

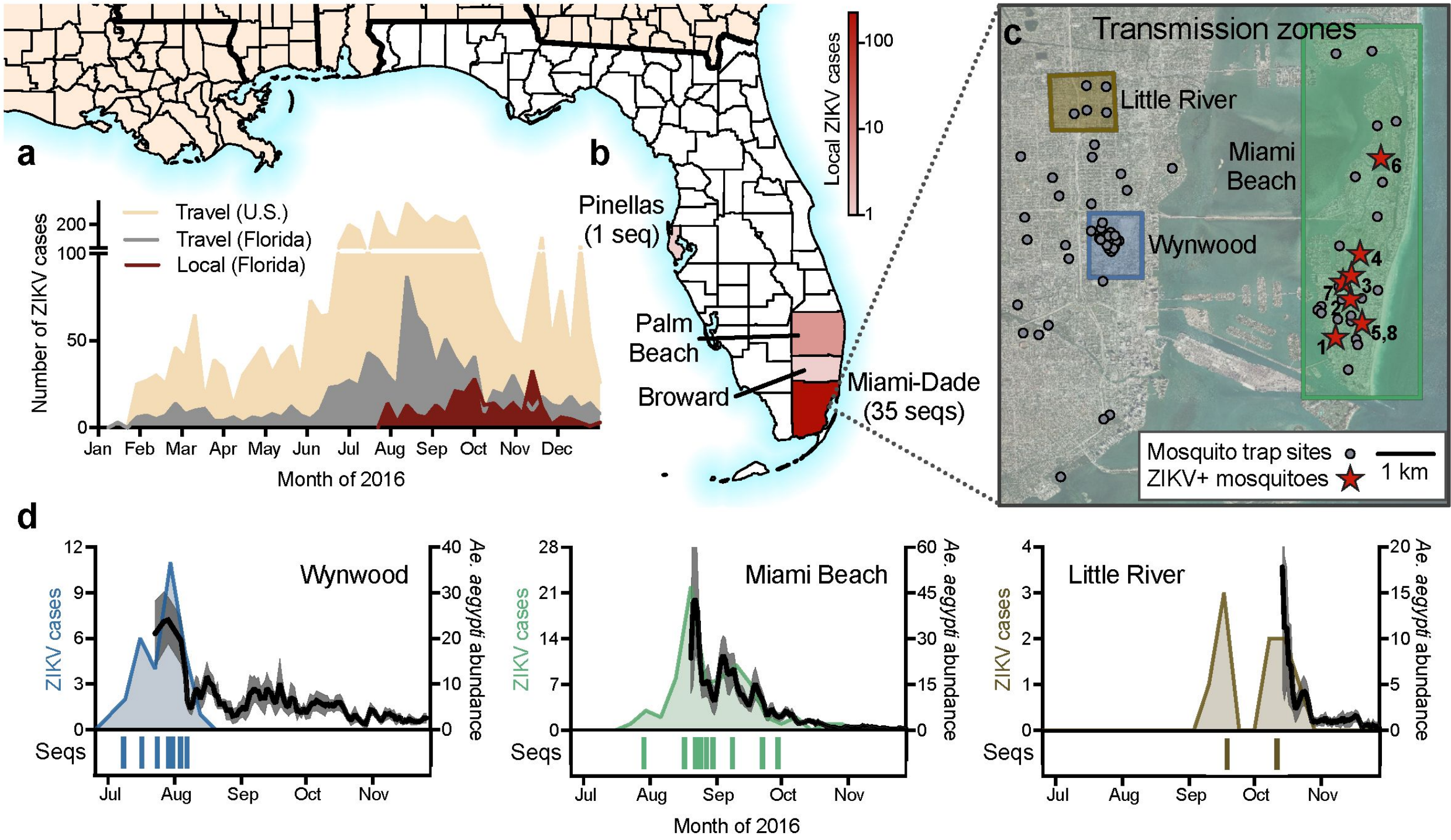
Project proposal

Due next Friday (March 31st)

