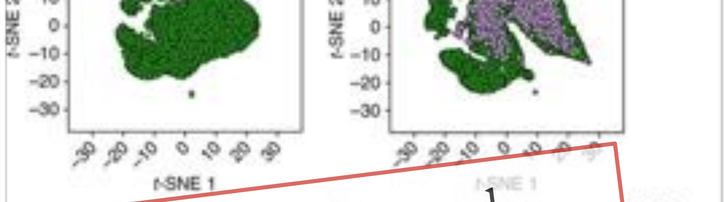
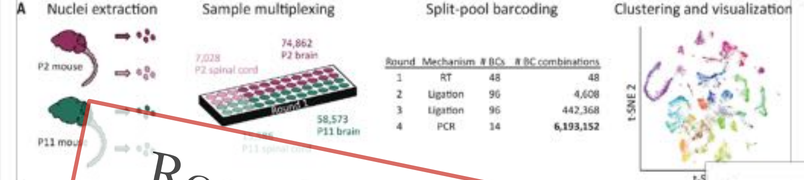
Interactive Visual Analysis of Single-Cell Data with HSNE

Thomas Höllt, Vincent van Unen, Nicola Pezzotti, Na Li, Marcel J.T. Reinders, Elmar Eisemann, Frits Koning, Anna Vilanova, and Boudewijn P.F. Lelieveldt

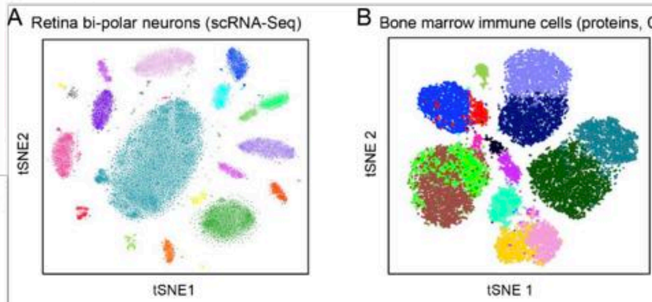
t-SNE

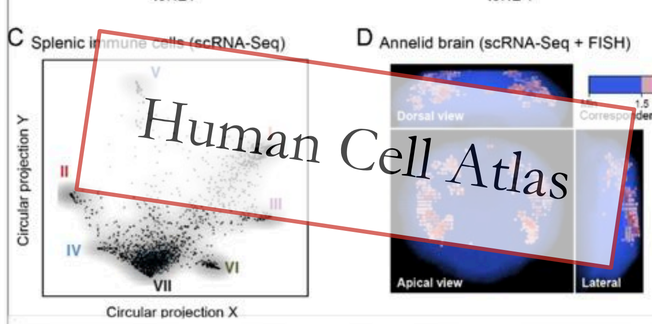


Haghverdi et al.
Nat. Biotech, 2018



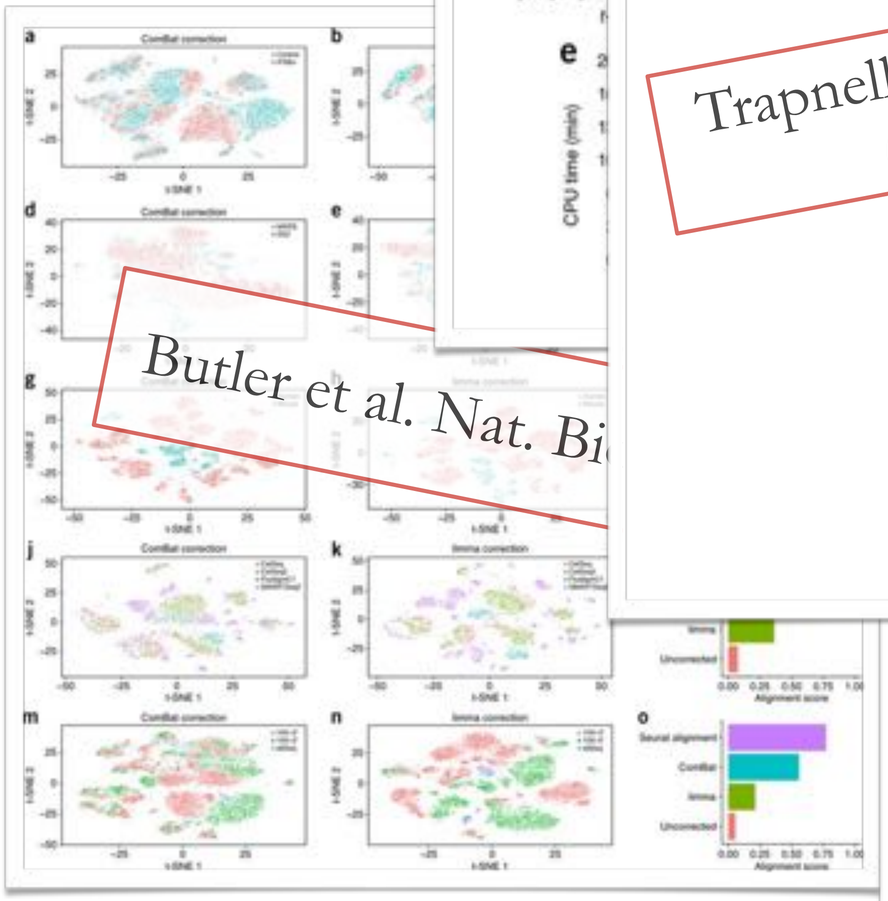
Rosenberg et al.
Science, 2018



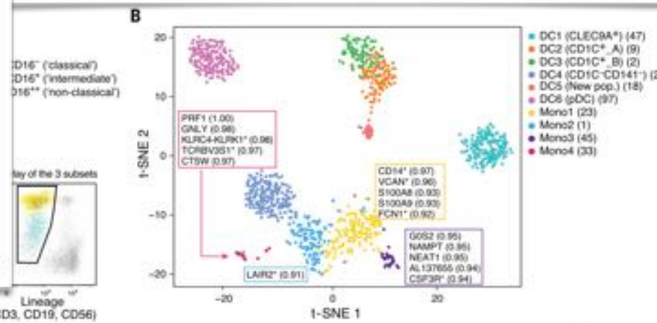


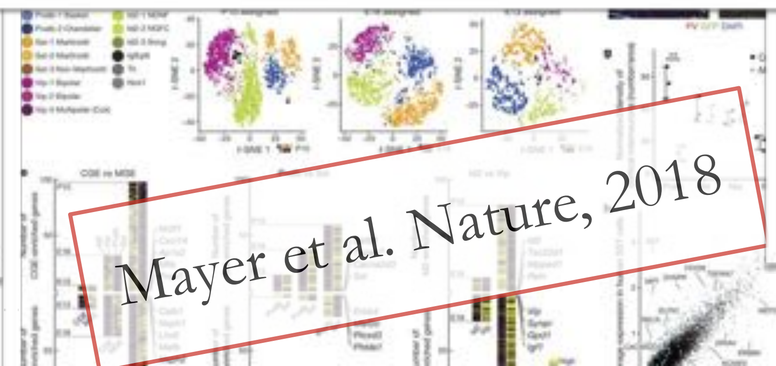
Human Cell Atlas

Trapnell, ISMB Keynote
(Saturday)



