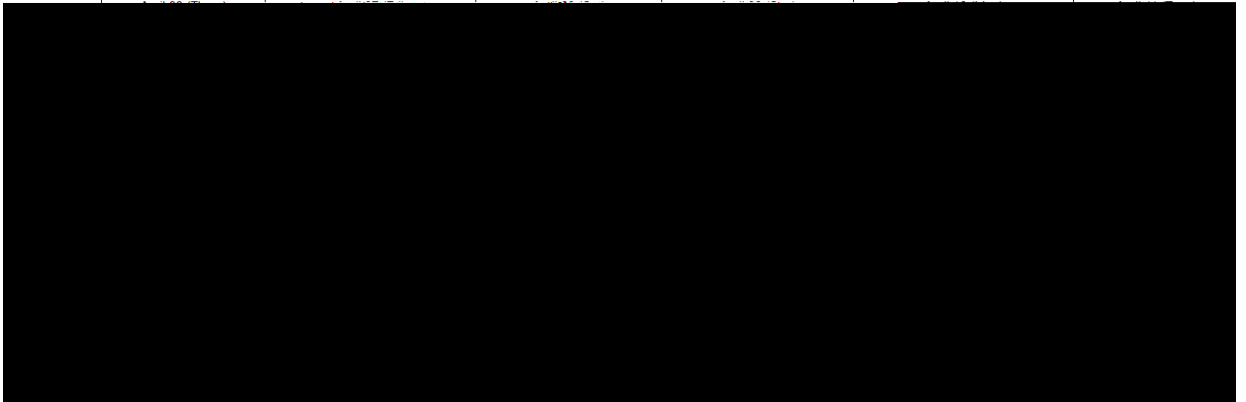


- How to analyze RNA-seq, ChIP-seq and Proteomics data
- How to use the latest *Xenopus* genomic resources in my research
- How to handle large-scale data in the public database
- How to analyze single-cell transcriptome data (*Xenopus* & others)



- Taejoon Kwon (UNIST, Korea)
- Leonid Peshkin (Harvard Medical School)
- ChangHee Lee (Harvard Medical School)
- Konrad Thorner (XenBase)
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