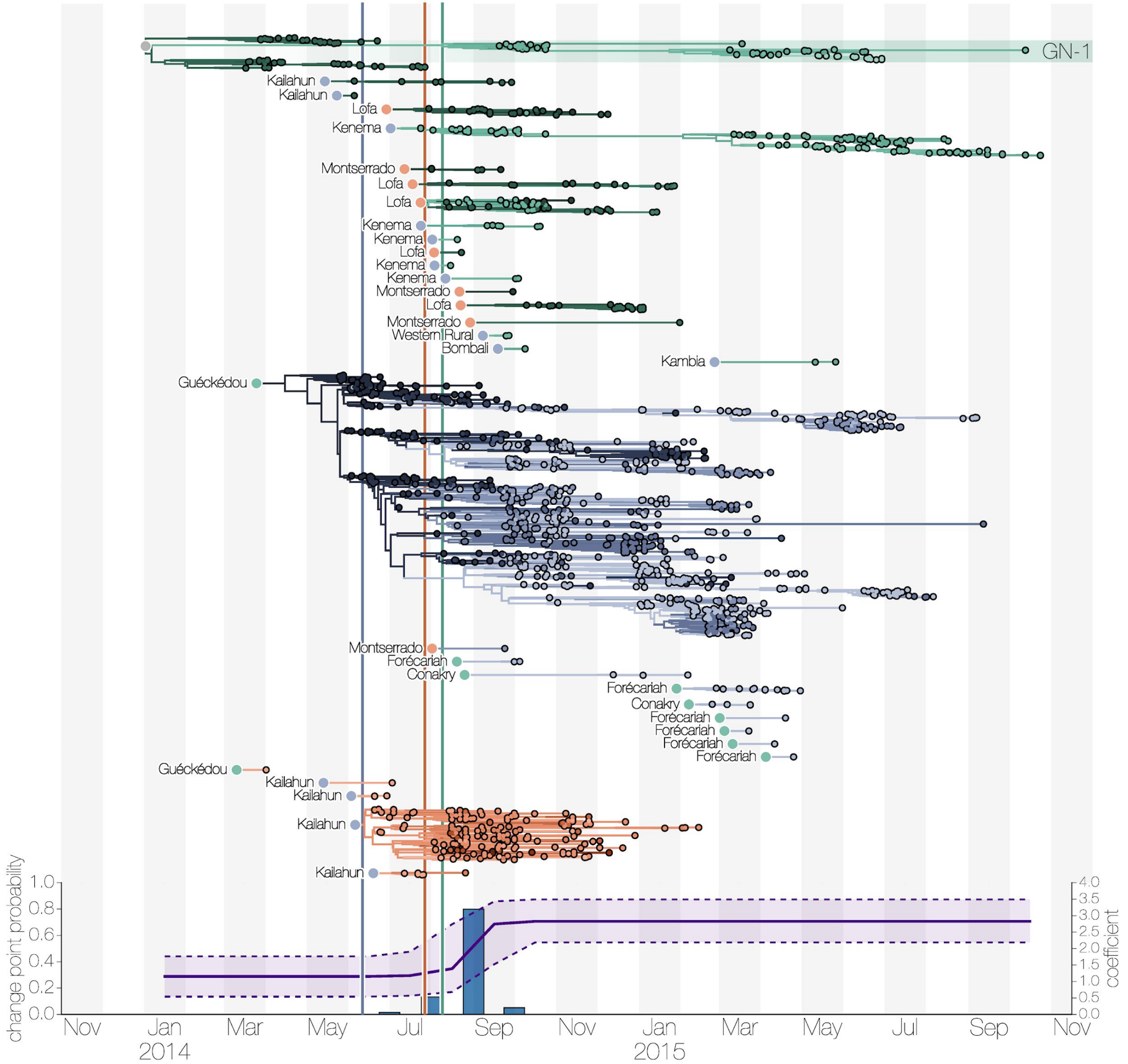
1 page description of what you plan to focus on for your final project.