Butler et al. Nat. Bi





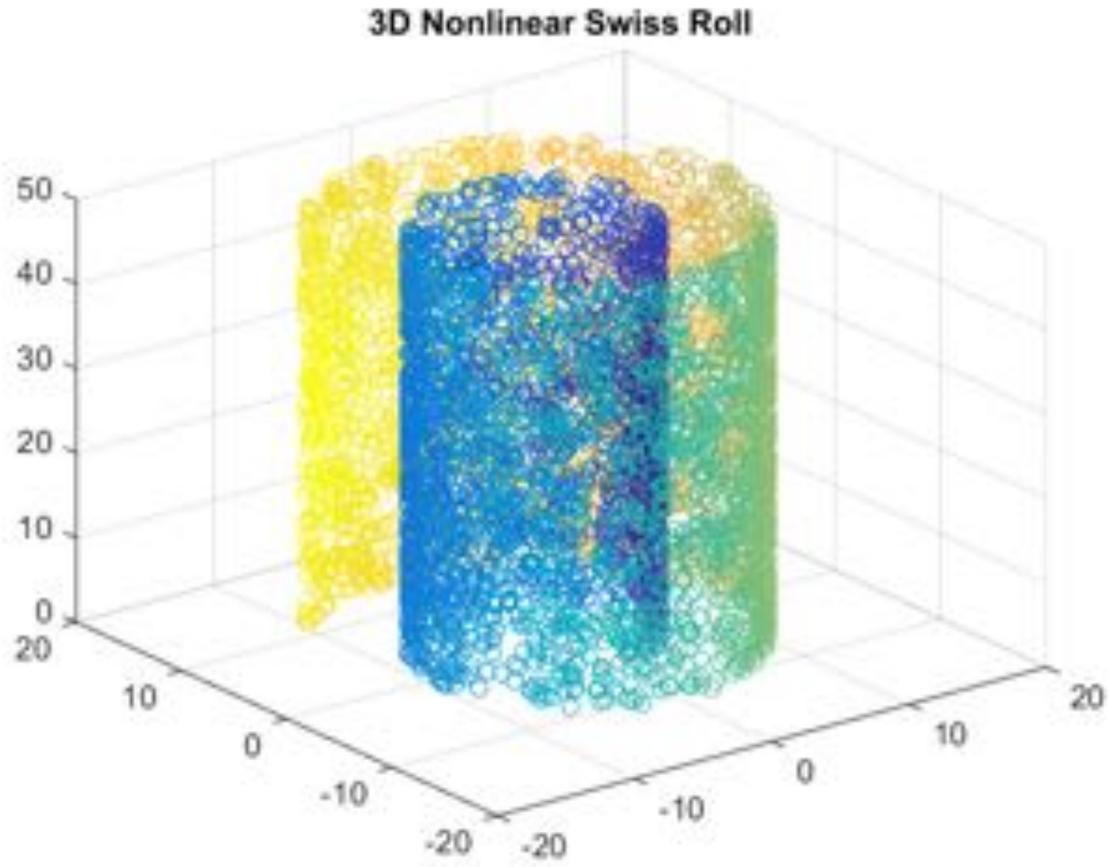
Mayer et al. Nature, 2018

Villani et al. Science, 2017

t-SNE

- Non-linear dimensionality reduction
  - Compute local neighborhoods in hi-D
  - Model low-D to preserve neighborhoods

  ⇨ Preserves high-D clusters!



- Computationally intensive
- Crowding problem

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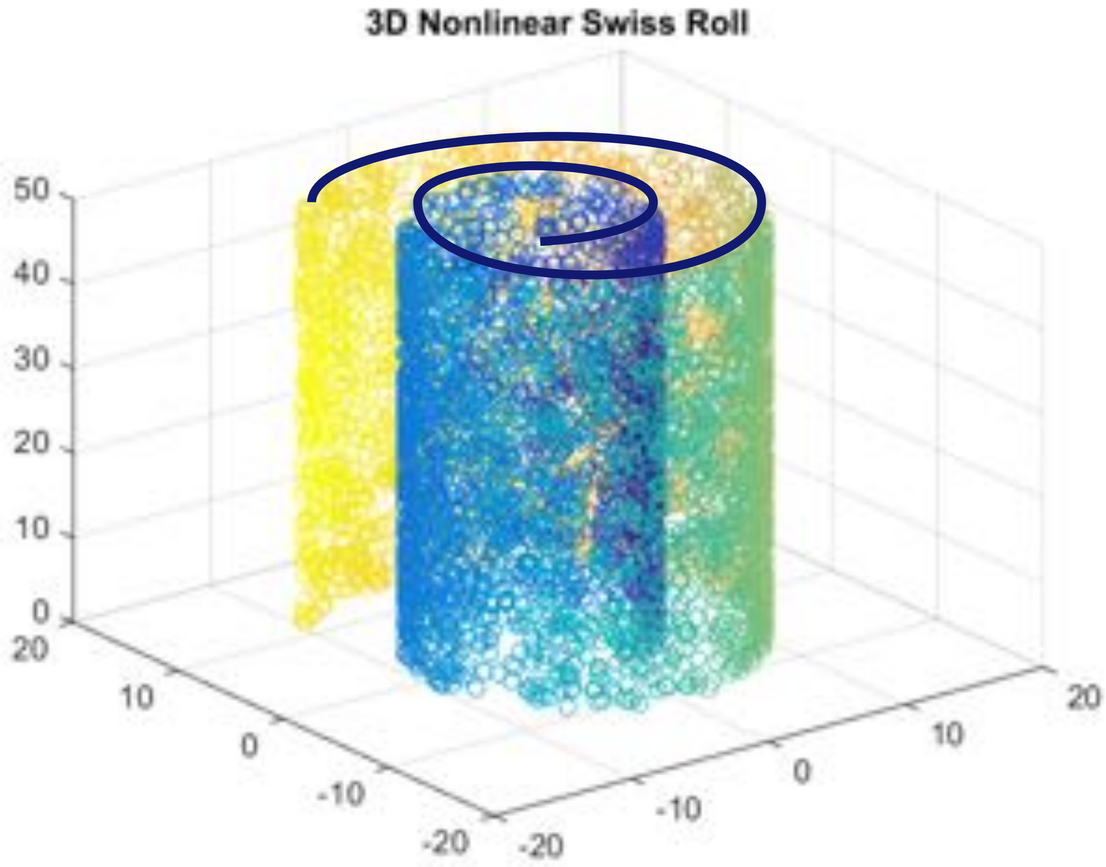

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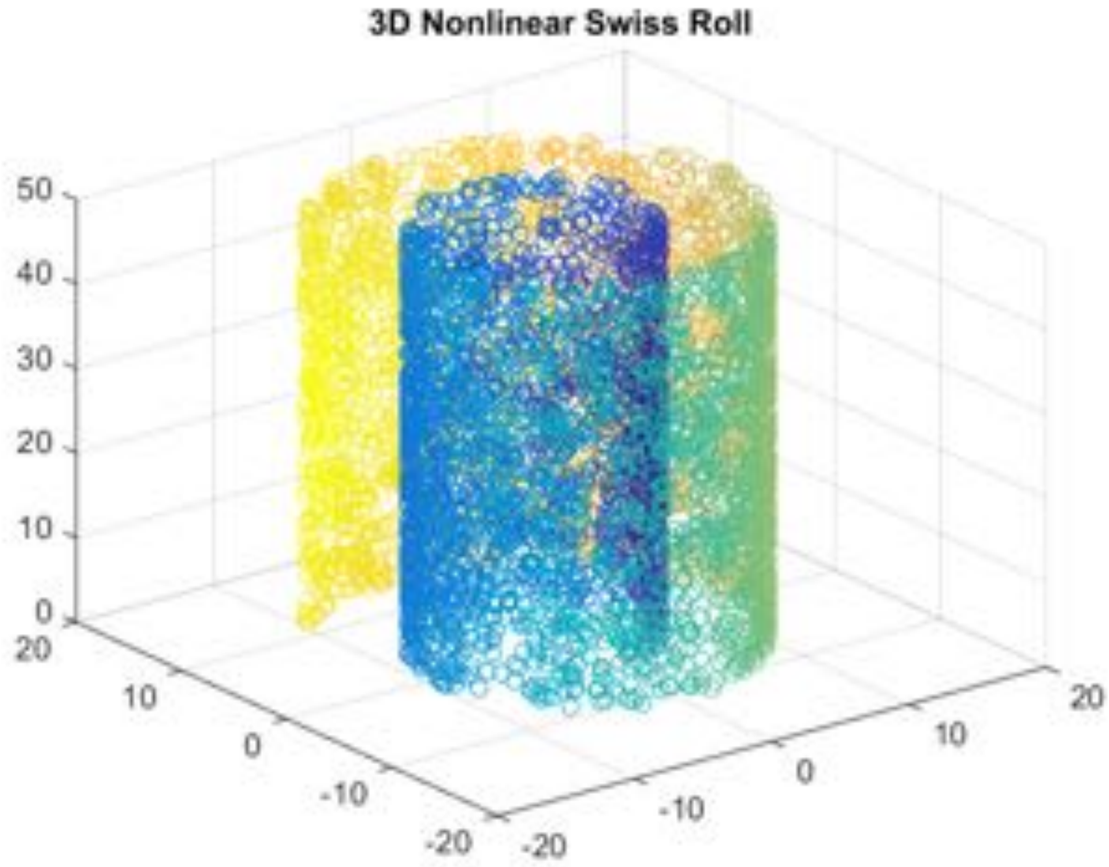

