BRIGHAM AND WOMEN'S HOSPITAL

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Department of Medicine
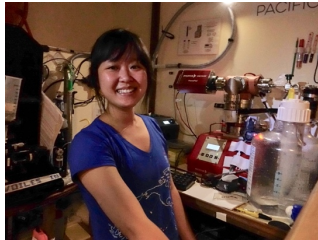*Channing Division of Network Medicine*

Channing Microbiome Seminar
December 16 (Friday), 2022, 9AM-10AM (EST)

Zoom: https://us02web.zoom.us/j/81070959105?pwd=RFJNd3dSZmR6dXJZNjJiYVVzQ3NEQT09
Meeting ID: 810 7095 9105
Passcode: 984617

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Deep Learning for Predicting 16S rRNA Gene Copy Number

Abstract: Culture independent 16S rRNA gene metabarcoding is a commonly used method in microbiome profiling. To achieve more quantitative estimates, i.e., the true cell abundances, we need to resolve the variable 16S RNA copy numbers (GCN) for different community members. Currently, there are several bioinformatic tools available to estimate 16S GCN, either based on taxonomy assignment or phylogeny. Here we present a novel approach ANNA16, Artificial Neural Network Approximator for 16S GCN, a deep learning-based method that estimates GCN directly from the 16S gene sequence strings. Based on 19,520 16S data (rrnDB database), we show that ANNA16 outperforms the commonly used algorithms. Interestingly, Shapley Additive exPlanations (SHAP) shows that ANNA16 can identify unexpected informative positions in 16S DNA sequences without any prior phylogenetic knowledge, which suggests potential applications beyond GCN.

Bio: *Dr. Lin a biological oceanographer. She received her PhD from Nicholas School of the Environmental at Duke University. She was an Assistant Professor at Duke Kunshan University in China, and currently she is an Assistant Professor in Department of Life Sciences at Texas A&M University – Corpus Christi. She studies marine microbiome and how they regulate energy and carbon fluxes in a changing climate.*

Hosted by Yang-Yu Liu

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