Graphical Concepts

Spring 2023
PCfB Class 9
March 24, 2023



Grubaugh et al. 2017, Nature

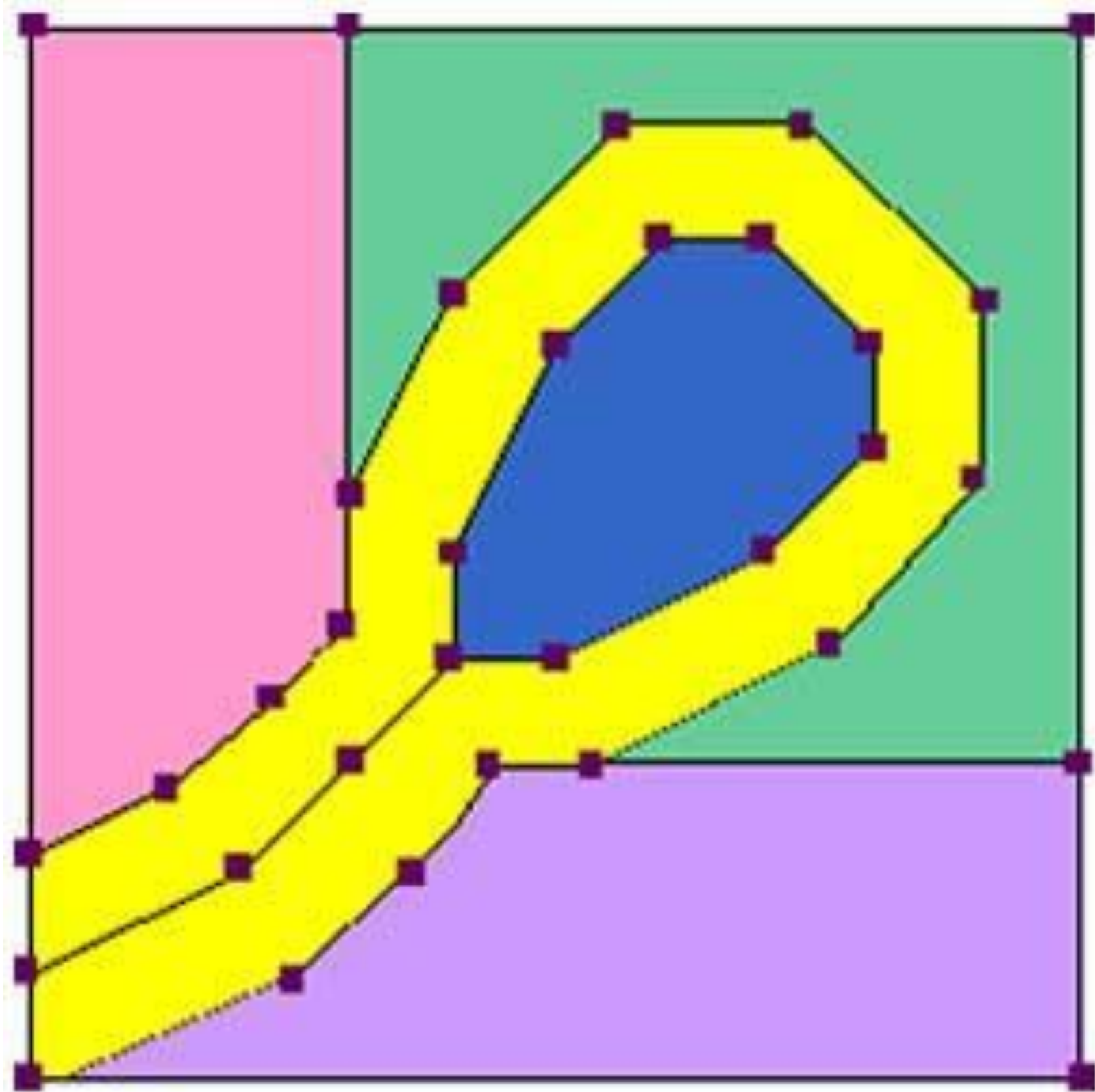


Dudas et al. 2017, Nature

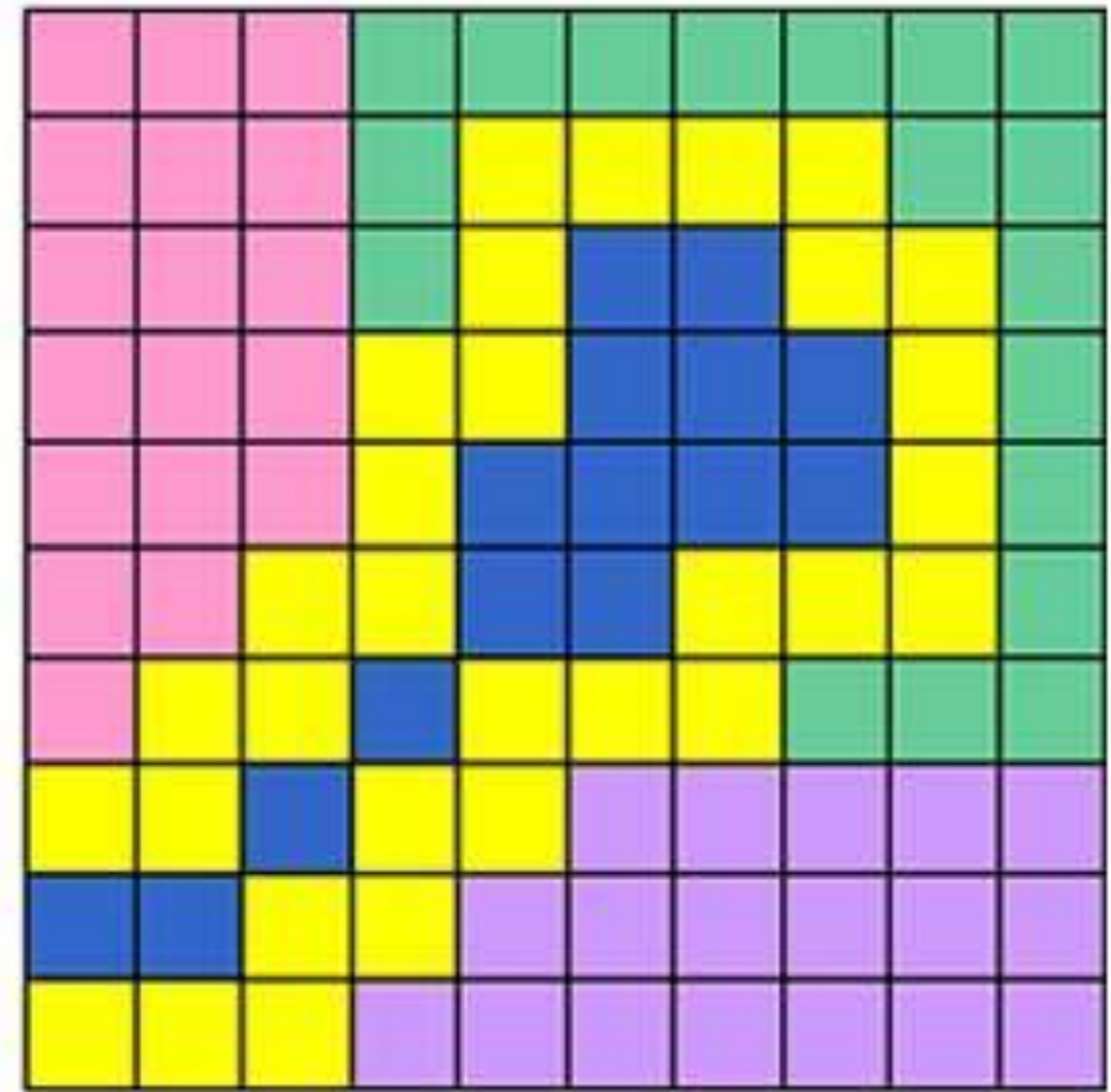
