Thursday

9:30  **Arrival / welcome coffee**

10:00 **Welcome notes**

10:05  Tom Tubbesing
Unravelling microbiome adaptations in three production scale biogas plants

10:30  Benedikt Osterholz
*Metagenomics-Toolkit: The flexible and efficient cloud-based metagenomics workflow with machine learning-enabled resource allocation*

10:55  **Break**

11:25  Andreas Rempel
The panagenomics workbench

11:50  Luca Parmigiani
Comparing pan genome graphs using Panacus

12:15  Leonard Bohnenkämper
Rearrangement-based small parsimony

12:40  **Lunch**

13:40  Manuel Feser
On the way to plant data commons

14:05  **Keynote:**  Jianxu Chen
*Image analysis for optical microscopy in the era of AI*

14:45  **Break**

15:00  Maximilian Wolf
Meta-analysis and bias correction of fecal metaproteomic datasets

15:25  Emanuel Lange
A roadmap for the MPA-Pathway-Tool towards simplified modeling and data integration

15:50  Muhammad Elhossary
Alternative approaches for genome-wide identification of bacterial small RNAs based on sequencing data

16:15  **Break**

16:45  Vanessa Scharf (application)
Construction and analysis of knowledge graph representation of bacterial small RNAs and their interactions

17:10  Luna Pianesi (application)
Graph neural networks and explainable AI for a new Aurora kinase inhibitor

17:35  **End of program**

19:00  **Dinner / Social Event**
Hicc Upp (Wittener Straße 205)
Friday

9:00  **Start of program**

9:00  Daniel Göbel, Michael Beckstette
      *CloWM – Cloud based Workflow Manager*

9:45  **Hands-on-session: Working with CloWM**
      (in parallel: faculty meeting)

10:30 **Break**

11:00 **Tutorial continued**
      (in parallel: faculty meeting)

12:30 **Lunch / End of program**