Single Cell RNA-seq in VEuPathDB

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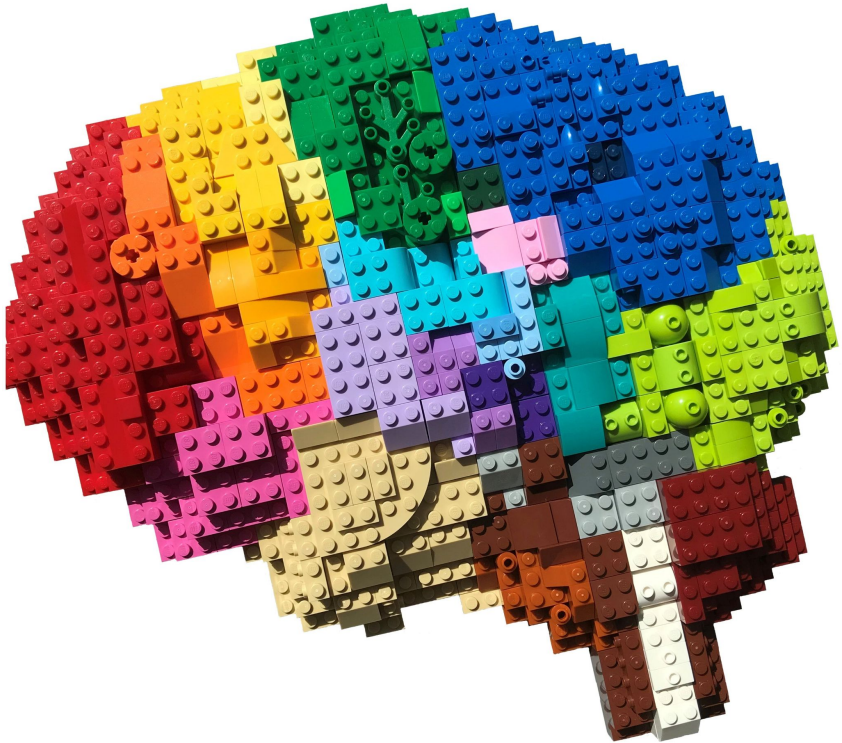
Why Do Single Cell Analysis?



- Most biological samples aren’t clean isolates of a single cell type
- Some tissues are very heterogeneous and hard to dissect
- Single celled organisms may not be conducting biological functions synchronously
- Even lab samples are often not as homogeneous as we like to think

Image Credit: @BoXia7 (Twitter)

Why do Single Cell Analysis?

- When you sequence RNA in bulk, you mix your heterogeneous cells together
- You can distinguish strong signals, but weaker signal are masked
- It is difficult to associate signals with different cell types

Image Credit: @BoXia7 (Twitter)

Why do Single Cell Analysis?

- Single cell analysis allows us to distinguish individual cell types
- This enables us to attribute signal in our data to specific cell populations
- We can also find weak signal associated with small populations of cells

Image Credit: @BoXia7 (Twitter)

Why do Single Cell Analysis?

- Further analysis can help us reconstruct how these cell populations are physically related to each other (spatial transcriptomics)
- Useful for exploring host-parasite or vector-parasite interactions

Image Credit: @BoXia7 (Twitter)

Why do Single Cell Analysis?

- Or we can infer developmental trajectories by ordering cells
- This is particularly useful in parasitology for:
  - Examining processes that can't be synchronised
  - Finding intermediate cells between known lifecycle stages

Image Credit: @BoXia7 (Twitter)

How Does It Work?

