Project proposal

Due next Friday (March 28th)

1 page description of what you plan to focus on for your final project.
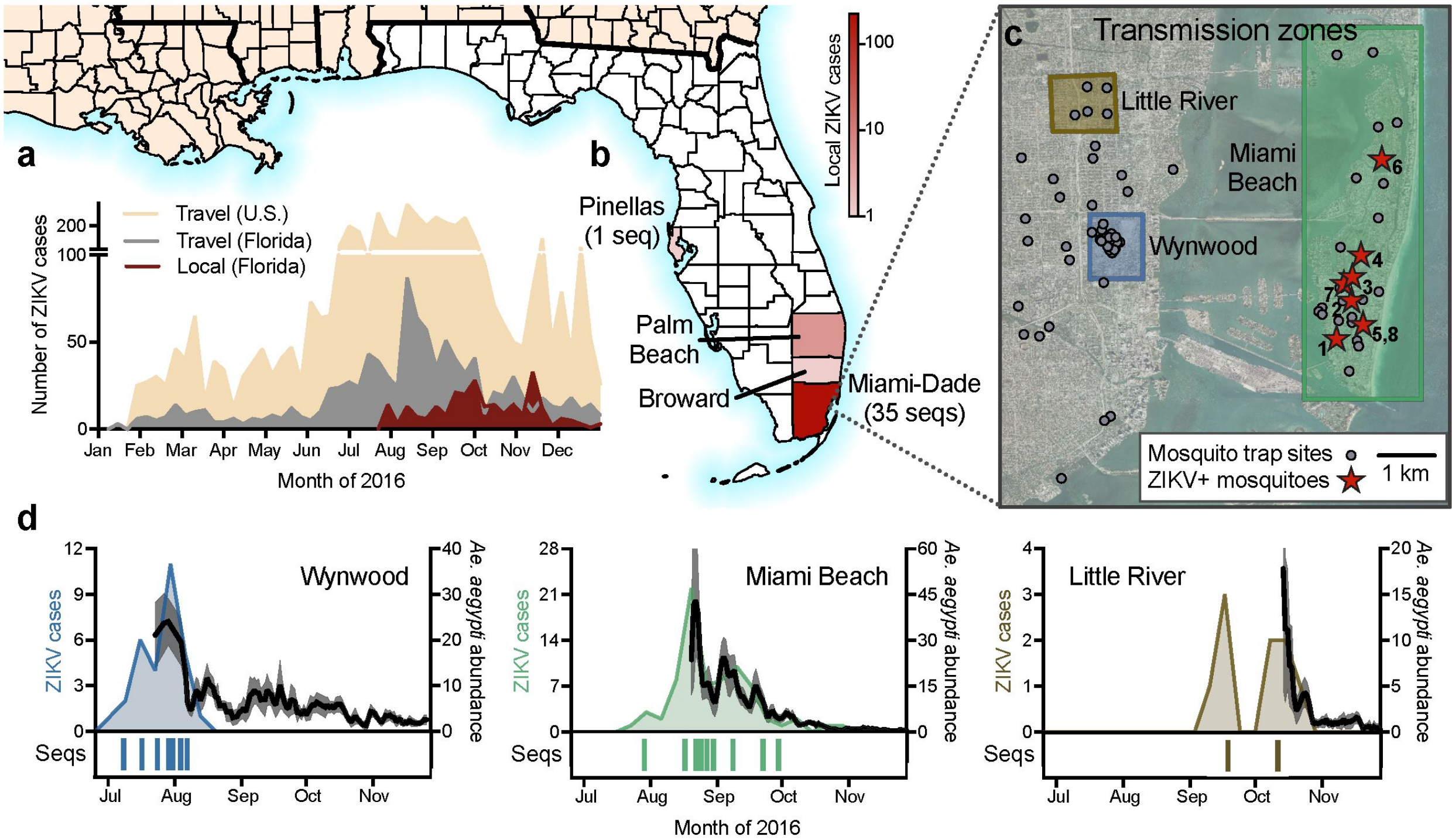
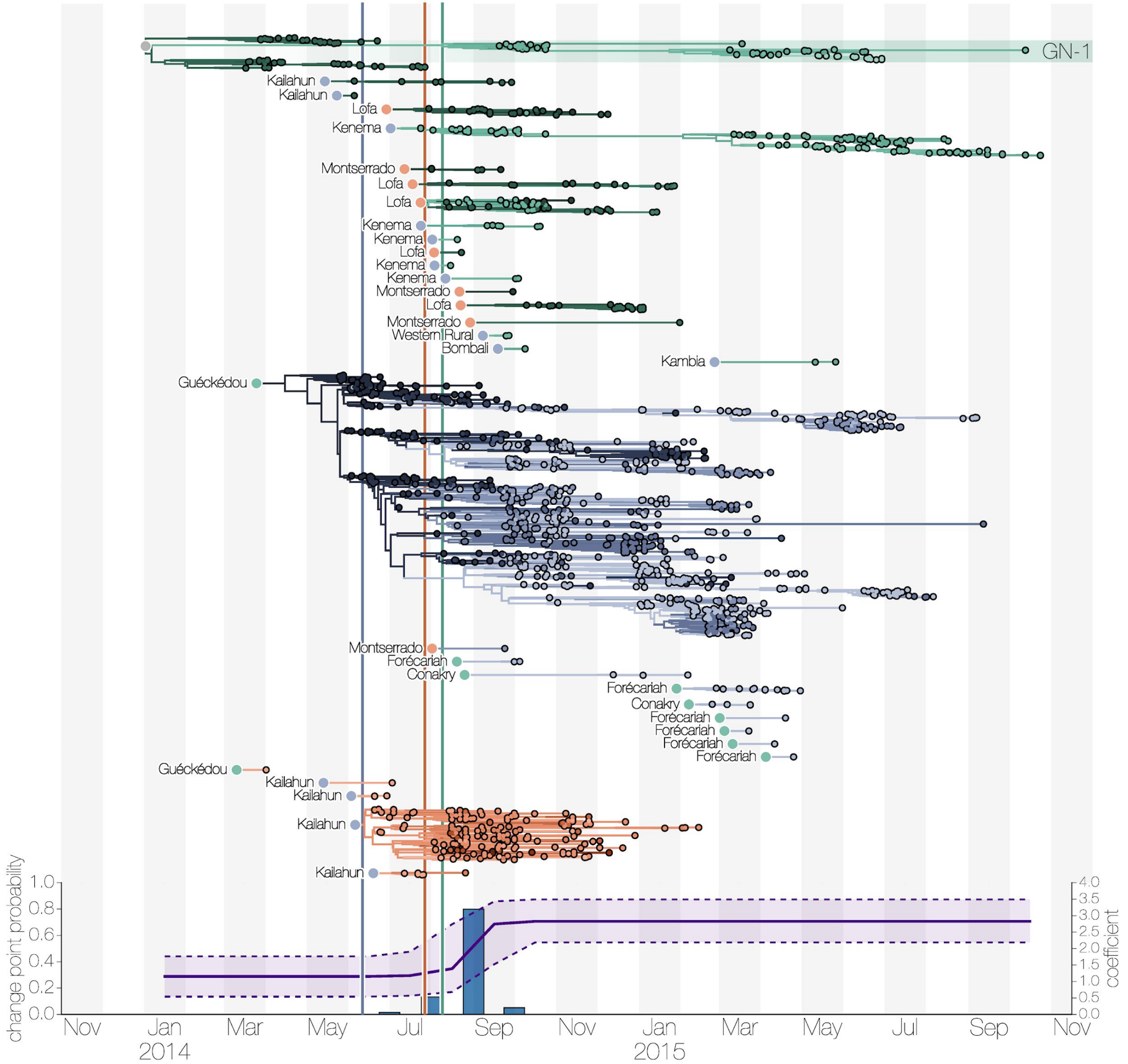***Extra credit for including a BioRender figure in proposal***

