Data-driven precision medicine approaches to cancer

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Cancer Background

- Mass of cells
- Heterogeneity
Single Cell Sequences

- Seurat - R toolkit for single cell genomics
- Filter based on QC metrics (ex: total number of molecules detected in a cell)
- Identify highly variable features
- Determine dimensionality of dataset (look at p-values)
- Cluster Cells
Patient Data

- Look at DNA
- Compare treatment success
- Gene expression difference
Application

- Identify tumor/aggressiveness
- More effective treatment
Acknowledgements

Thank you

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