deNBI-epi Berlin

# Computational epigenomics tools and training BIMSB

FKZ 031L0101B

Wolfgang Kopp, Alison C McGarvey, Scott A Lacadie, Uwe Ohler, Altuna Akalin
Max Delbrueck Center, The Berlin Institute for Medical Systems Biology, Germany

Short description of the project

We offer reproducible tools, services and training for the epigenomics and genomics data analysis community.

de.NBI Services and Tools
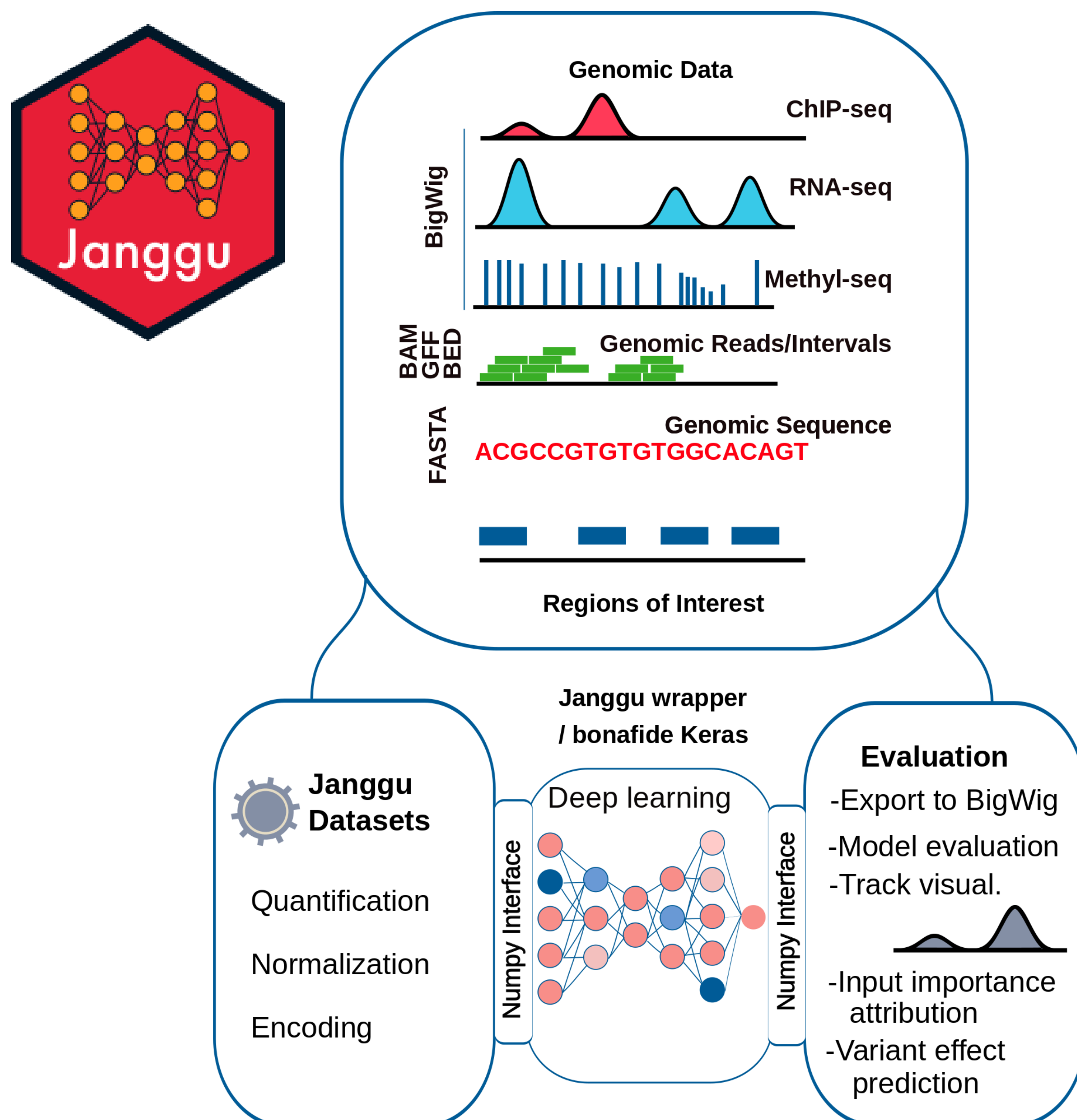
Pre-print (under review)
Source: **github.com/BIMSBbioinfo/janggu**
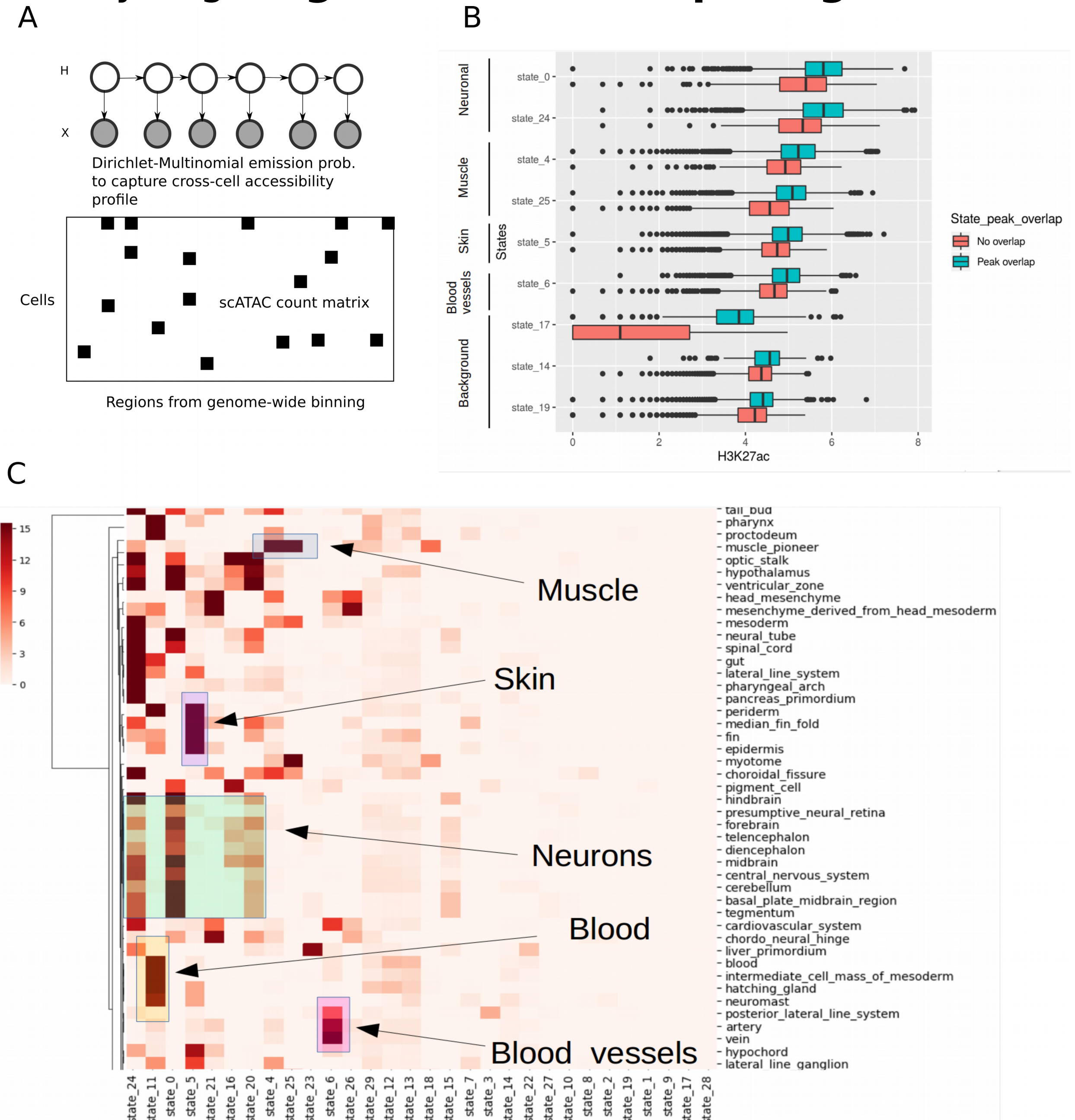Downloads (Feb 9, 2020): **21k>**
Highlighted in de.NBI Use Cases brochure

