## **BayBioMS** "Advanced Mass Spectrometry"-Seminar

Under the direction of

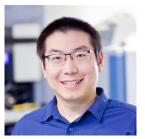
BayBioMS baybioms@tum.de www.baybioms.tum.de



Benedikt Bächler (Metabolomics, substitute for Karin)



Dr. Christina Ludwig (Proteomics)



Dr. Chen Meng (Bioinformatics)

When: Monday 24.06.2019, 5pm Where: iGZW, conference room 3<sup>rd</sup>

floor, Gregor-Mendel-Strasse 4

Doors open at 4:45 pm Free beer, drinks and snacks will be served!!

## **BayBioMS proudly presents our special guest speaker:**

## Brendan MacLean University of Washington

"Skyline - A software solution for quantitative mass spectrometry studies in proteomics and metabolomics"



Skyline is a freely-available and open source software tool for analyzing proteomic as well as metabolomic mass spectrometry data in a targeted fashion. Over the last decade, Skyline has emerged as the most popular analysis software in the field of targeted proteomics. Brendan MacLean is the principal investigator of Skyline and responsible for all aspects of design, development and support in creating the Skyline Environment and its growing worldwide user community.

