

# Unraveling Immunogenomic Diversity in Single-Cell Data

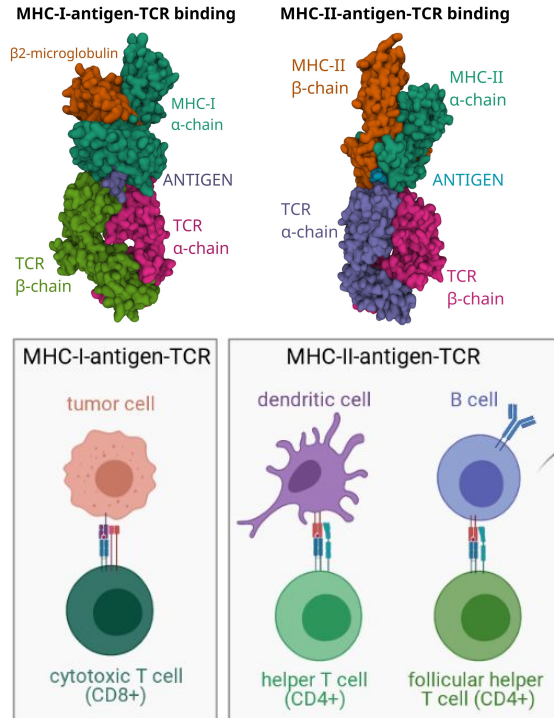
**Ahmad Al Ajami**<sup>1,2,3</sup>, Jonas Schuck<sup>1,2,3</sup>, Federico Marini<sup>4</sup>, Katharina Imkeller<sup>1,2,3</sup>

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**Grand Rapids**  
**25 July 2024**

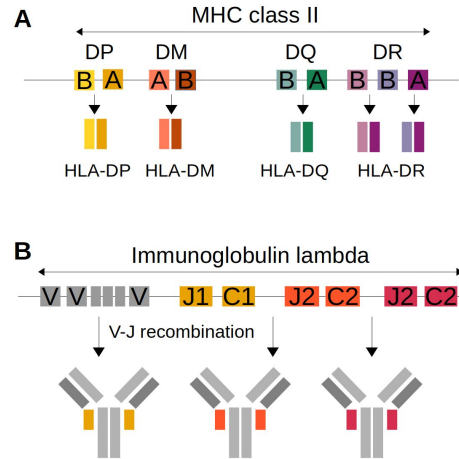
# Structural diversity of receptors

- Receptors that coordinate antigen specificity in immune responses



# Genetic mechanisms of structural diversity

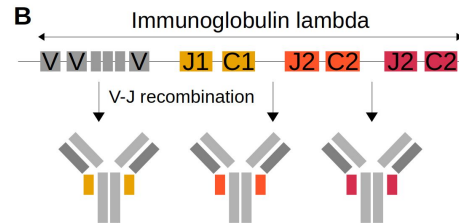
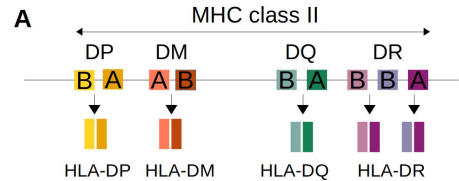
**Polygeny:**  
Multiple similar genes  
encode same function



Gene group	Number of <b>similar genes</b> (incl. pseudogenes)
<i>IGHG</i>	5
<i>HLA-DRB</i>	8
...	...