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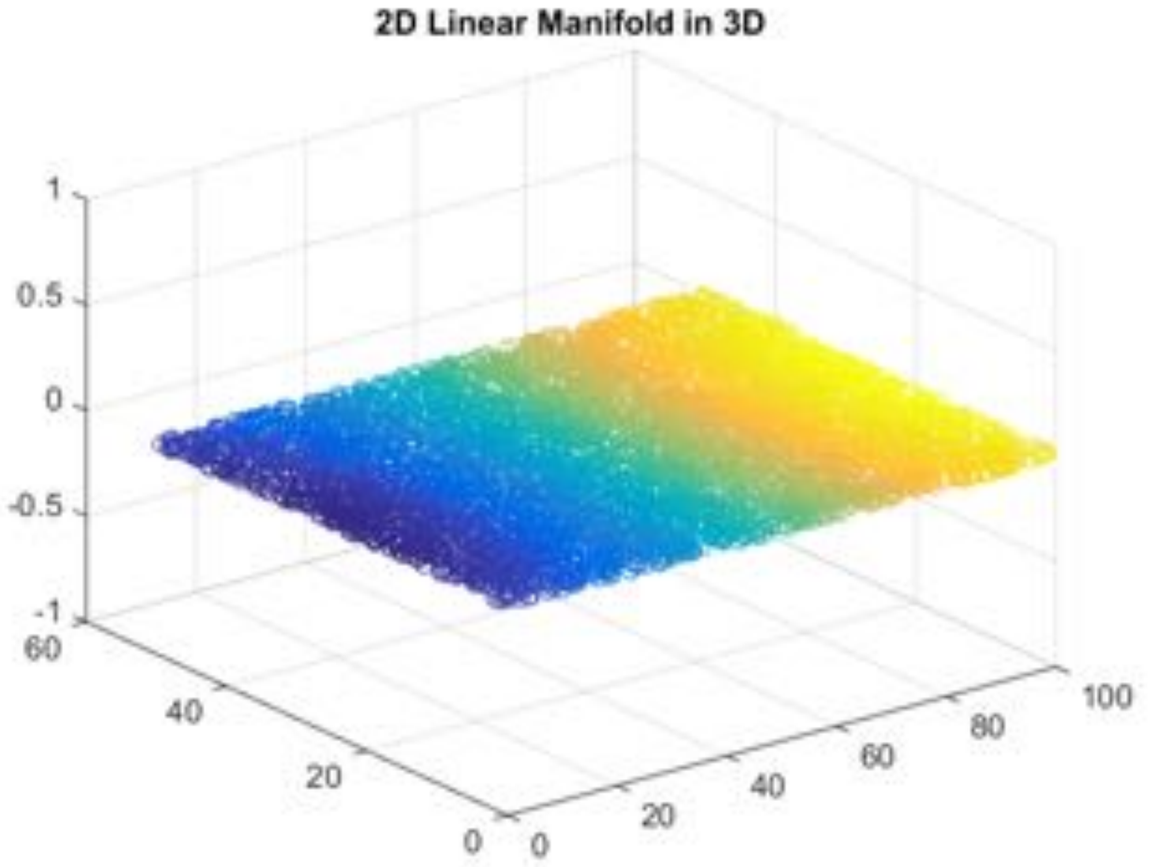

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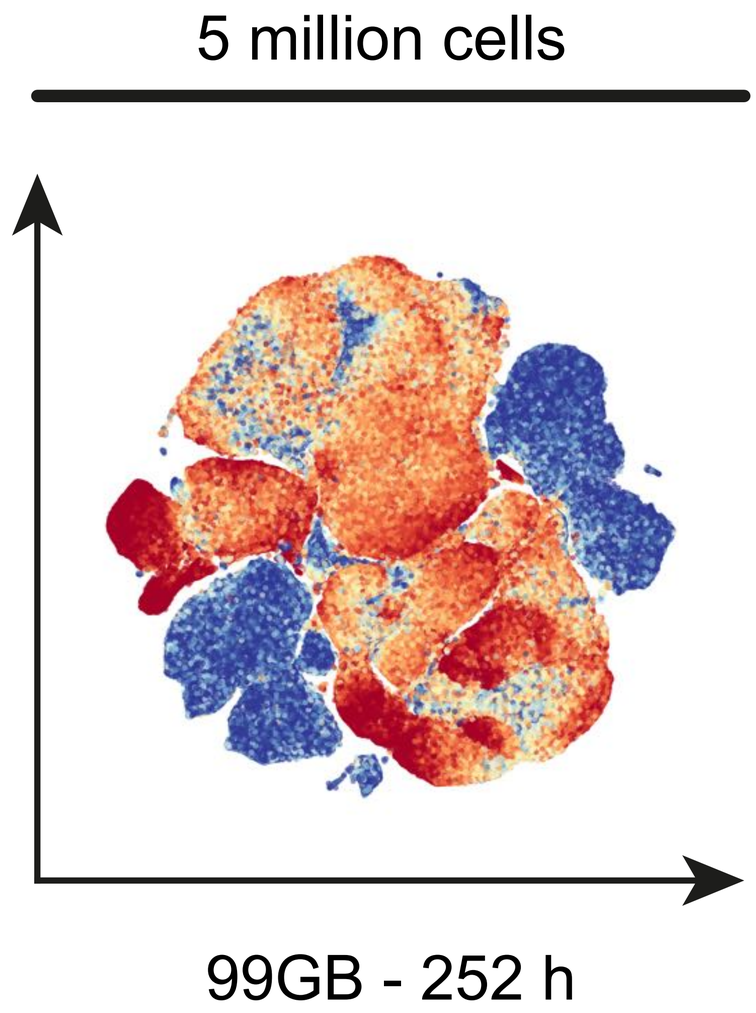
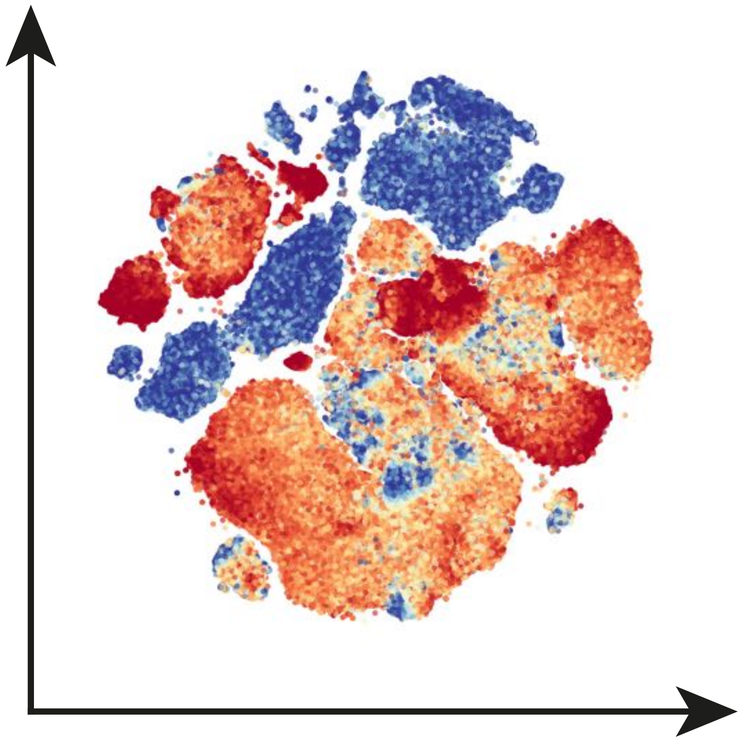
Crowding



