. In a network, high-degree nodes were called "Hub", which enriched more survival related genes than lower degree ones. **Conclusion** Hub nodes in gene regulatory networks promise to be potential features for molecular subtyping.

Detailed achievements:
- Hub nodes in gene regulatory networks promise to be potential features for molecular subtyping.

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