

Single cell sequencing

Boris Tichý (CEITEC-MU), Andreas Sommer (VBCF) 24. 09. 2018

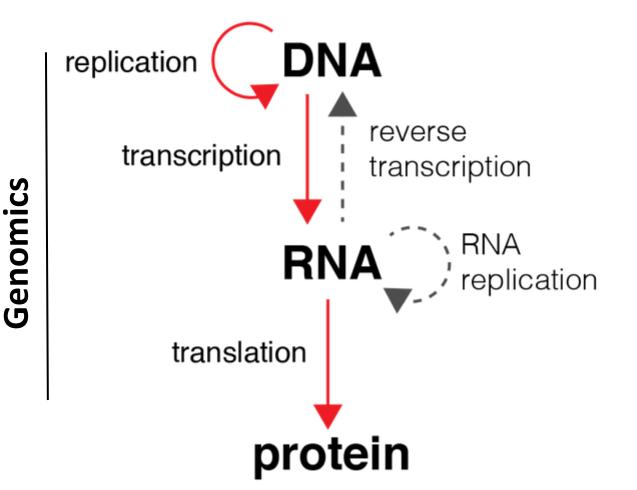






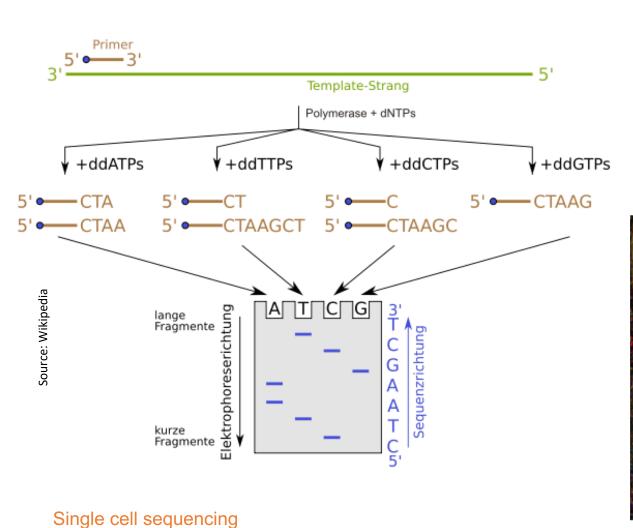
<u>Genomics Tools:</u> Microarrays PCR Sanger FISH ... **NGS**

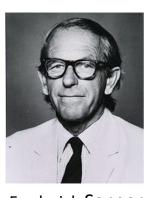
(Next Generation Sequencing)











Frederick Sanger

- <text>
 - ♦ First full human genome
 - ♦ Large Sequencing centers from 6 countries,
 - Hundreds of dedicated scientists
 - \diamond Approx. 10 years
 - \diamond > 3 billion USD



2005









"A new generation of non-Sanger-based sequencing technologies has delivered on its promise of sequencing DNA at unprecedented speed, thereby enabling impressive scientific achievements and novel biological applications." **nature methods: method of the Year 2007**

2010

-

Massive Parallelization of sequencing reactions!