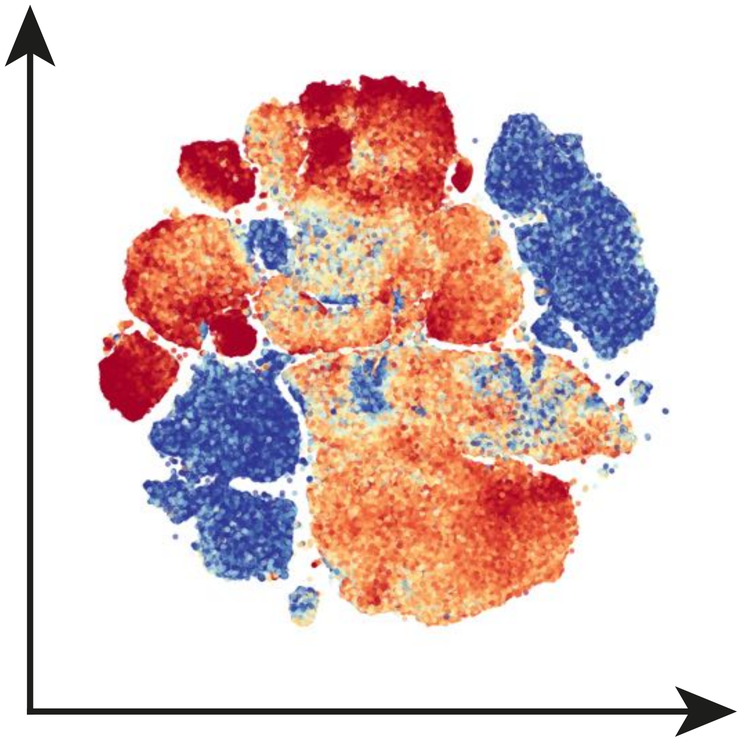
Crowding

1 million cells



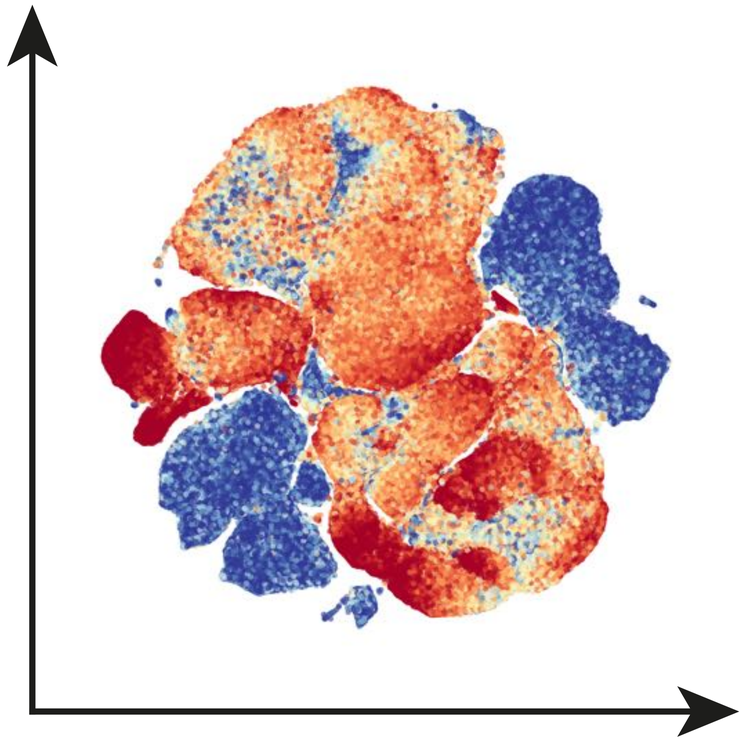
16GB - 19.5 h

2 million cells



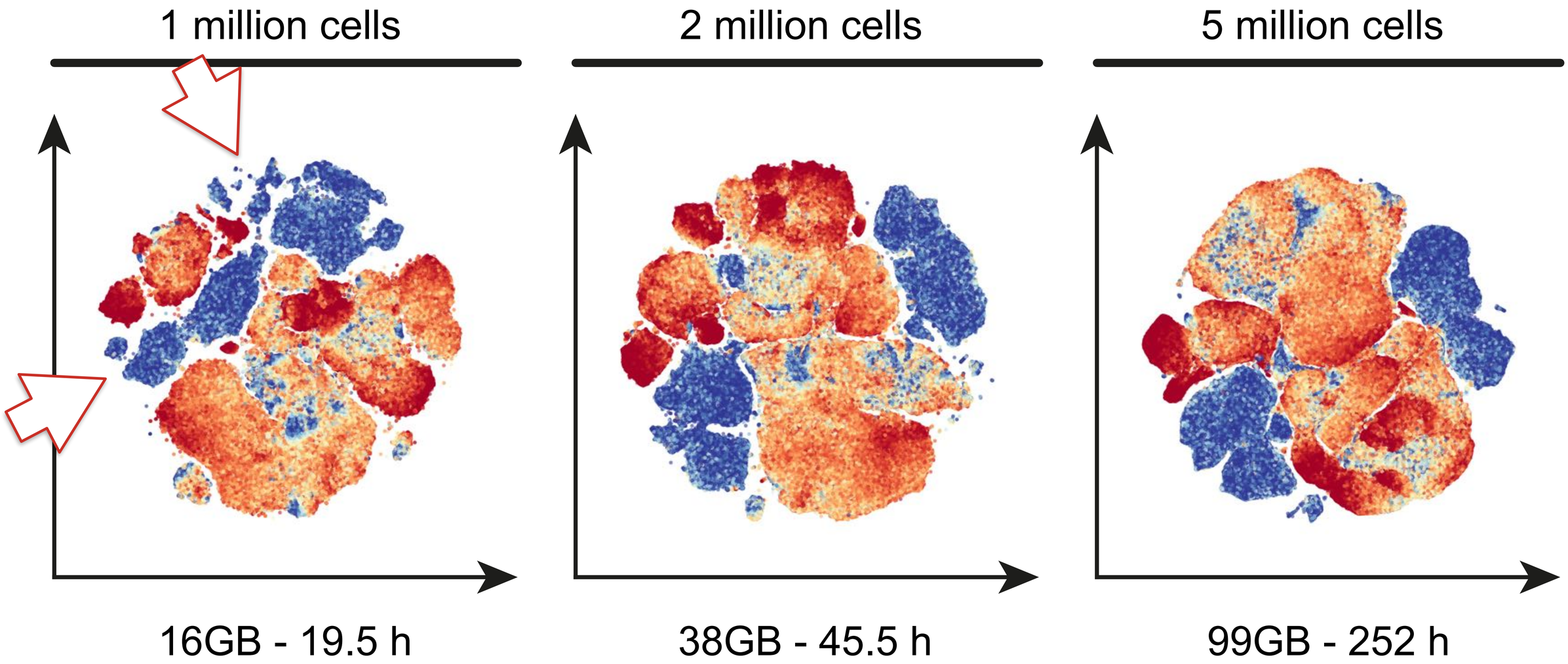
38GB - 45.5 h

5 million cells



99GB - 252 h

Crowding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2 million cells
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HSNE