Objectives

- Overview of graphical concepts
- Exposure to editing programs

Types of digital images



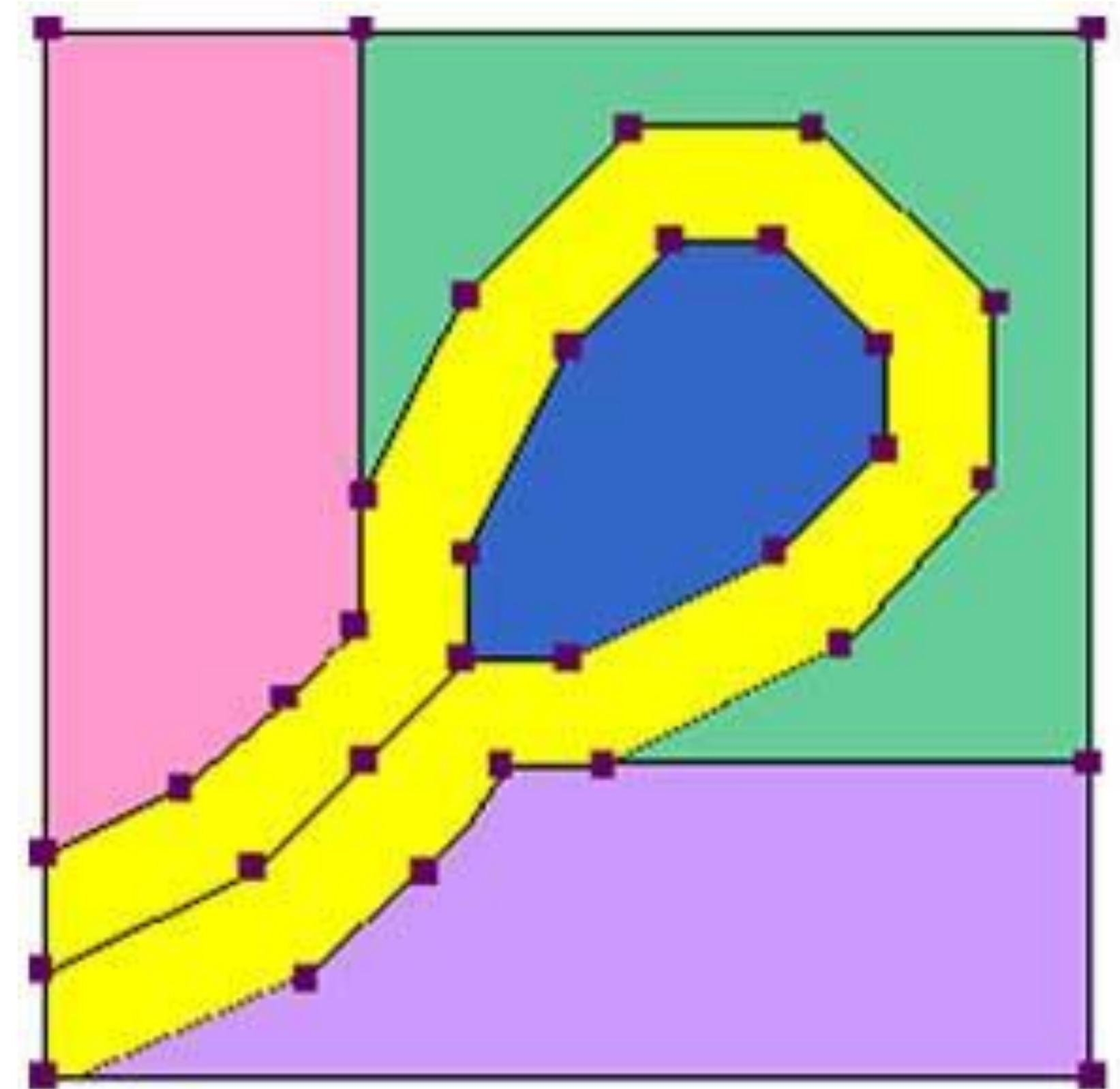
vector-based



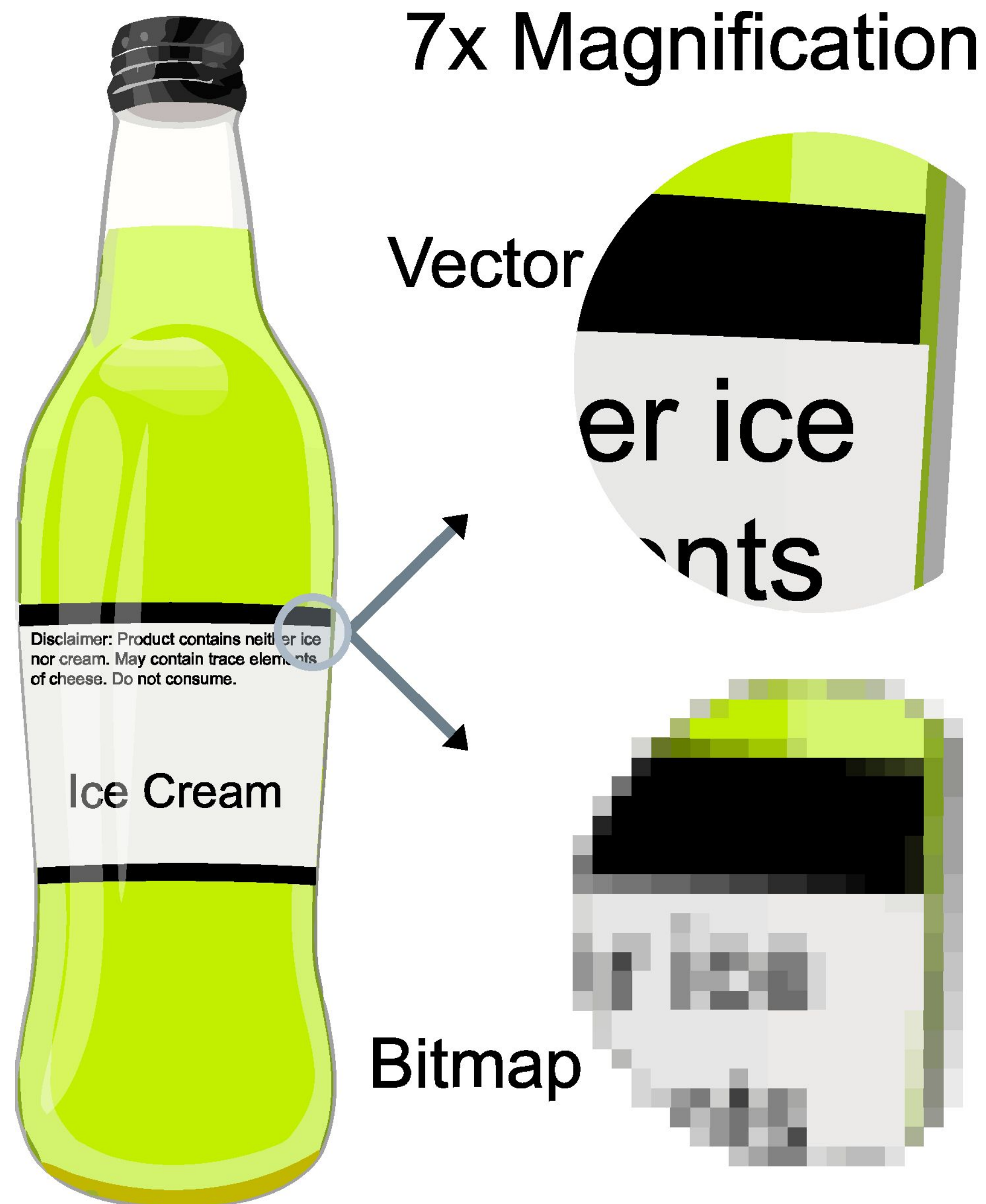