Jul 24, 2018

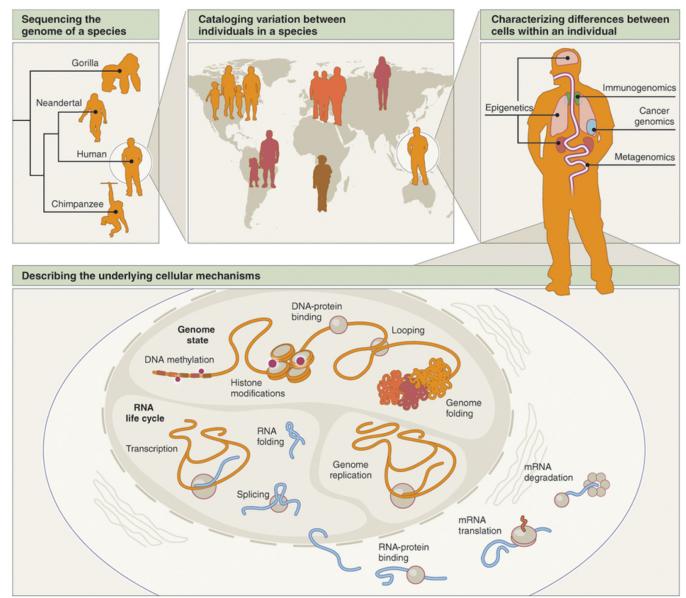


GRI Staphylococcus Genome Set Reveals Bug's Host-Switching History Aug 13, 2018 When rese **Deep Whole-Genome Sequencing Diagnoses Early Infantile** aureus isol Epileptic domestic a Aug 17, 2018 **Researchers** International Consortium Sequences, Annotates Bread testing could Wheat Reference Genome The consortiu Research | 17 September 2018 which has be Genomic history of the Sardinian population Cost pe researchers. Analyses of 3,514 whole-genome-sequenced individuals from Sardinia indicate that within-island substructure and sex-biased processes have impacted the genetic history of Sardinia, providing new insight into the demography of ancestral Sardinians. \$1k Charleston W. K. Chiang, Joseph H. Marcus [...] John Novembre \$100 Nature Genetics, 1–9 2001 2003 2007 2013 2017 2005 2009 2011 2015

Protocols, Flexibility



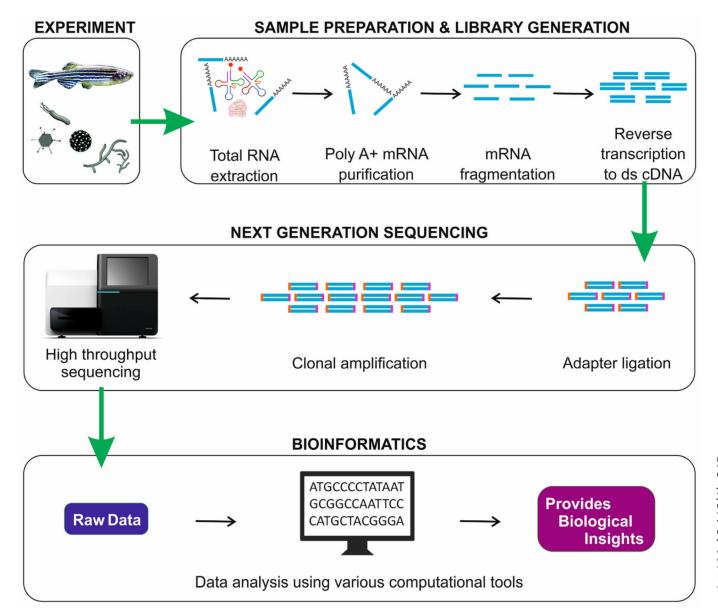




Nature Biotechnology 30, 1084–1094 (2012)



mRNA Sequencing



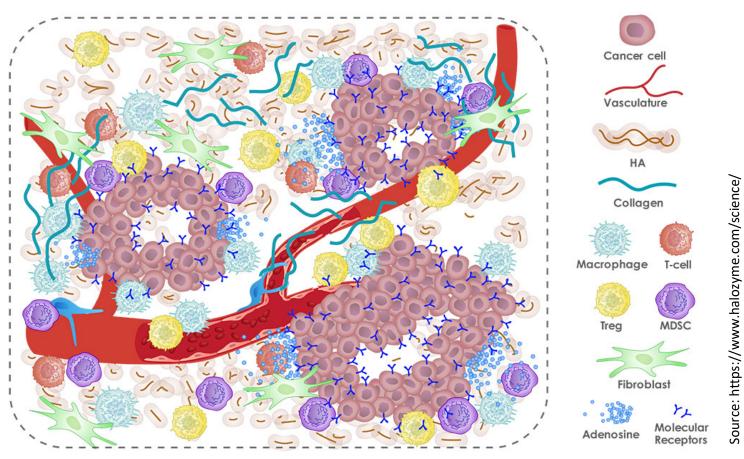
Single cell sequencing

Int J Mol Sci 19(1): 245.