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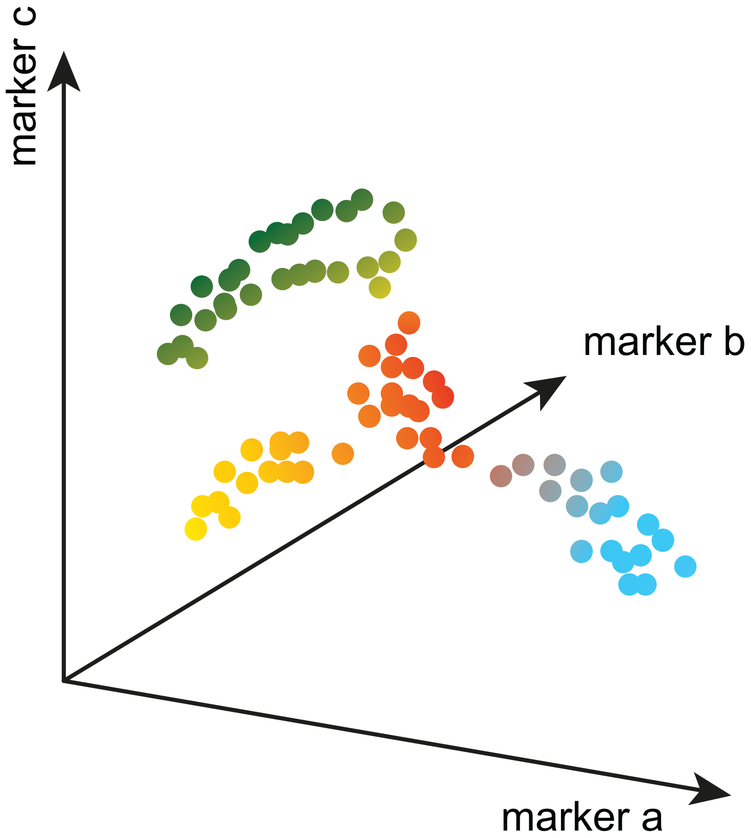
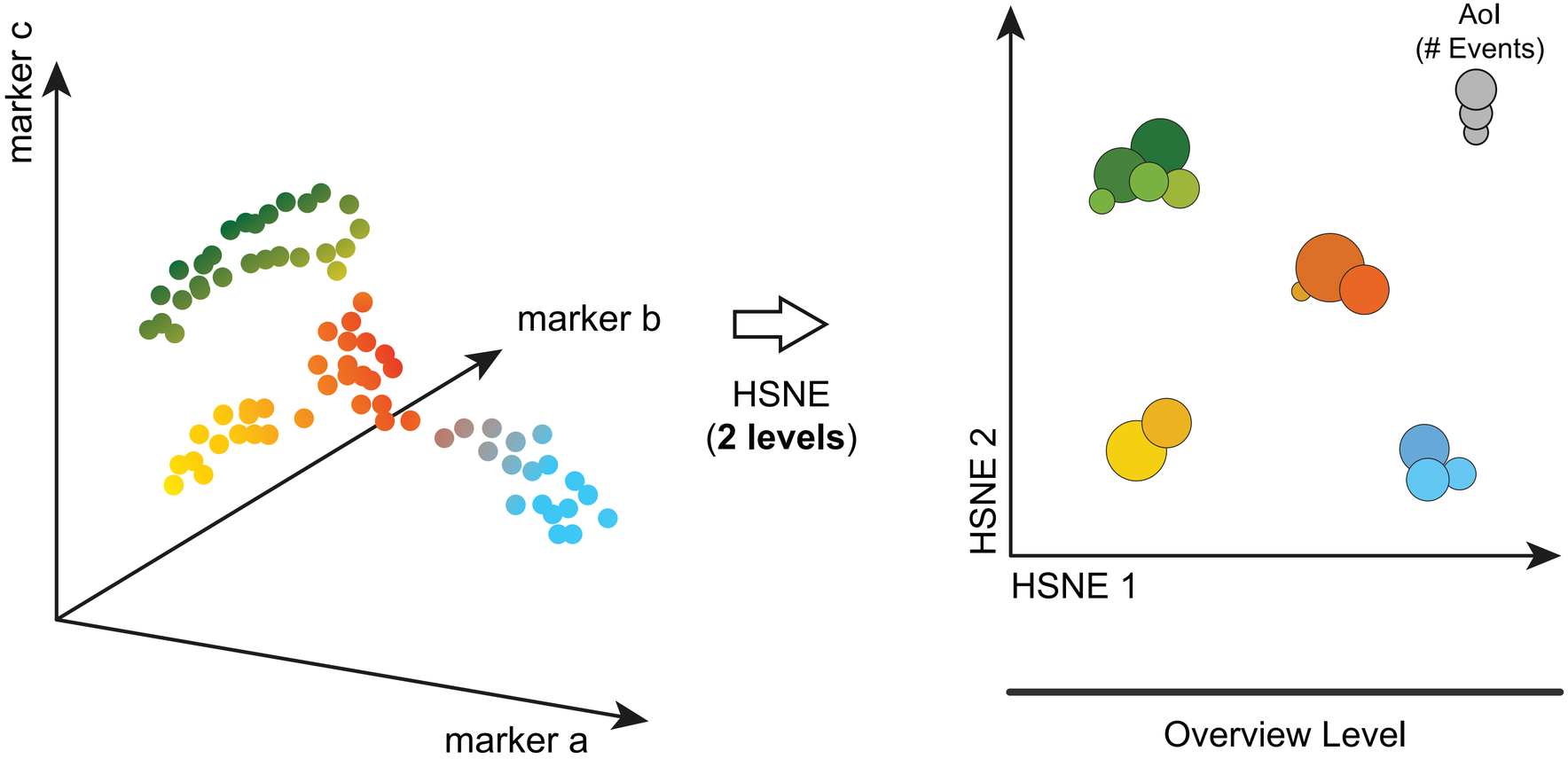
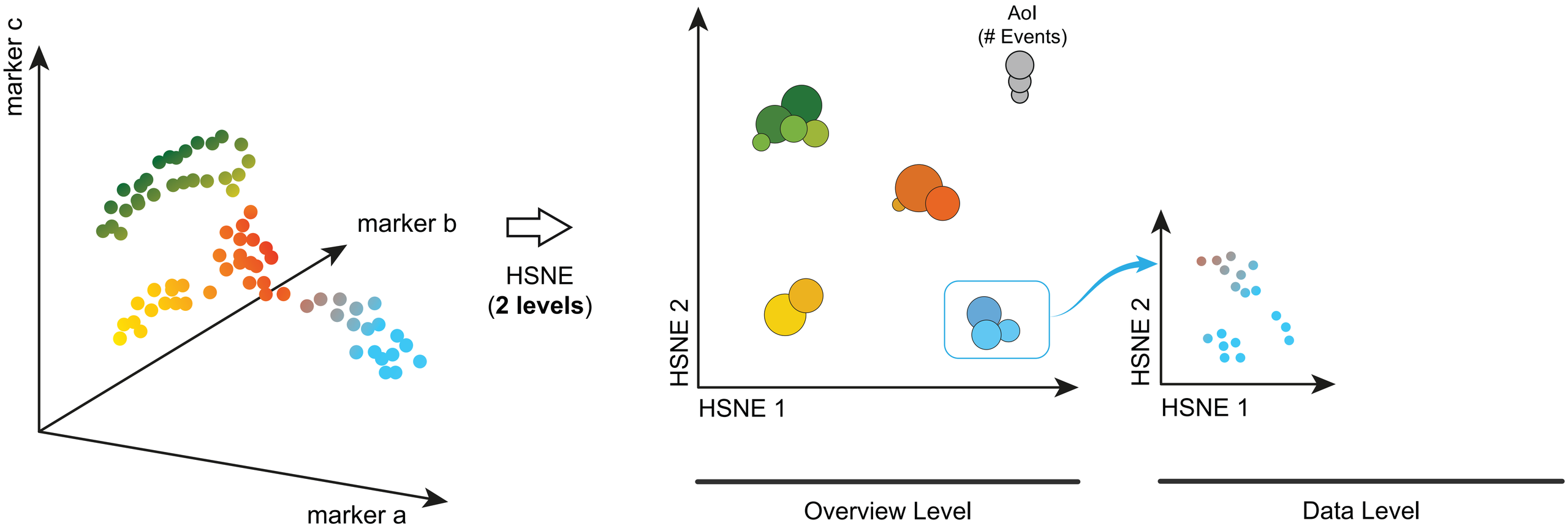


HSNE


marker c
marker b
marker a
HSNE
(2 levels)
AoI
(# Events)
HSNE 2
HSNE 1
Overview Level

HSNE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HSNE 2
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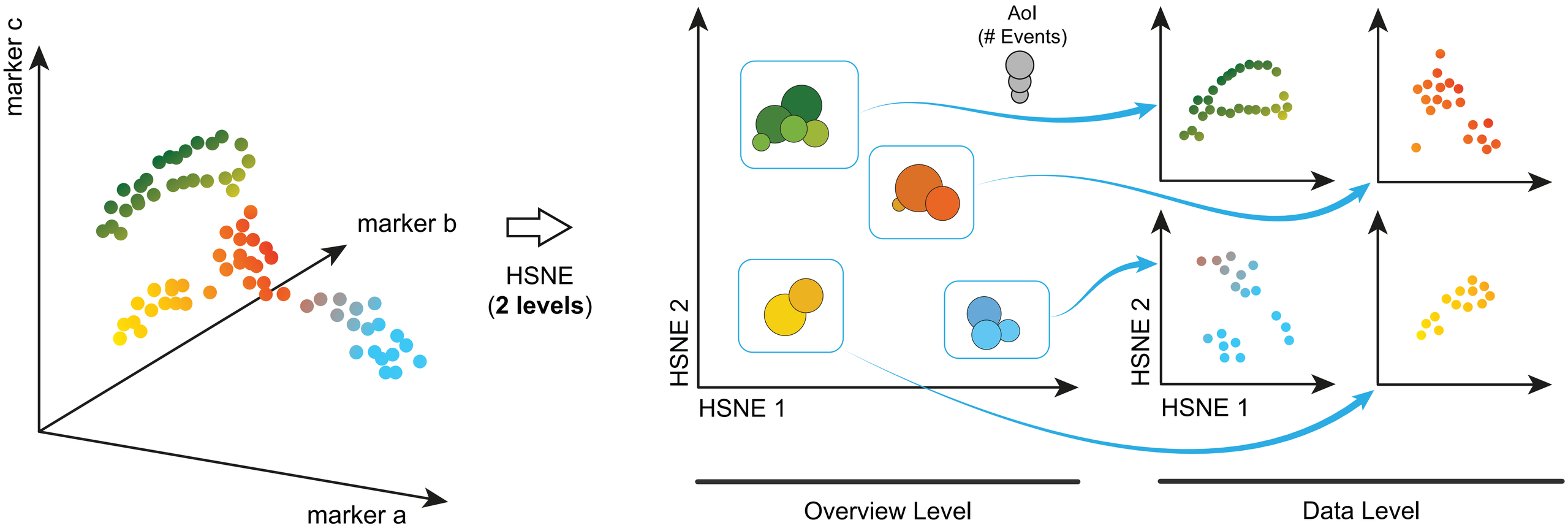
HSNE 2
HSNE 1
Overview Level
Data Level