Check-in

Graphical Concepts

Spring 2023
PCfB Class 9
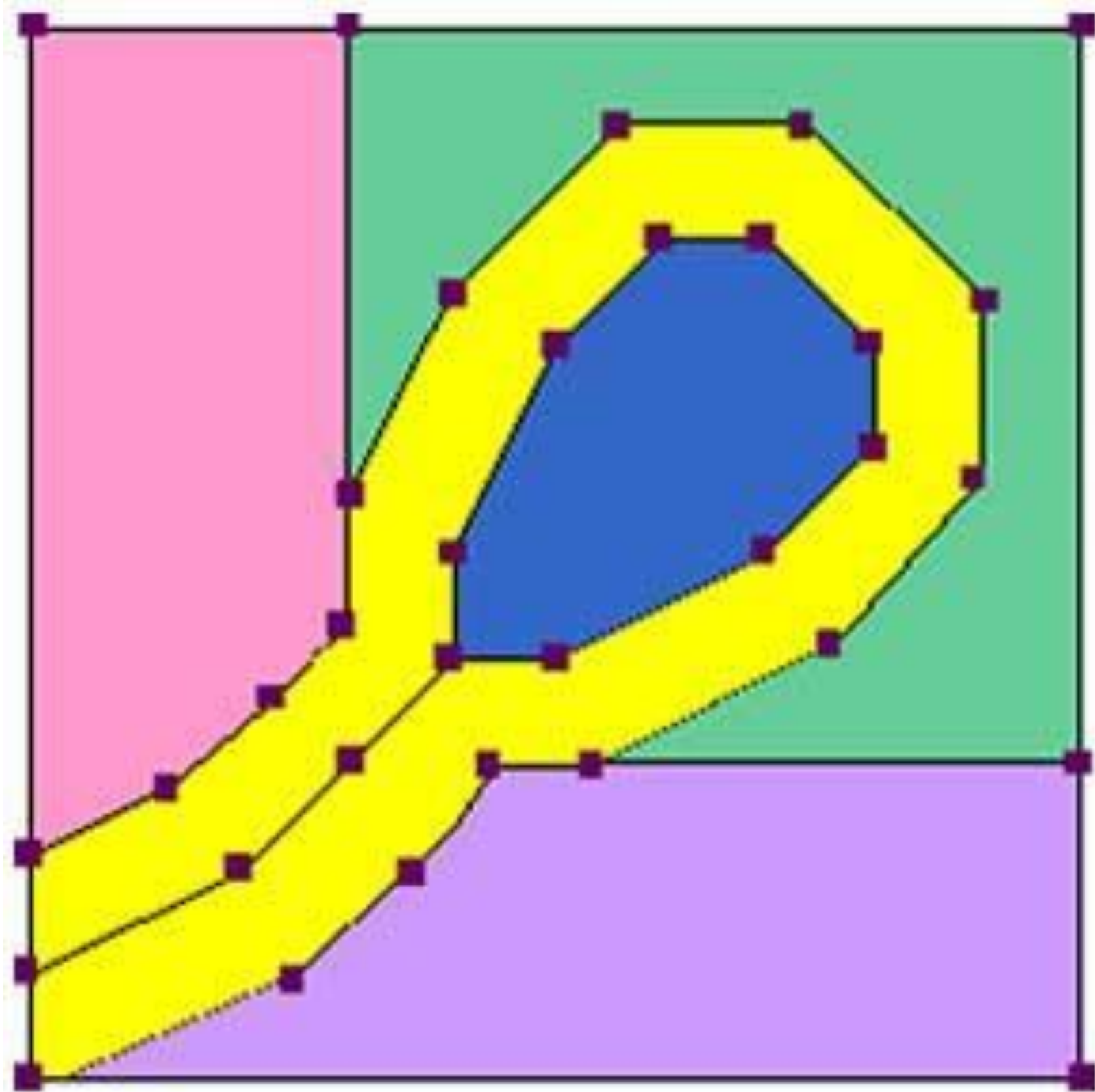March 24, 2023

Grubaugh et al. 2017, Nature

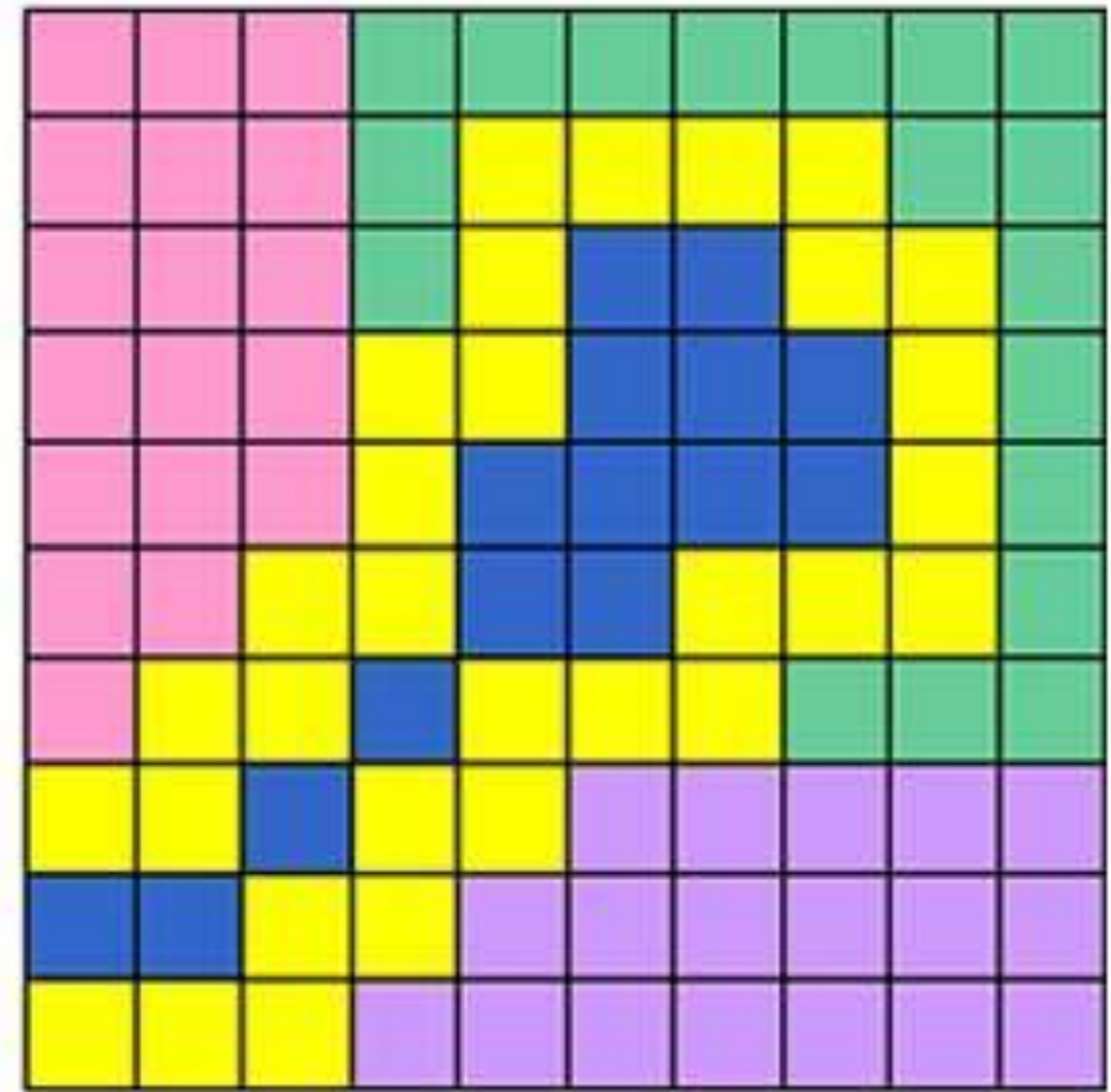**Dudas