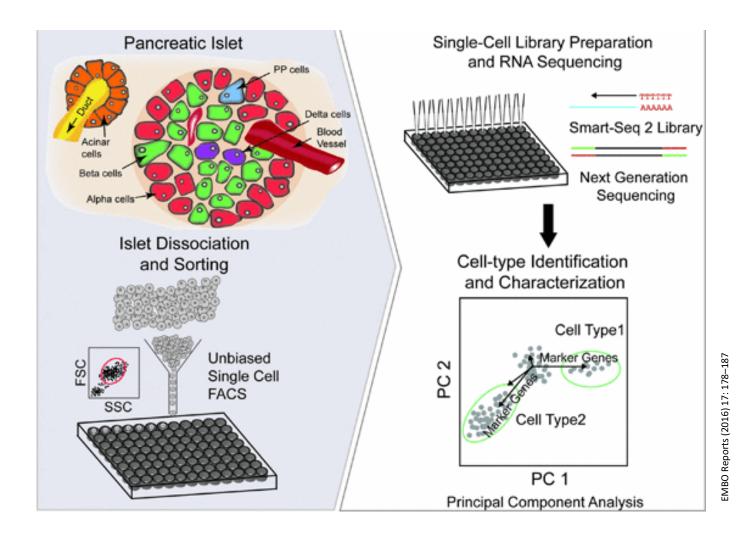


The Tumor Microenvironment



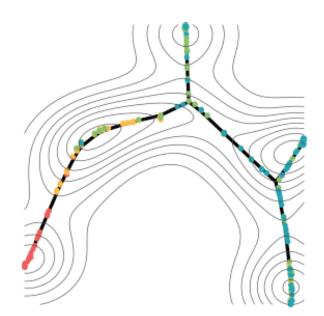
Single RNA cell sequencing

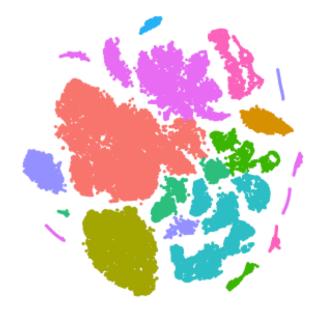




Data Analysis







Pseudotime

Build single-cell trajectories with the software that ntroduced pseudotime. Find cell fate decisions and the genes regulated as they're made.

Clustering

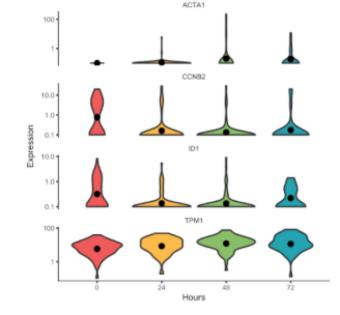
Group and classify your cells based on gene expression. Identify new cell types and states and the genes that distinguish them.

Differential expression

Find genes that vary between cell types and states, over trajectories, or in response to perturbations using statistically robust, flexible differential analysis.

Source: 10X Genomics

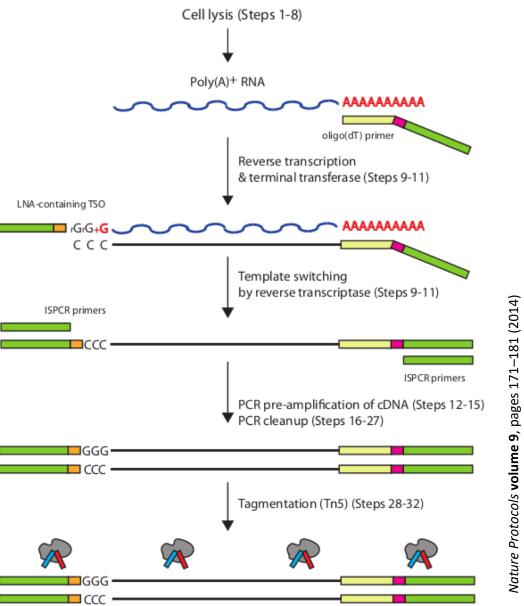




Smart-seq 2







Pilot project introduction

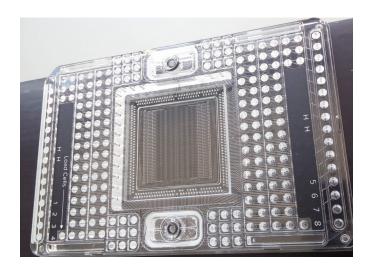


- Project partners:
 - VBCF NGS Core Facility, CEITEC Genomics Core Facility
- Complementary equipment/expertise:
 - Library preparation expertise, NGS sequencers, FACS, LCM, Fluidigm C1
- Basic project idea:
 - Set up a protocol for single cell RNA sequencing used at both sites
- Project goal:
 - Broadening the range of our services based on requirements of our users
- End-users:
 - Academic users (eg. oncology research)