HSNE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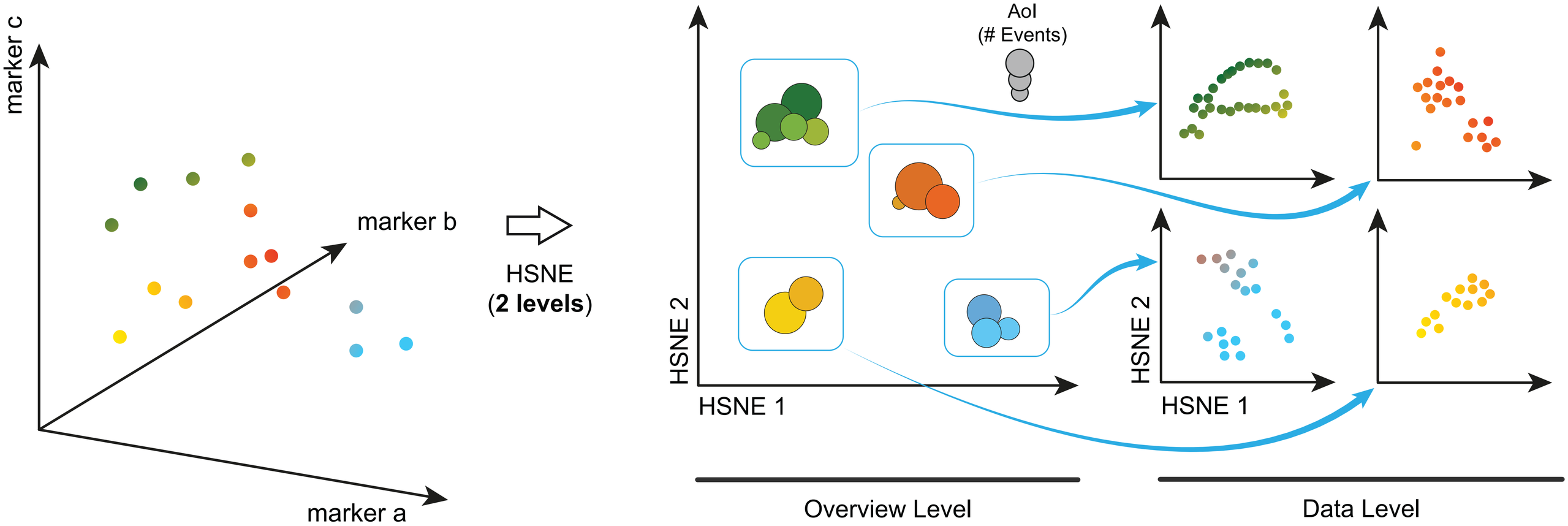
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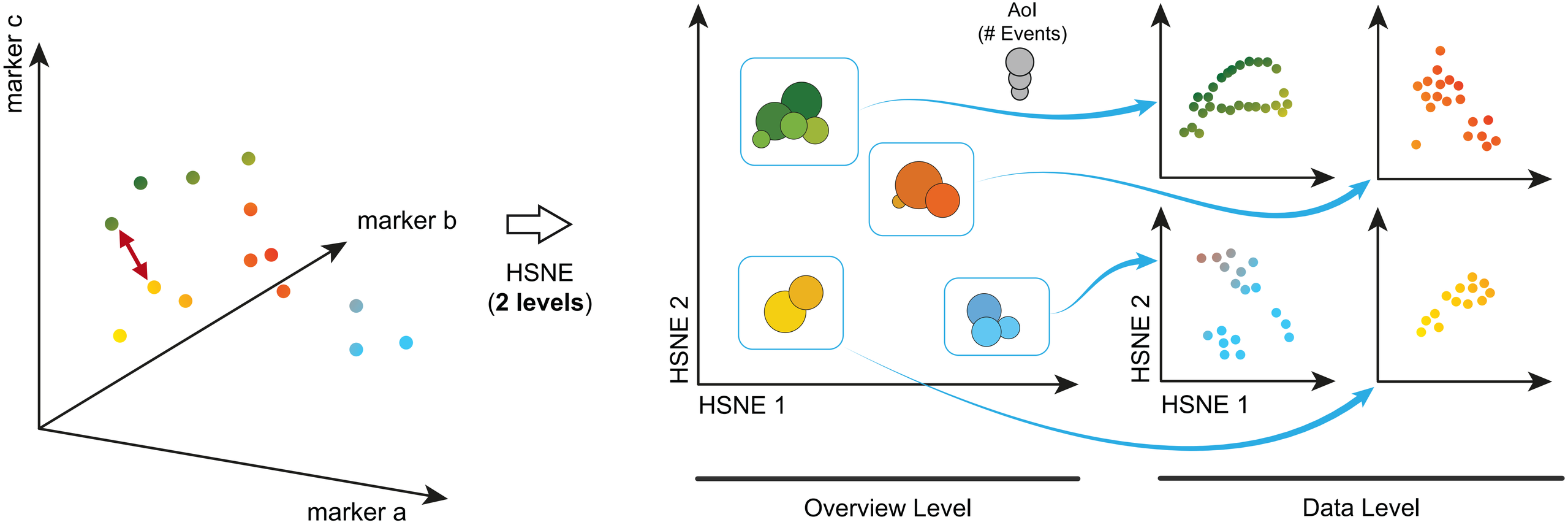