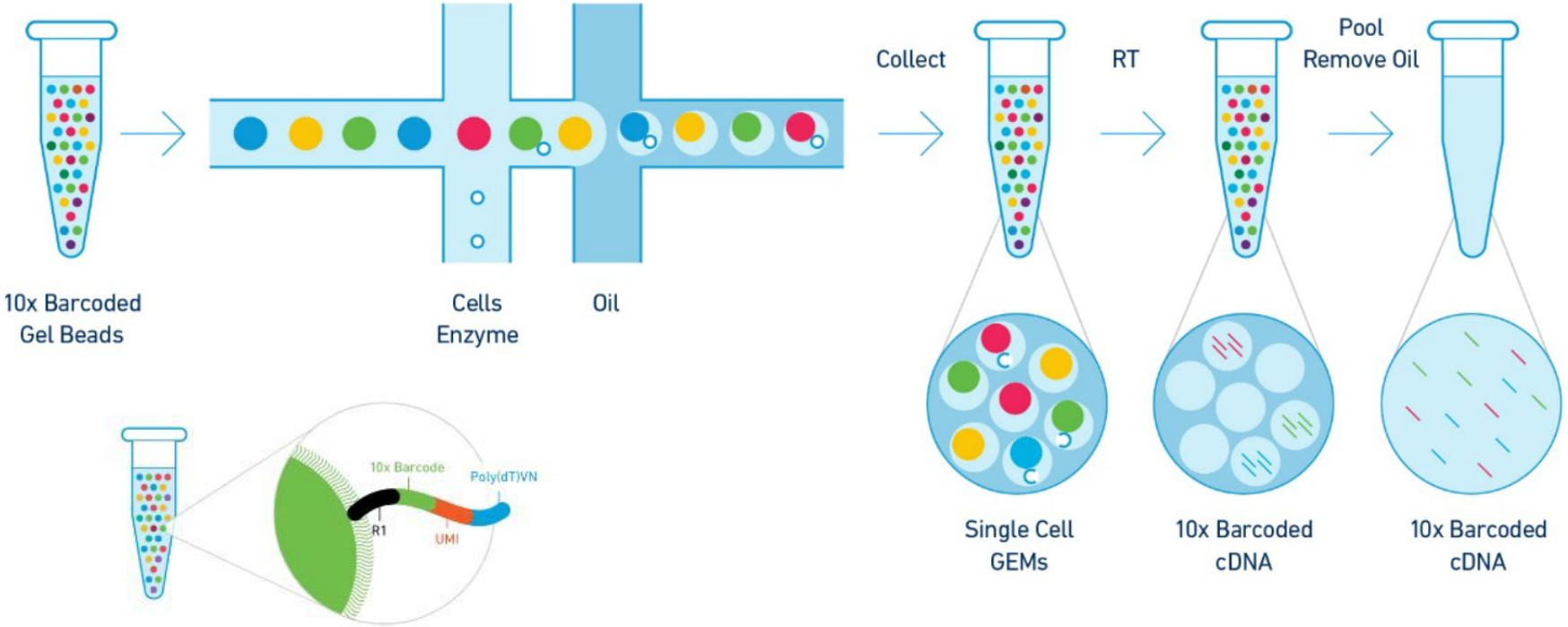


Image Credit: 10x Genomics

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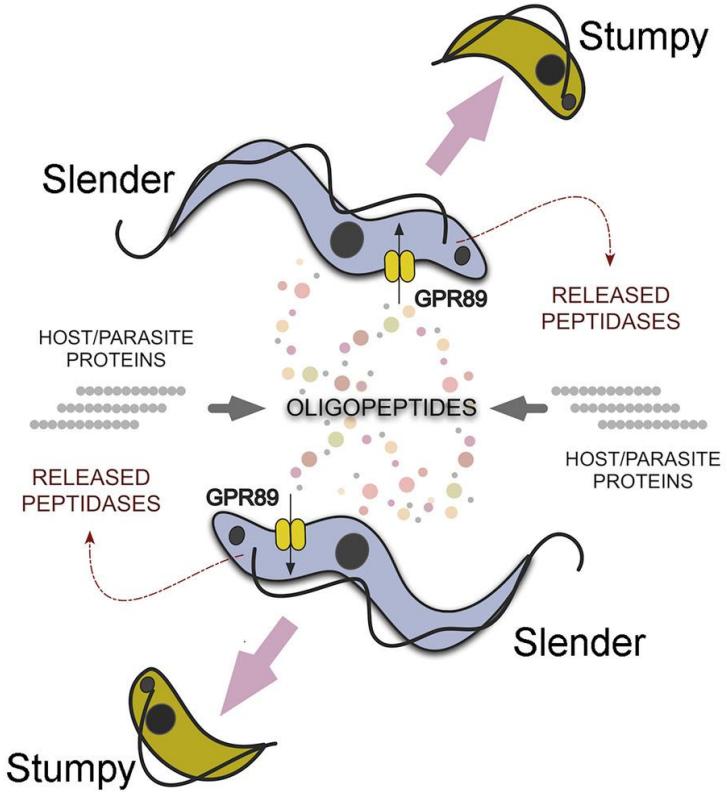
Quorum Sensing in *Trypanosoma brucei*



- Long slender morphological forms in the bloodstream are replicative but not transmissible
- Short stumpy forms are adapted for transmission but cannot replicate
- Regulation of the differentiation process is poorly understood

Rojas et al, Cell 2019