**Identifying conserved host response for virus infections such as Covid-19**

Clinical presentations of COVID-19 are highly variable, and while the majority of patients experiences mild to moderate symptoms, 10%–20% of patients develop pneumonia and severe disease. We recently performed the first single-cell RNA-sequencing of blood cells to determine changes in immune cell composition and activation in mild versus severe COVID-19 over time.[1] A recent study based on multi-cohort analysis of host immune response identifies conserved protective and detrimental modules associated with severity across viruses[2,3]. Therefore, we hypothesized that viral infections induce a conserved host response and the conserved response is associated with disease severity. In this project, we will 1) implement the analysis framework for identifying conserved host response and 2) apply it to transcriptome data from multi-cohorts of COVID-19 and other virus infected patients.

**Possible benchmark topics include:**

1. A Benchmark for transcriptome data pre-processing
2. Benchmarking the methods for identifying host response signatures in transcriptome data
3. Benchmarking the meta-analysis methods across multiple cohorts
4. Application of implemented analysis framework to patients' data from e.g. COVID-19 and influenza.
5. Validation of virus responding signatures using independent datasets

**An ideal candidate should have:**

- Good background in programming (Python or R).
- Interest in performing biological data mining.
- Experiences with RNA-sequencing or omics data is a plus.
- Love to read and explore scientific articles, preferably every day.
- Pro-active in learning new things, preferably every day.

Interested students are encouraged to email to Prof. Dr. Wolfgang Nejdl, nejdl(at)kbs.uni-hannover(dot)de and Prof. Dr. Yang Li, yang.li(at)helmholtz-hzi(dot)de for discussions.

**References:**

1. Schulte-Schrepping, J. *et al.* Severe COVID-19 Is Marked by a Dysregulated Myeloid Cell Compartment. *Cell* **182**, 1419-1440.e23 (2020).
2. Andres-Terre, M. *et al.* Integrated, Multi-cohort Analysis Identifies Conserved Transcriptional Signatures across Multiple Respiratory Viruses. *Immunity* **43**, 1199–1211 (2015).
3. Zheng, H. *et al.* Multi-cohort analysis of host immune response identifies conserved protective and detrimental modules associated with severity across viruses. *Immunity* **54**, 753-768.e5 (2021).