Project implementation

- Approach/methodology
 - Library protocols based on SMART-Seq2 method
 - Open solution according to Picelli 2014
 - Solution using Fluidigm C1 + commercial kit
- Implementation
 - Implementation of Smart-Seq2 at VBCF \rightarrow transfer of the protocol to CEITEC
 - Staff exchange (Filip Pardy at VBCF)
 - Implementation of Smart-Seq2 on Fluidigm C1 at CEITEC

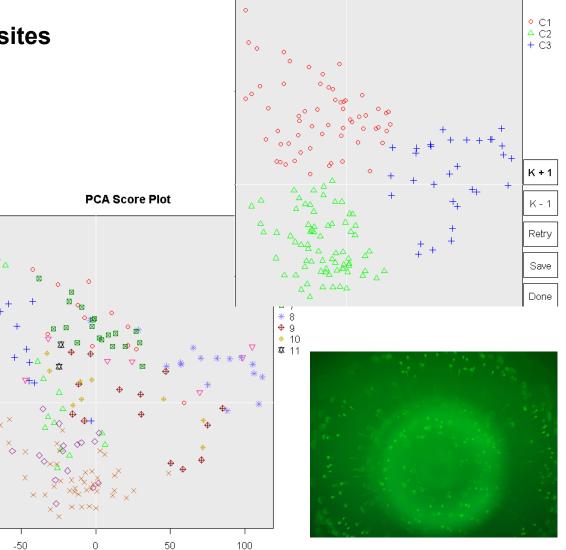


Picelli et al., Nature Protocols 2014

Project results



PCA Clustering Plot (K = 3)



- Results:
 - Method for single-cell RNA sequencing at both sites

100

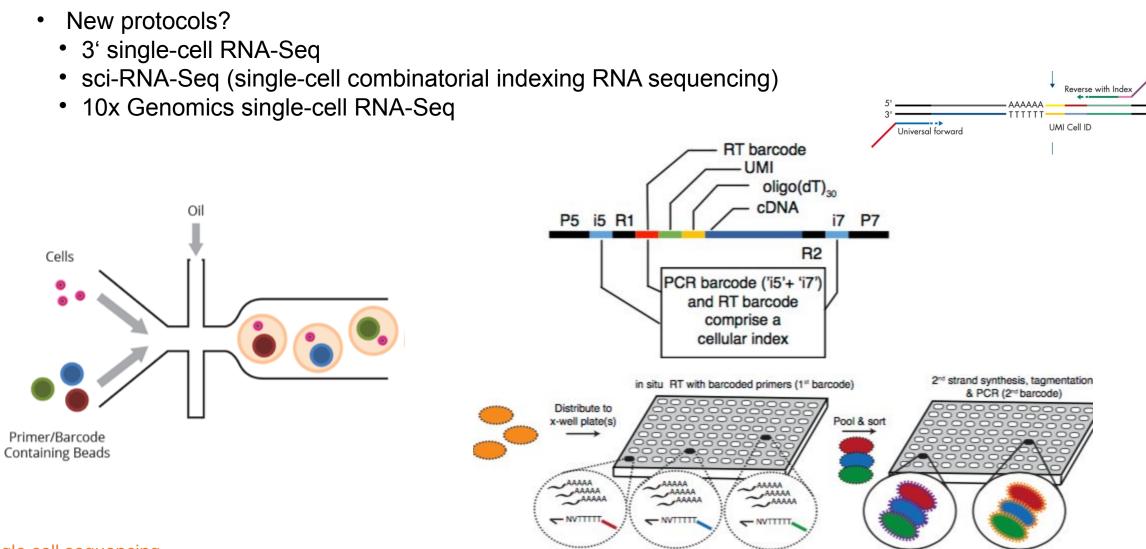
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- Benefits for the users:
 - No averaging of gene expression
 - Screening for cell subpopulations

Single cell sequencing



Future