# Genetic mechanisms of structural diversity

**Polygeny:**  
Multiple similar genes  
encode same function



**Hyperpolymorphism:**  
Multiple alleles  
for one gene

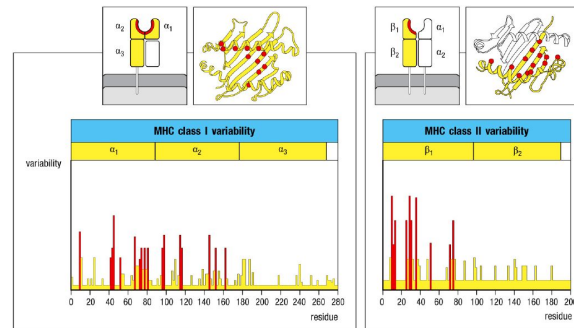


Figure 6.21 Janeway's Immunobiology, 9th ed. (© Garland Science 2017)

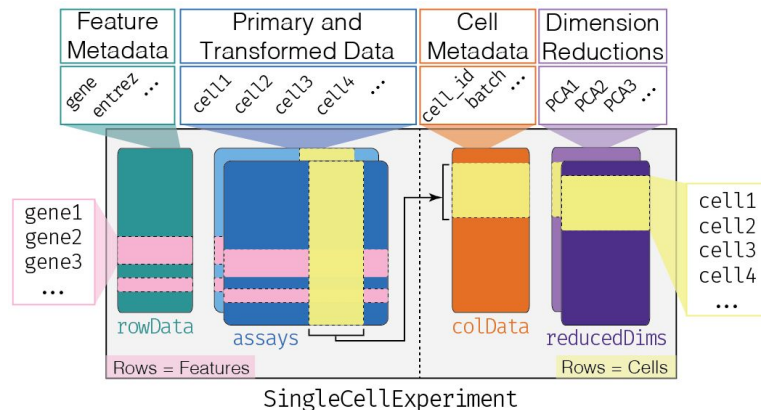
Gene group	Number of <b>similar genes</b> (incl. pseudogenes)
<i>IGHG</i>	5
<i>HLA-DRB</i>	8
...	...

Gene group	Number of <b>alleles</b> (incl. pseudogenes)
<i>IGHG</i>	71
<i>HLA-DRB</i>	~4200
...	...

Source: IMGT and IPD-IMGT/HLA

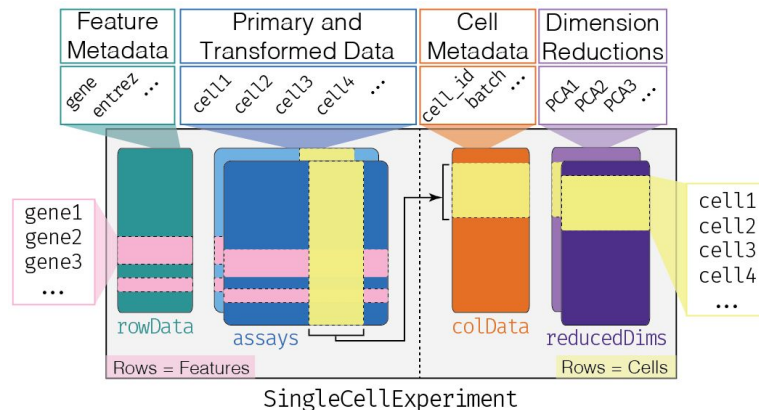
# Typical transcriptomic analysis workflow

1. For each sequencing read:
  - a. identify cellular barcode
  - b. identify unique molecular identifier (UMI)
  - c. map read to reference genome
2. Count unique transcripts per gene and barcode using UMI
3. Generate feature count matrix (genes x cells)
4. Downstream analysis
  - a. dimension reduction
  - b. clustering
  - c. differential gene expression
  - d. ...