pixel-based

Vector-based images

- Composed of independent shapes
- Each shape editable as a unit

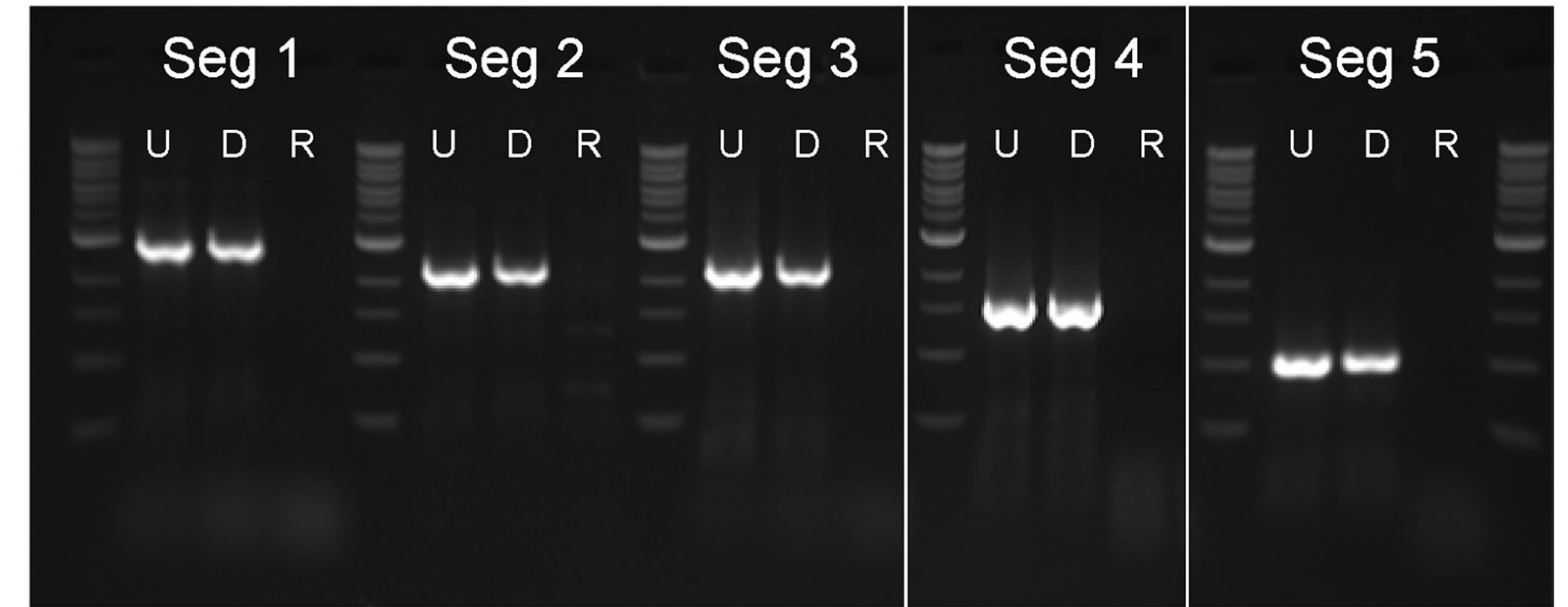
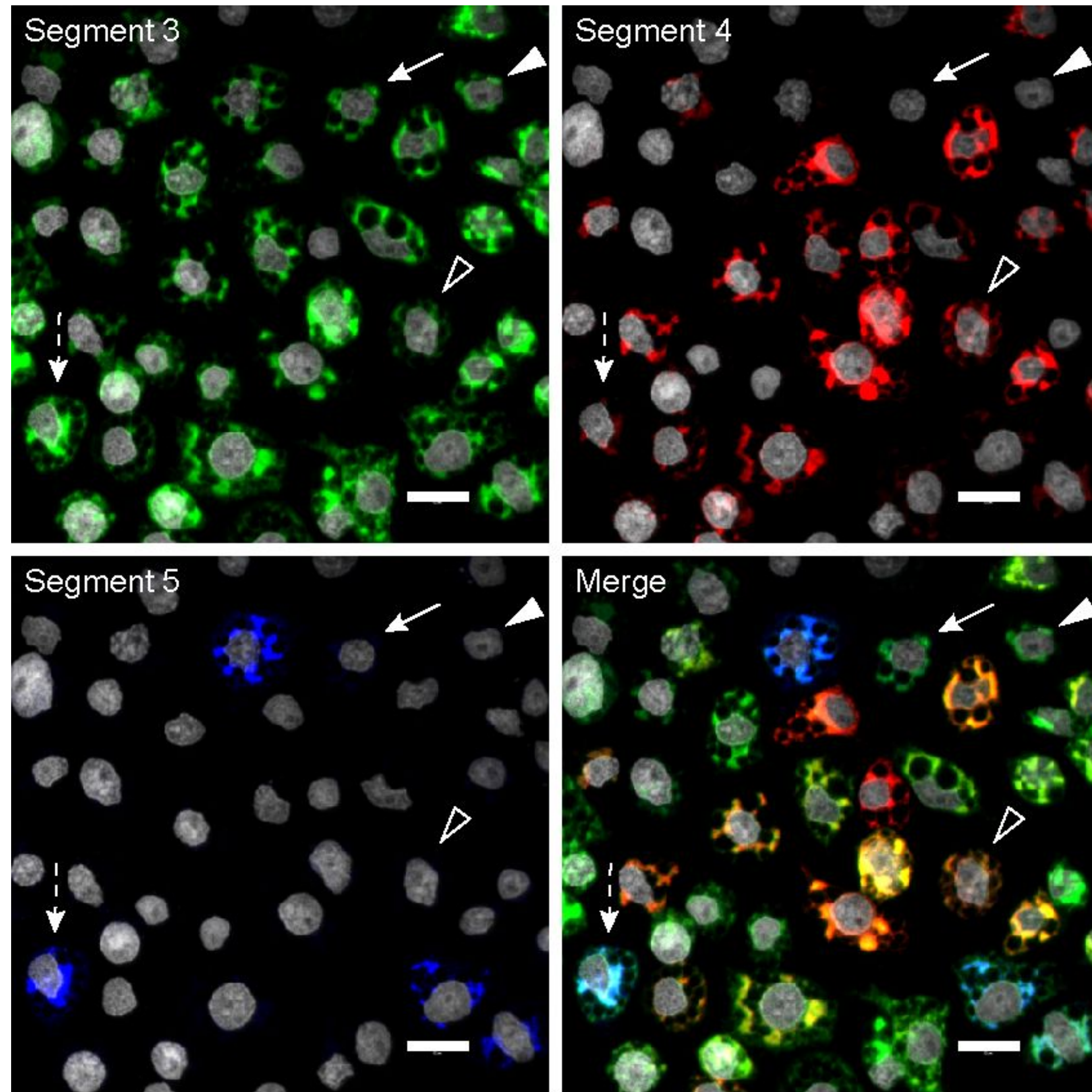