et al. 2017, Nature**

Objectives

- Overview of graphical concepts

- Exposure to editing programs

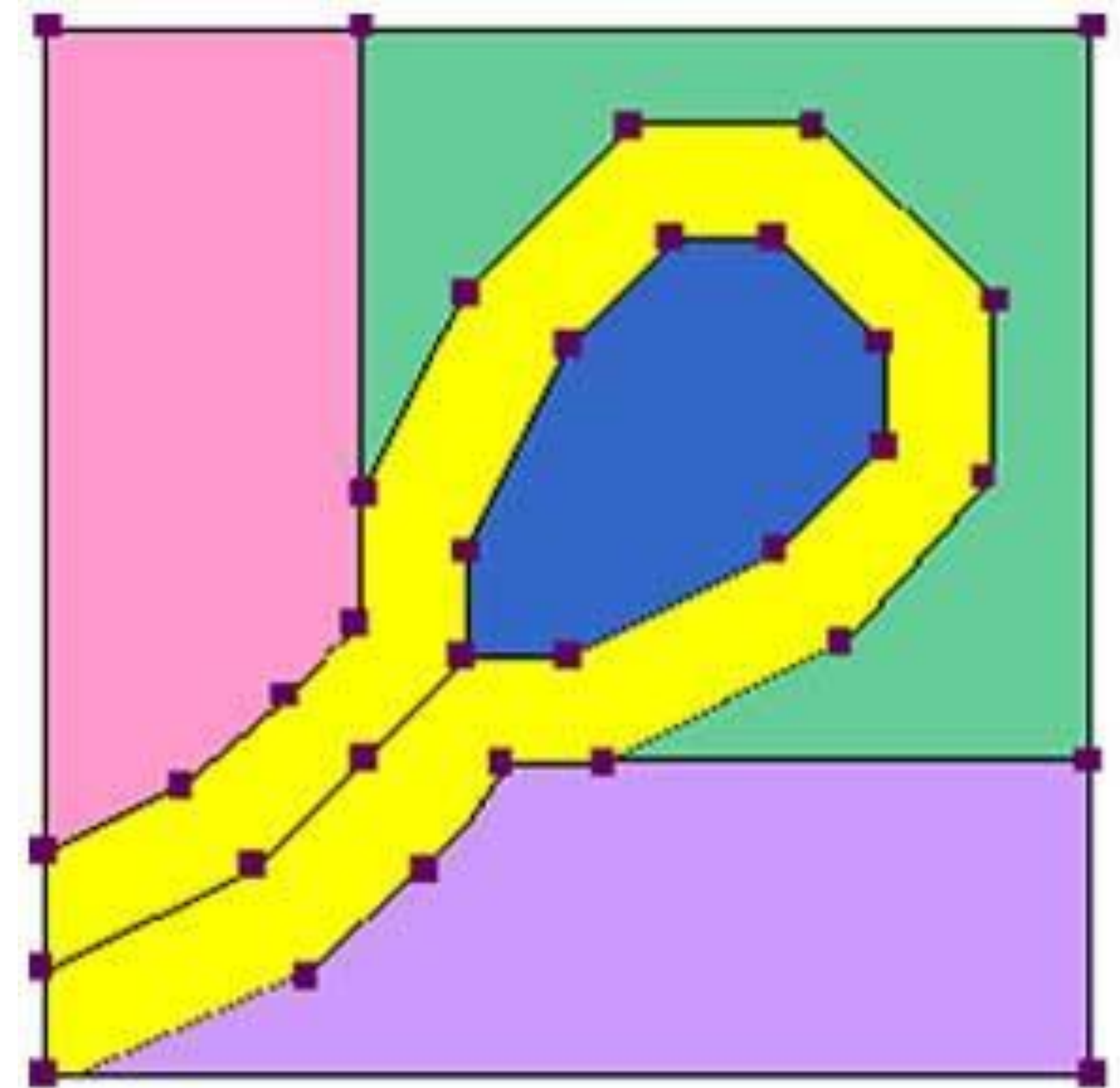# Types of digital images