# Typical transcriptomic analysis workflow

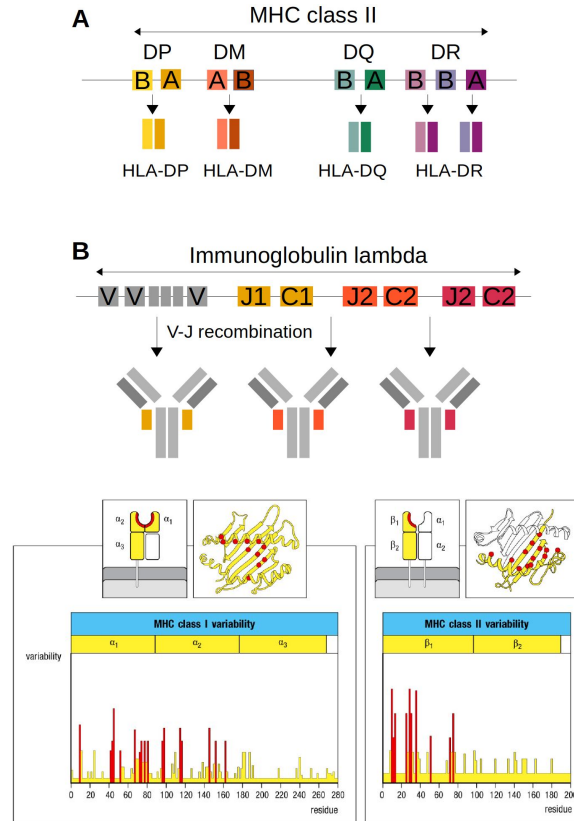
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# Allelic diversity and polygeny pose a bioinformatic challenge

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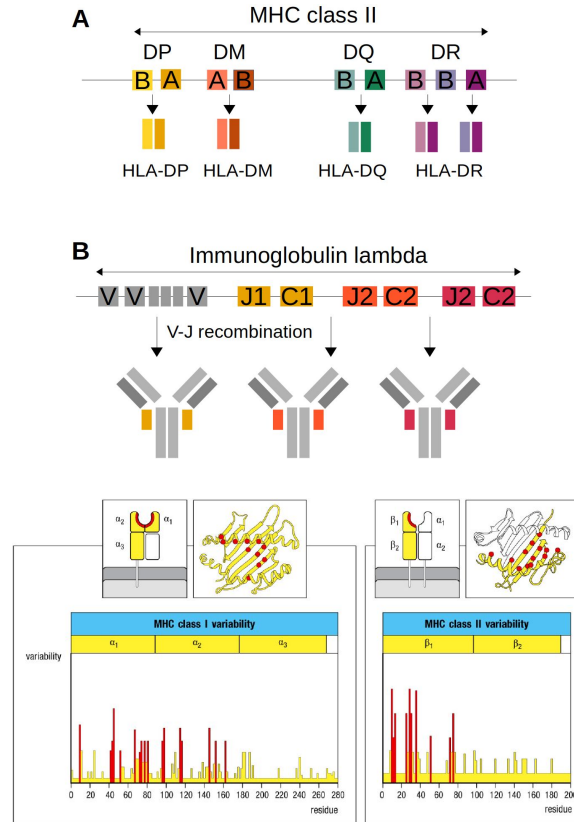
**Bioinformatic challenge**

Cross-mapping: uniquely  
mapping to the wrong gene

# Allelic diversity and polygeny pose a bioinformatic challenge

**Polygeny:**  
Multiple similar genes  
encode same function

**Hyperpolymorphism:**  
Multiple alleles  
for one gene



**Aim**

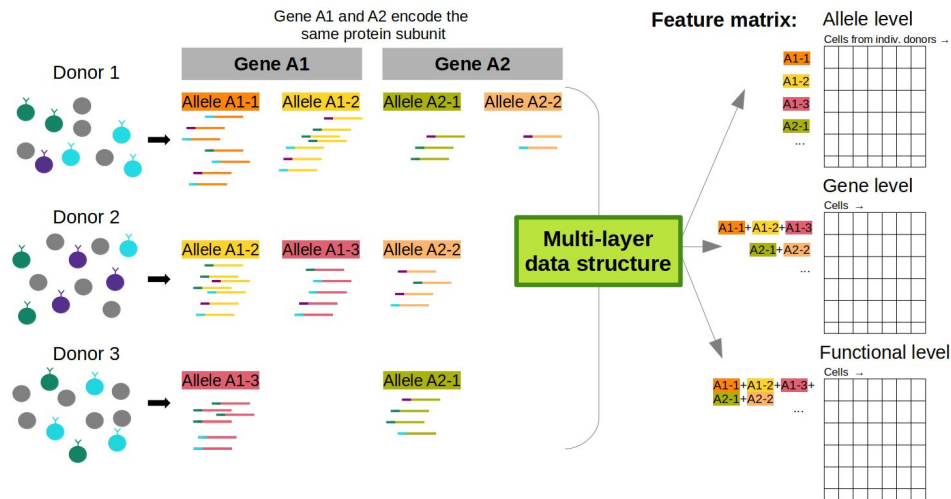
To perform quantification of  
allele-specific expression for  
immunogenomic analysis