Use vectors whenever possible!

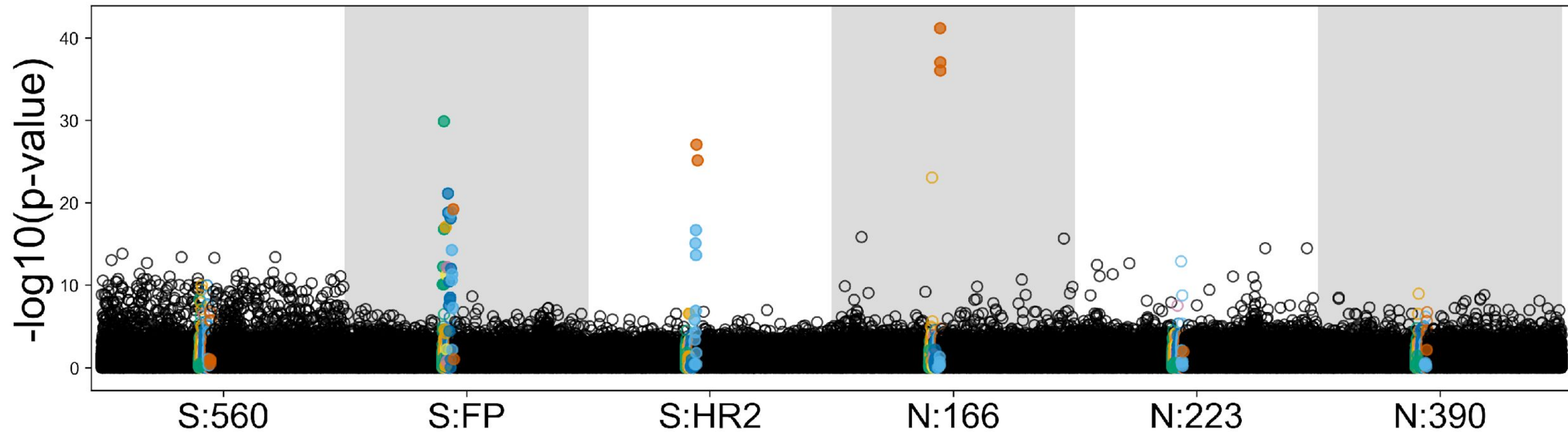


- Maintain clarity at any size
- Easy to edit
- Can always convert to pixels
- Searchable

1st exception = photographs



2nd exception = complex figures



How to generate vector images

- Draw images from scratch
- Trace a photograph
- Export from most programs

Know your file formats!