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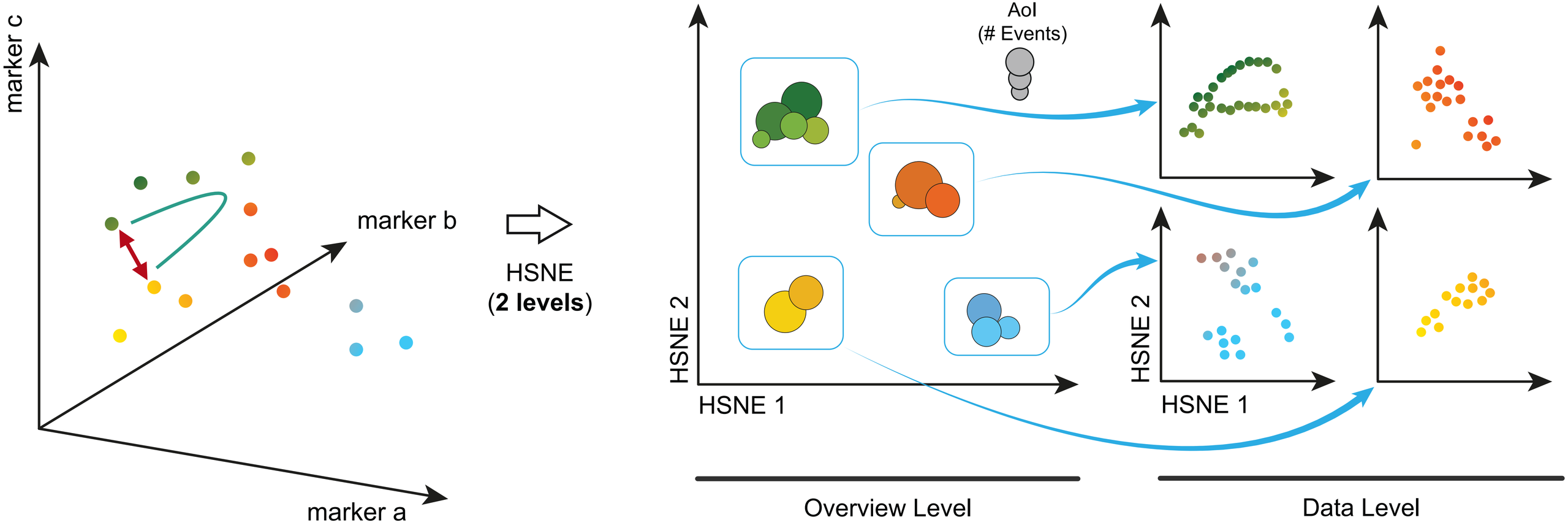
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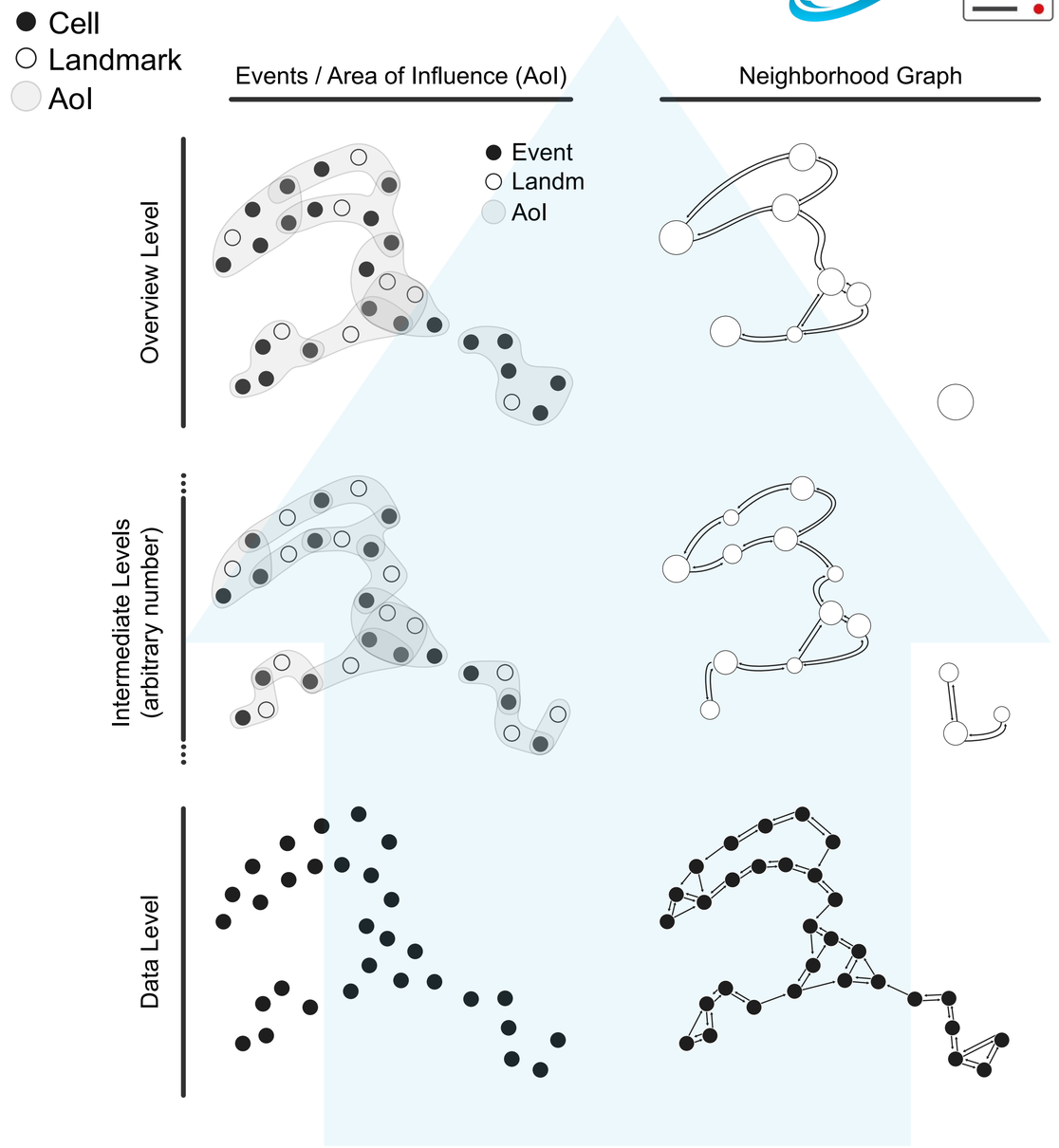
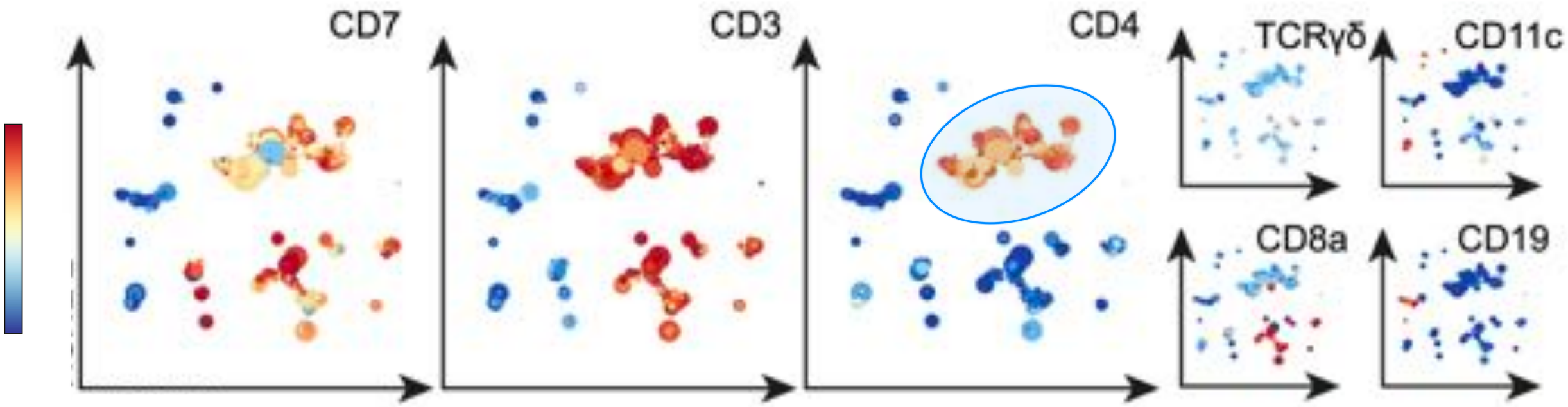
HSNE - Construction

