

## PROGRAM

### DAY 1 ATAC methodology and bioinformatics – adaption to different species

(Presentations 15 + 5 min)

1100-1130 Lunch

1130 Welcome, Peter Aleström

#### PART I: ATAC method

1140 Leif Lindeman (NMBU): ATAC - general and experimental procedure

1200 Jorke Kamstra (Utrecht Univ.): ezh2 control of the epigenome

1220 Christiaan Henkel (NMBU): nanopore ATAC-seq?

1240 Matilde Mengkrog Holen (CIGENE): Frozen vs fresh samples

1300-1430 Coffee/Tea and Discussion: *Adaption to different species/tissues, High quality nuclei preparation, Tn5 enzyme and TD buffer, Library QC, scATAC-seq*

#### PART II: ATAC bioinformatic analysis

1430 Hien To (ELIXIR/CIGENE): ATAC-seq bioinformatics: Peak calling and TFBS motif prediction

1450 Lindeman (NMBU/CERAD): Zebrafish ATAC-seq bioinformatics pipeline(s)

1530 Discussion: *Bioinformatics “pipeline(s)”, adaption to different species*

1700 Dinner

### DAY 2 Hands-on ATAC library

*Leif Lindeman, Jarle Ballangby: Hands-on ATAC, max number of participants is 8.*

*Participants will learn to make ATAC libraries on 24 hpf zebrafish embryos.*

1000 Start of experiment based on Jarle Ballangby MSc and *den Broeder et al.* (ms in prep), Ezh2 treated zf embryo ATAC-seq protocol. All participants get one technical replica sample.

1600 Discussion of results