TIFF

PDF

AI

PNG

PSD

PS

SVG

GIF

EPS

BMP

JPEG

JPG

Working with vectors



Adobe Illustrator



Inkscape

Working with pixels



Adobe Photoshop

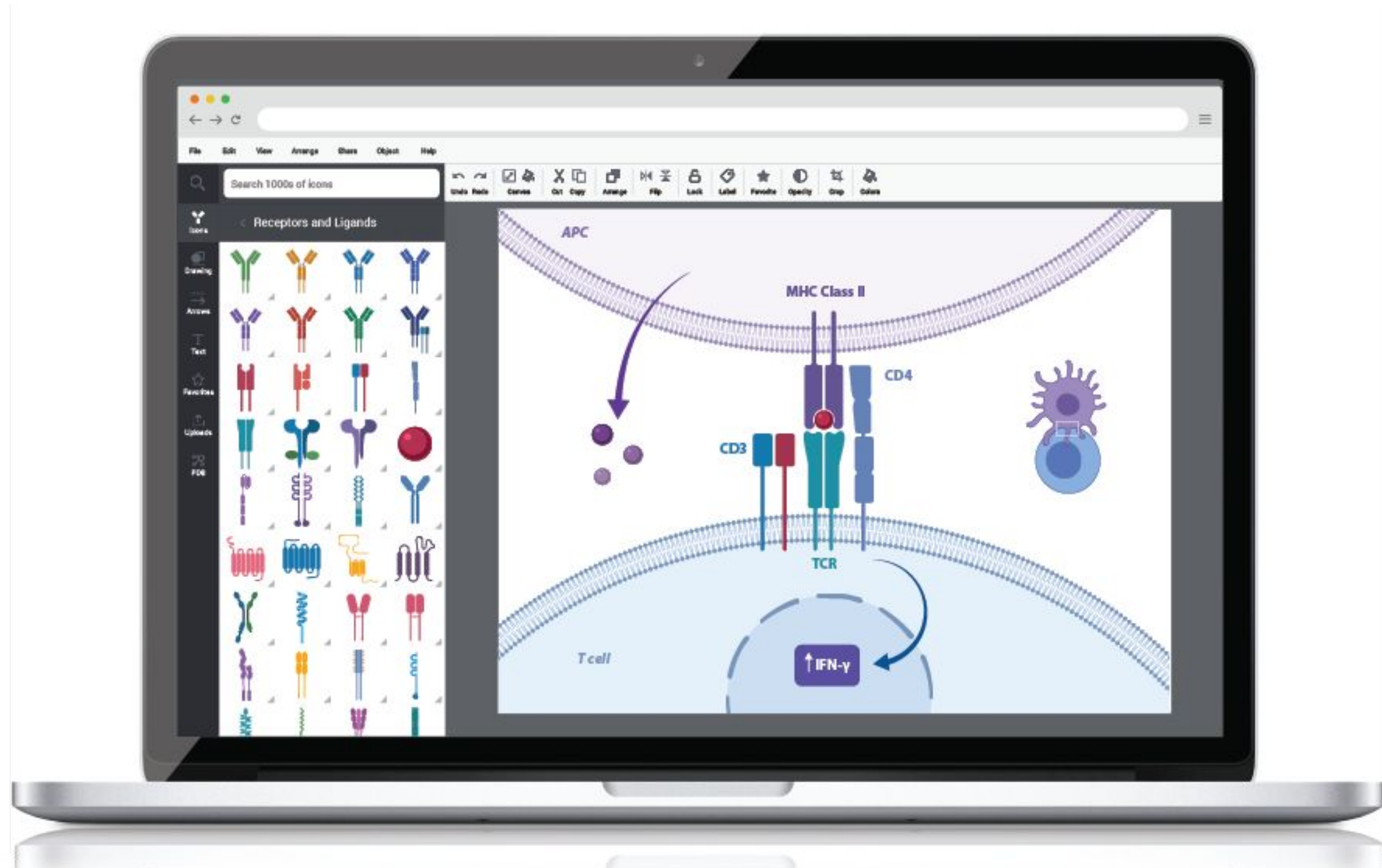


GIMP

Objective

Familiarize yourself with both
vector-based and pixel-based
graphics editing programs