# Implementation of allele and functional information

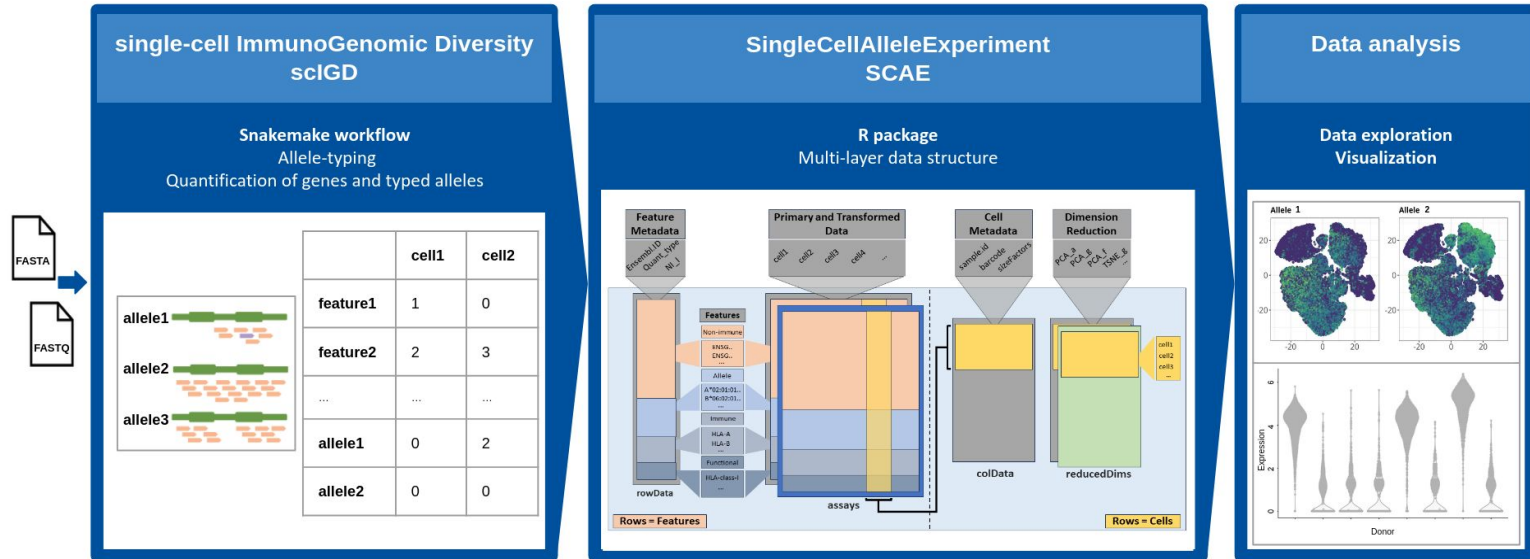
## *What we want*

- Building a multi-layer data structure for immune gene representation in single-cell data



# Workflow

## How to get there



- Example datasets present in *scaeData* – R/ExperimentHub data package

# Acknowledgements

## Project partner

Federico Marini

## Group of Computational Immunology

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 <https://agimkeller.github.io>



*scIGD*



*scaeData*



*SingleCellAlleleExperiment*