- Aggregate cells by *Landmarks*
- Landmarks selected based on local connectivity in neighborhood graph
- Cells represented by Landmark define Area of Influence (AoI)
- Similarity (above data level) defined by overlap AoI
- Retains non-linearity throughout the hierarchy

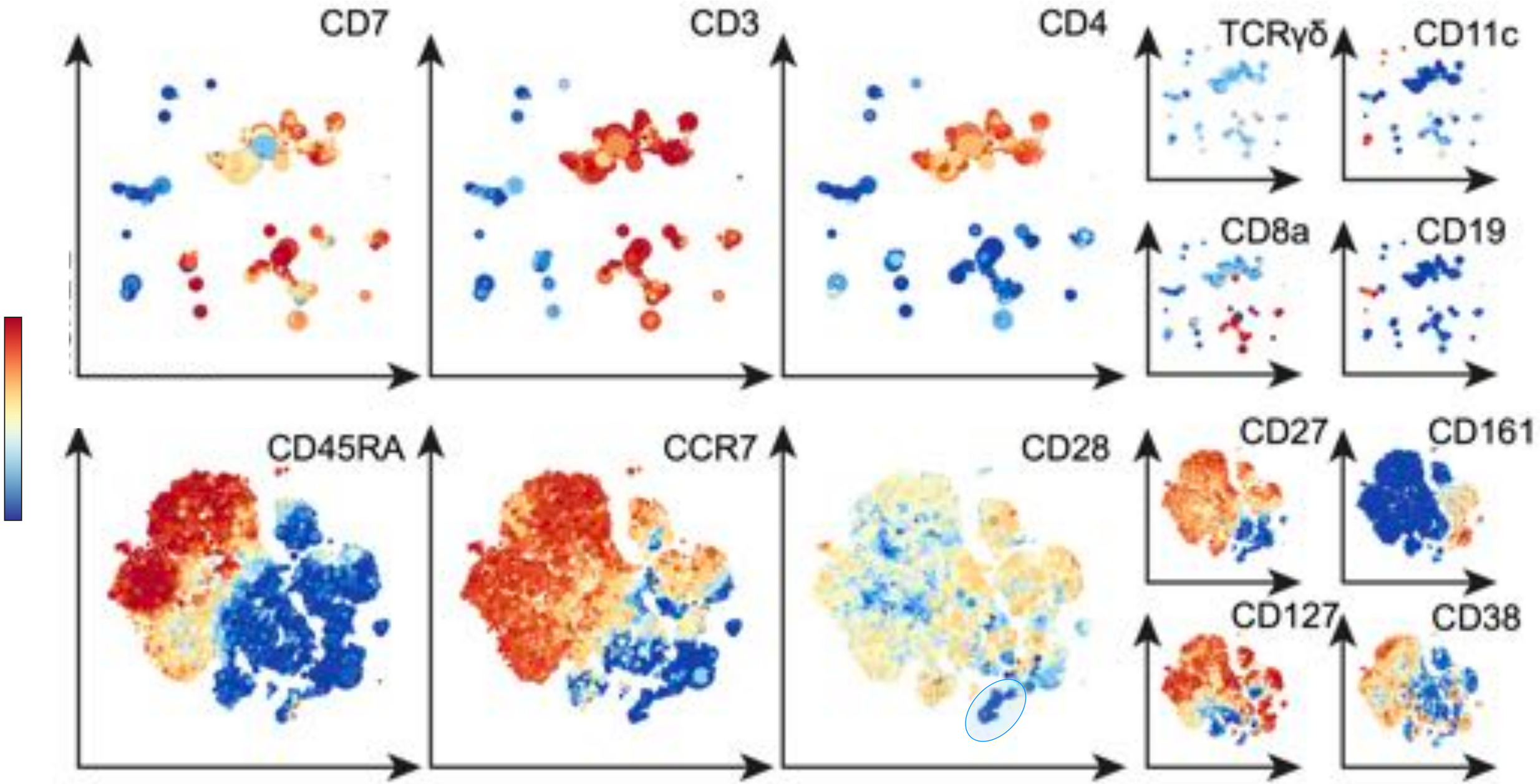


Interactive Exploration

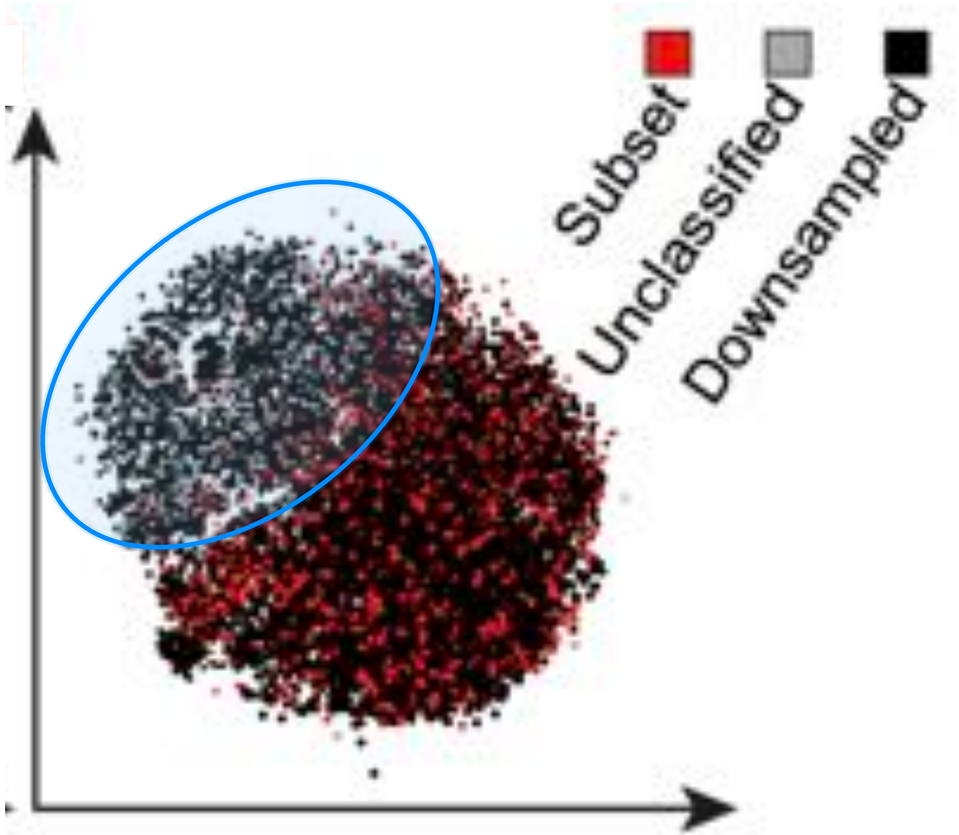
CD4+ T cells in blood and intestine



- Single-cell mass cytometry dataset on gastrointestinal diseases
- 5M cells, 40 dimensions (simultaneously measure proteins)
- Less than 30 minute computation time


CD7
CD3
CD4
TCRγδ
CD11c
CD8a
CD19
CD45RA
CCR7
CD28
CD27
CD161
CD127
CD38

CD4+ T cells in blood and intestine



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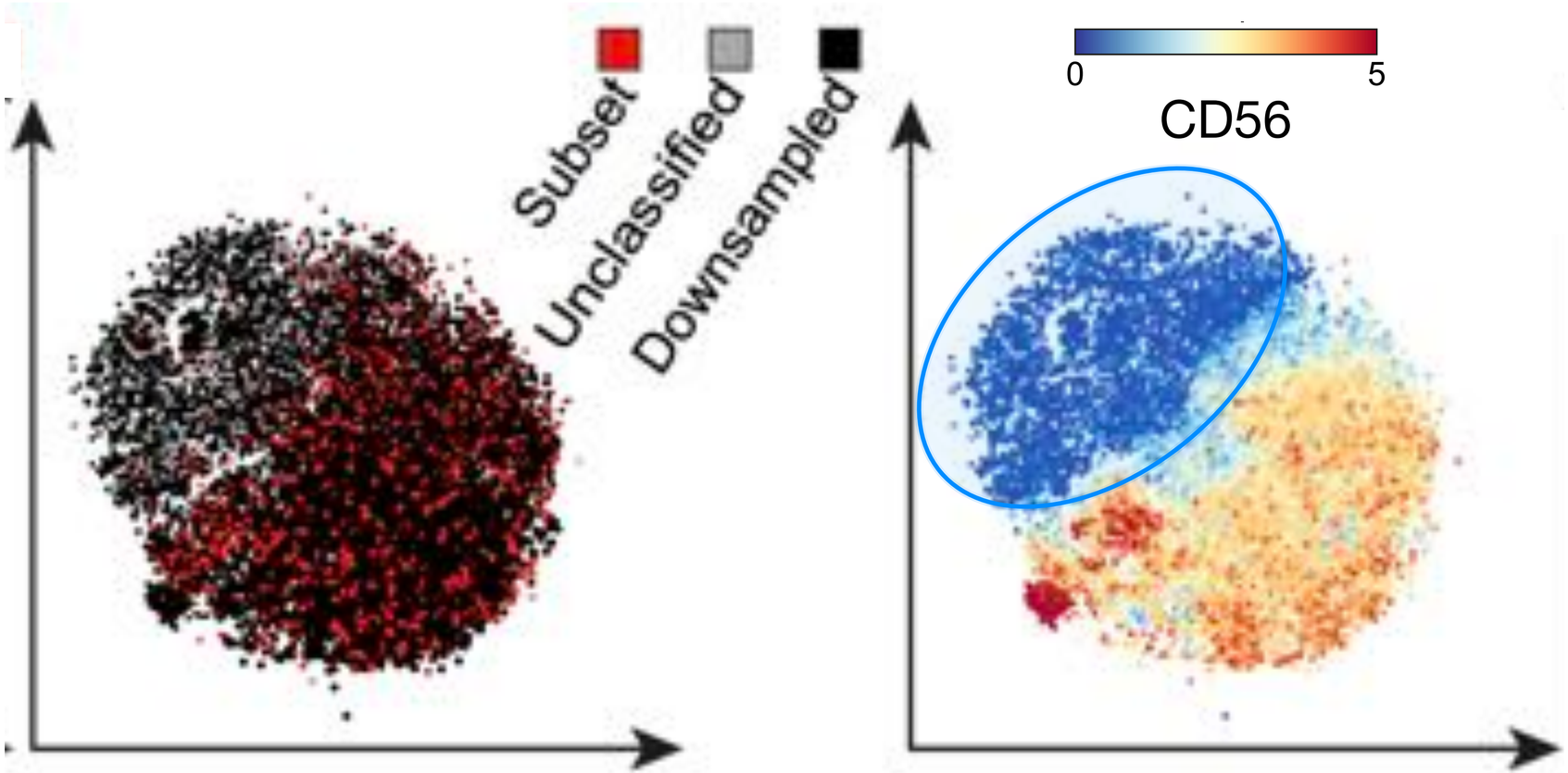

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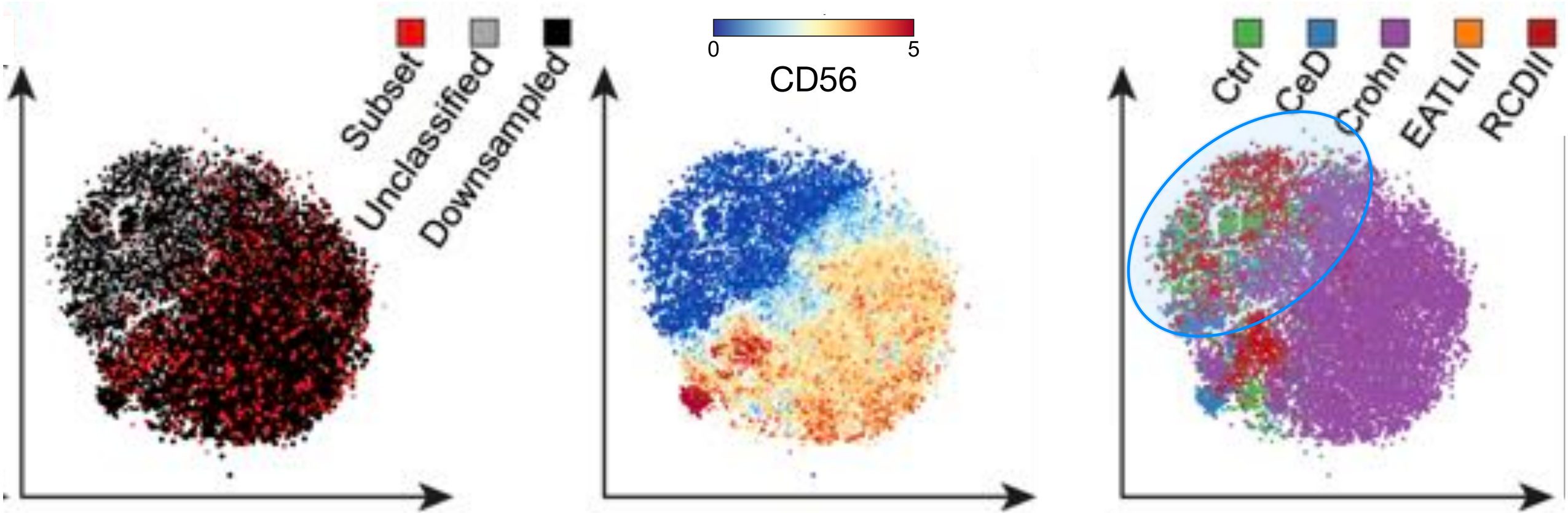

http://www.cytosplore.org
http://www.lcbc.nl

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STW / NWO Grant 12720 VAnPIRe
LKEB, IHB, LCBC @ LUMC
CGV @ TU Delft