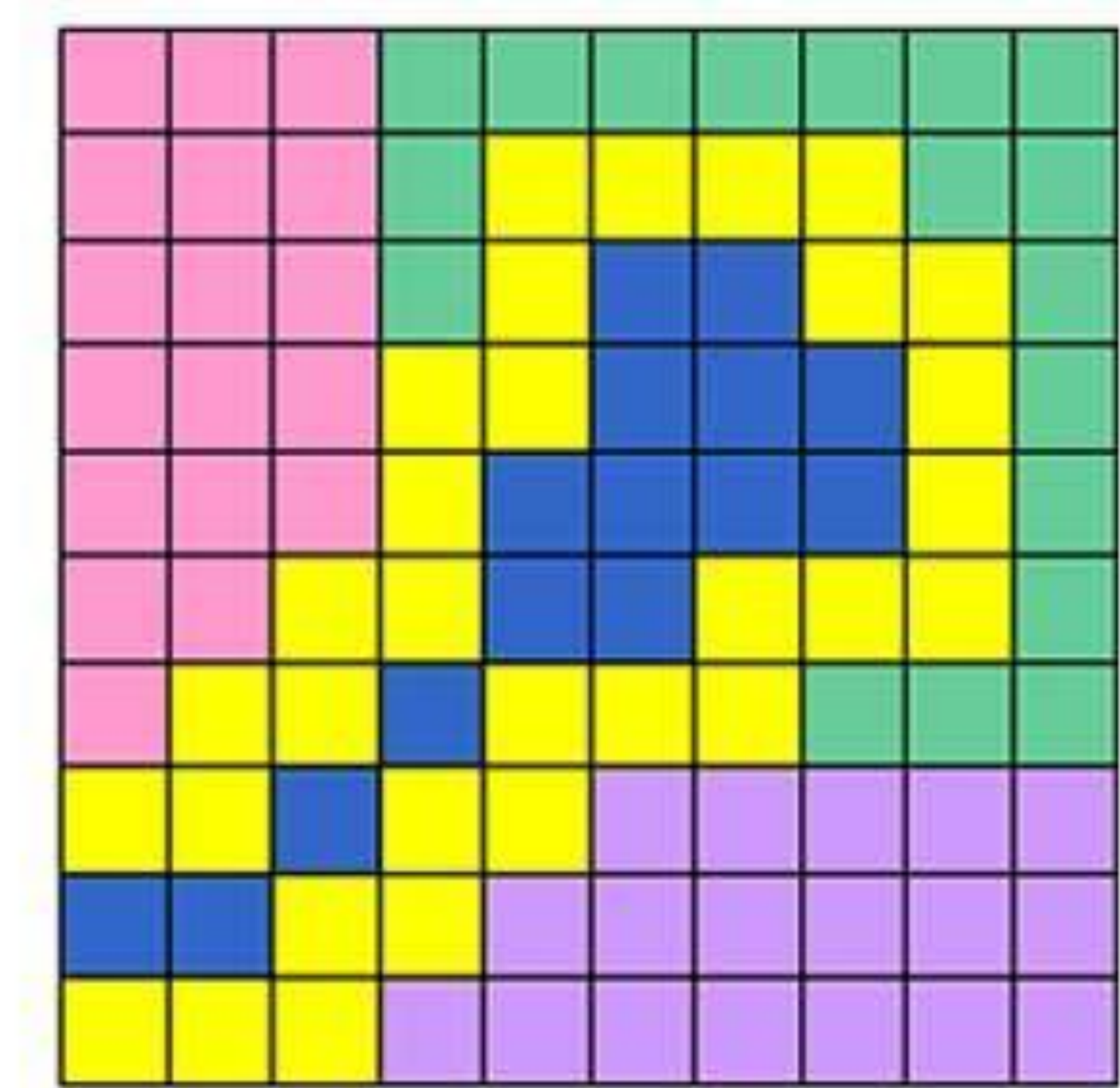vector-based

pixel-based

Vector-based images

- Composed of independent shapes

- Each shape editable as a unit

Pixel-based images (raster)

- Composed of squares of different colors

- Only editable by changing the colors of individual squares

Use vectors whenever possible!