BioRender

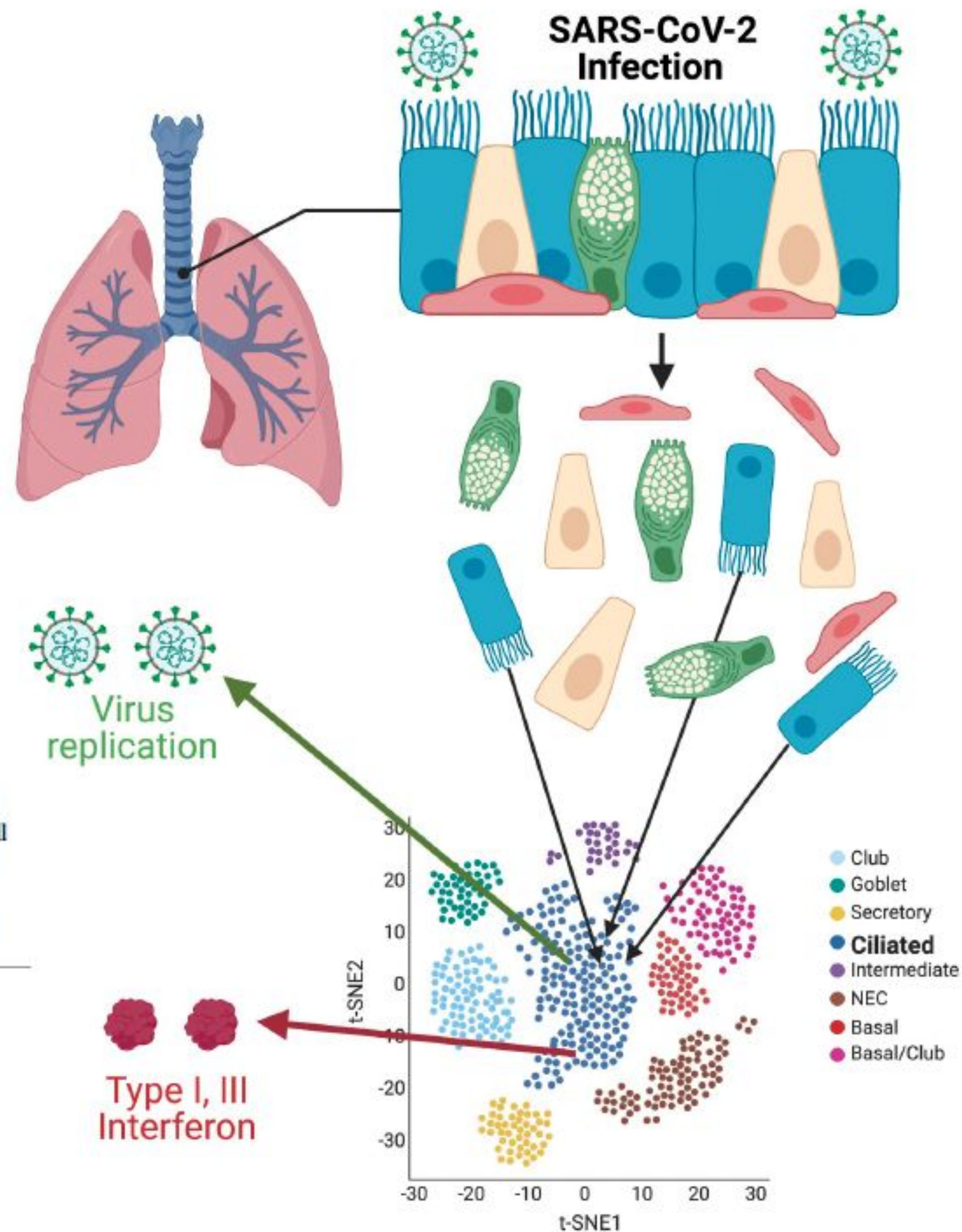


PRIMER

The first few days of a SARS-CoV-2 infection viewed at single-cell resolution

Tom Gallagher^{1*}, Paul B. McCray, Jr²

Fig 1. Single-cell resolution of SARS-CoV-2 infection. Primary cultures of well-differentiated bronchial epithelial cells, grown on permeable supports at ALIs, are infected with SARS-CoV-2, then separated for subsequent single-cell RNA sequencing. Using t-SNE statistical methods, cells with similar transcriptome profiles are group-clustered on two-dimensional plots. Individual cells containing SARS-CoV-2 RNAs and antiviral interferon transcripts are identified within clusters. Images were created with [BioRender.com](https://www.biorender.com/). ALI, air-liquid interface; SARS-CoV-2, Severe Acute Respiratory Syndrome Coronavirus 2; t-SNE, t-distributed stochastic neighbor embedding.



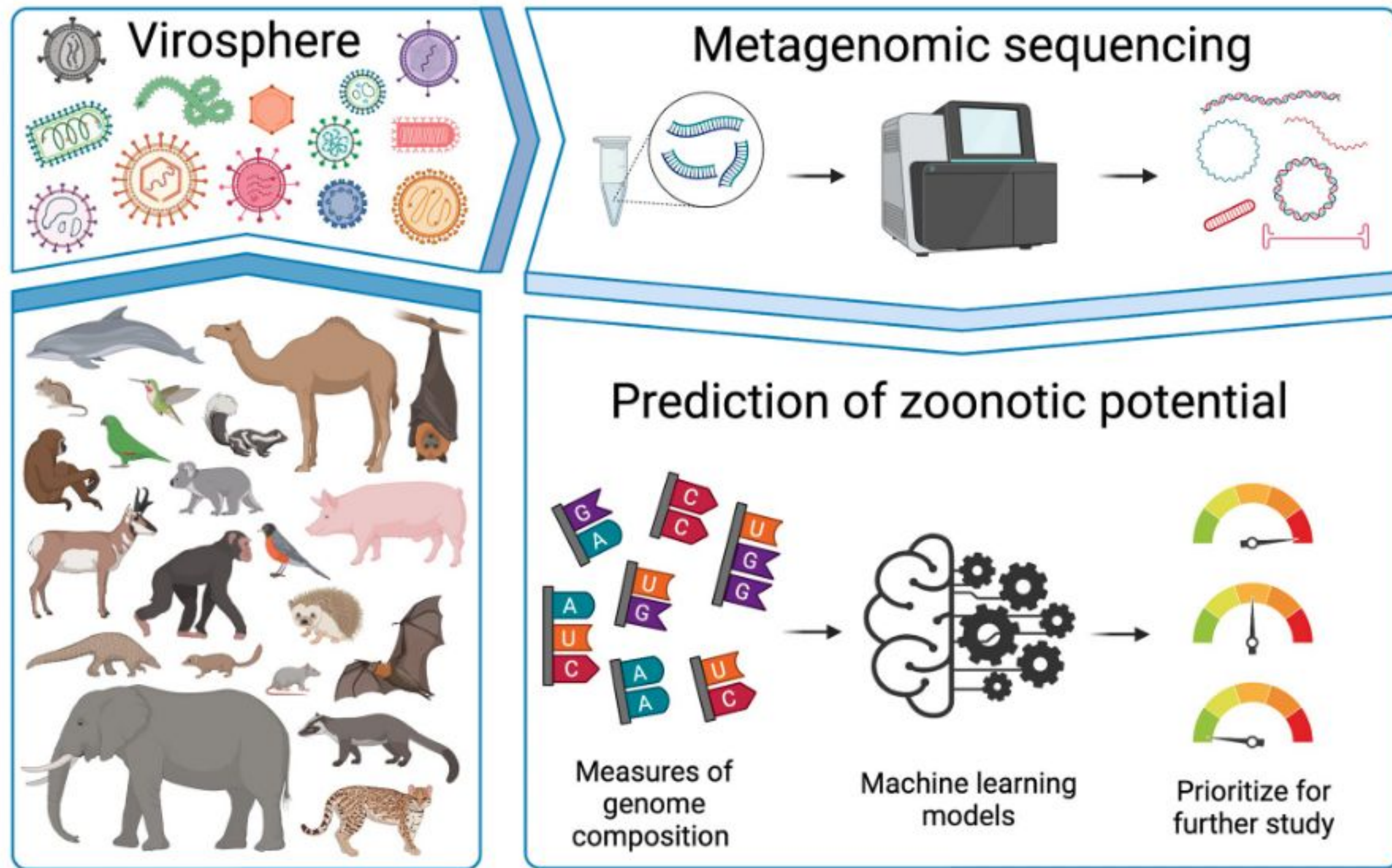


Fig 1. Predicting zoonotic potential using genomic signatures. Characterizing the diversity of viruses infecting non-human animals (i.e., the animal 'virosphere') is a critical component of pandemic prevention. However, current approaches for in-depth characterization cannot keep pace with the rate of sequence-based viral discovery driven by metagenomics. In this issue, Mollentze and colleagues present machine learning models that can prioritize novel viruses for follow-up studies based only on genomic signatures of zoonotic potential. Figure was created with BioRender.com.

BioRender Demo