Other Services:

Galaxy server maintenance at MDC: 100+ total users

General information on the project

- No. of staff paid from de.NBI grant (FTE): 1
- Other staff involved: 4

Progress report

### Analyzing single-cell ATAC-seq using HMMs

A) Segmentation of scATAC-seq data using HMM captures cell-type specific accessibility. B) Some states reflect regulatory activity as validated using H3K27ac. C) Functional annotation determined by state abundance around marker genes. (Data from McGarvey).

de.NBI Training and education

16 Number of courses

Yearly public courses on Computational genomics

273 Number of participants
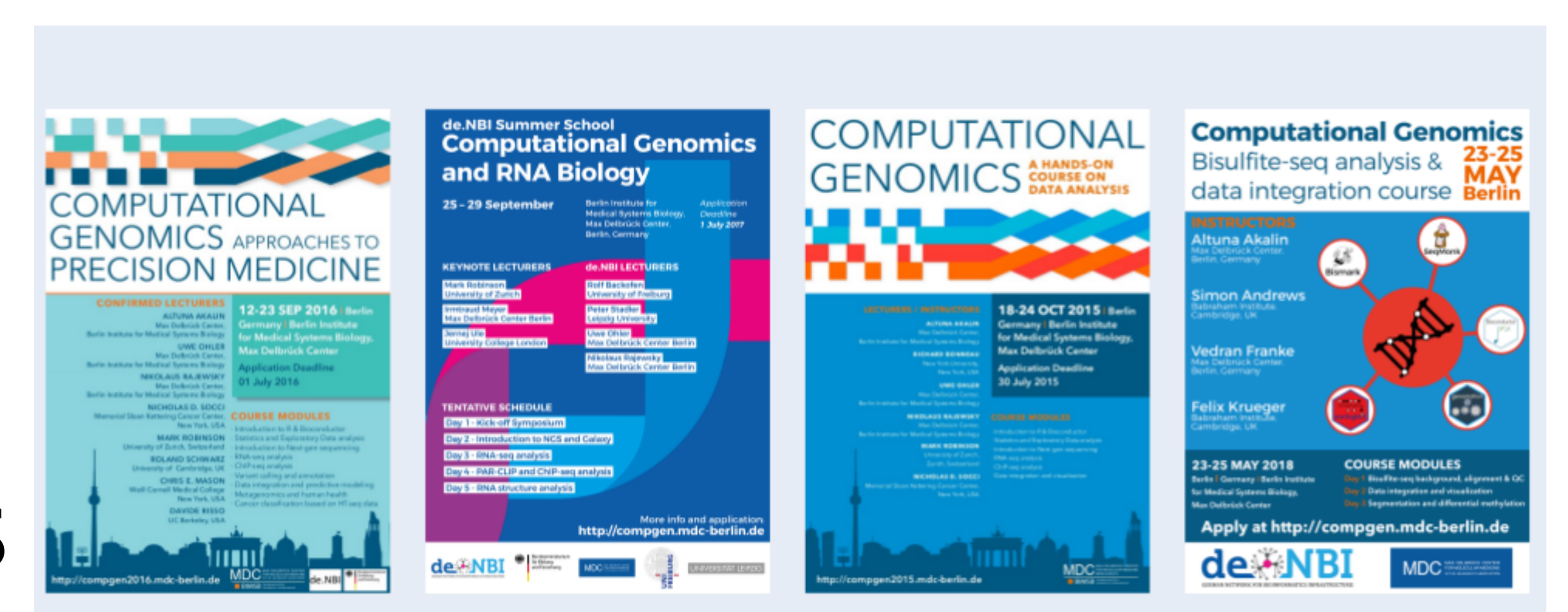
Publications

Janggu – Deep learning for genomics. Kopp, Monti, Tamburrini, Ohler, Akalin. Biorxiv, 2019.