7x Magnification

Vector

er ice
nts

Disclaimer: Product contains neither ice nor cream. May contain trace elements of cheese. Do not consume.

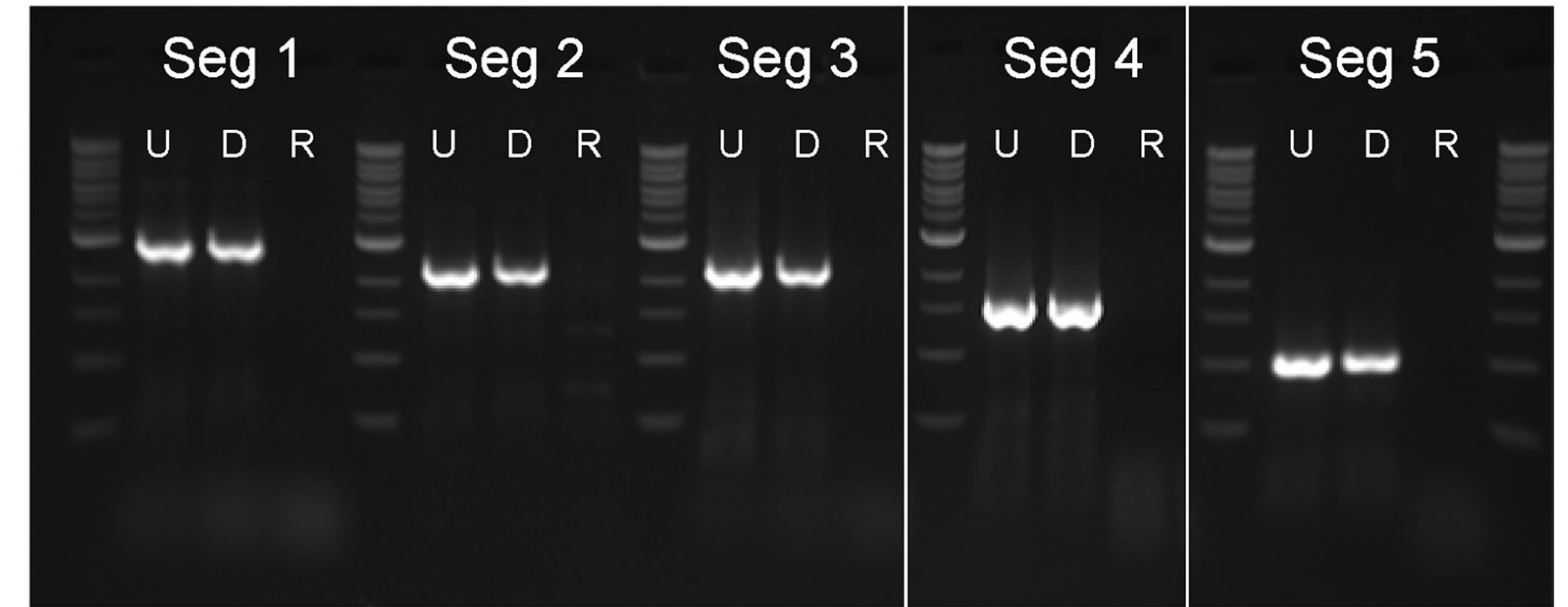Ice Cream

