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| Session/Day | **Day1 (22th, Tue, 1pm)**  **Place: 14A-109** | **Day2 (23th, Wed, 2:15pm)**  **Place: 14A-109** | **Day3 (28th Mon, 2:15pm)**  **Place: B11, ATC** | **Day4 (29th Tue, 2:15pm)**  **Place: B11, ATC** |
| Session1 | **Lecture 1** (KG)  Introduction of SVs and bulk genomics approaches | **Lecture 2** (KG)  Introduction of Strand-seq and single-cell genomics approaches | **Bioinformatics practice 3**  (KG &HJ)  Software: BreakpointR  Data: Strand-seq  WT 20 good quality cells  Goal: Find breakpoint and explore it using UCSC genome browser | **Bioinformatics practice 5**(HJ)  Software: Mosaicatcher  Data: Strand-seq  Mixture (VAF20% BM510)  WT 80 cells + BM510 20 cells  Goal: Find out subclonel SVs and cells automatically |
| Session2 | **Bioinformatics practice 1**(HJ)  Software: Delly  Data: WGS  RPE1 WT  BM510  Mixture (VAF 20% BM510)  Goal: Detect clonal and subclonal somatic SVs | **Bioinformatics practice 2**(HJ)  Software: Plotting pipeline  Data: Strand-seq  WT 25 cells  (20 good quality + 5 bad quality cells)  Goal: Make overview plot, Quality checking | **Bioinformatics practice 4**  (KG & HJ)  Software: Plotting pipeline  Data: Strand-seq  Mixture (VAF20% BM510)  Goal: Manual identification of subclone | **Lecture 4** (WH)  Biological questions and new applications of Strand-seq  Evolution, inversion and TAD |

**Korbel Lab predoc course November 2019**

**Detecting genetic structural variation in the human genome in bulk experiments and single cells**

<https://github.com/jeongdo801/SV_practical_computational>