Bitmap
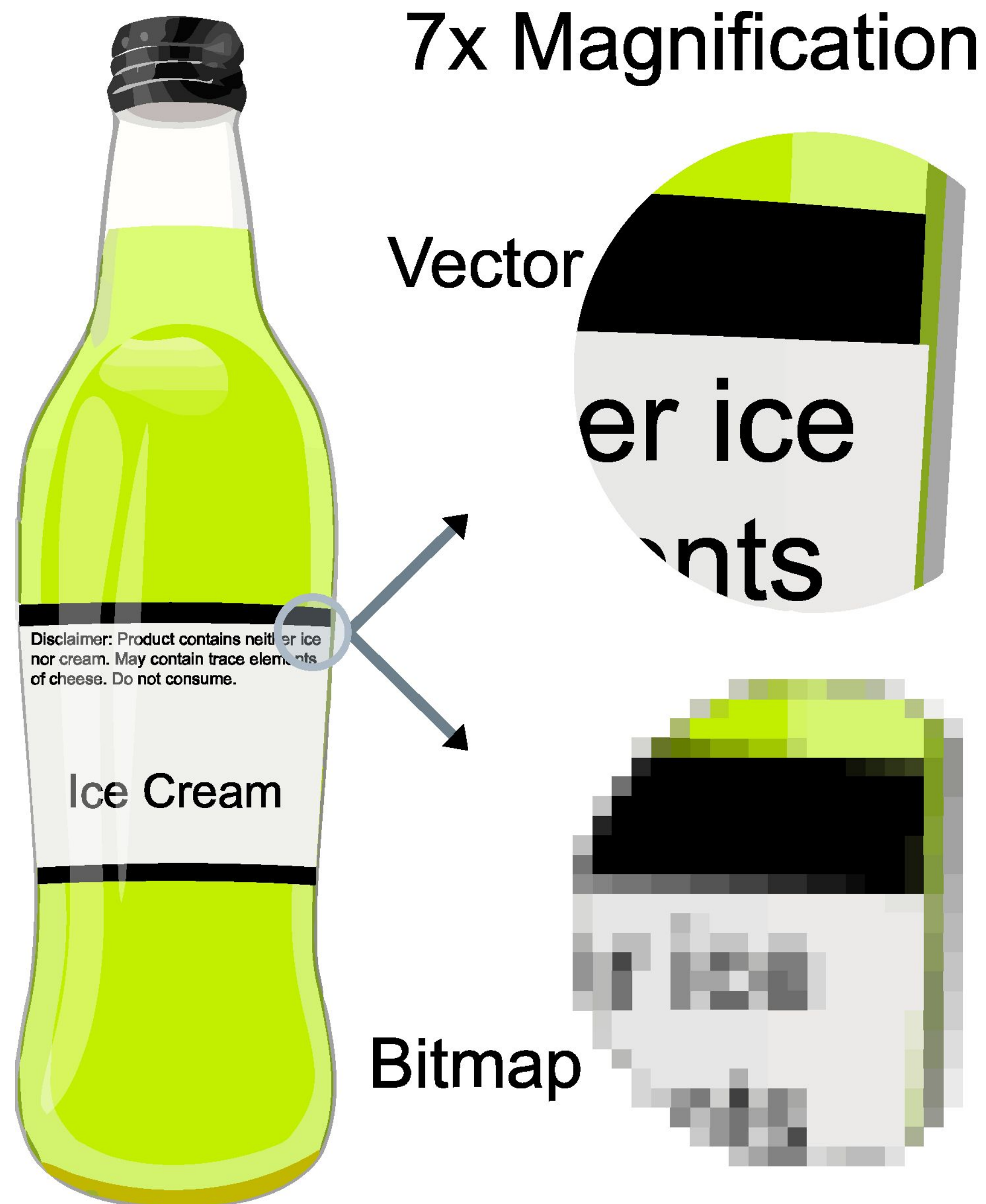
- Maintain clarity at any size

- Easy to edit

- Can always convert to pixels

- Searchable

1st exception = photographs
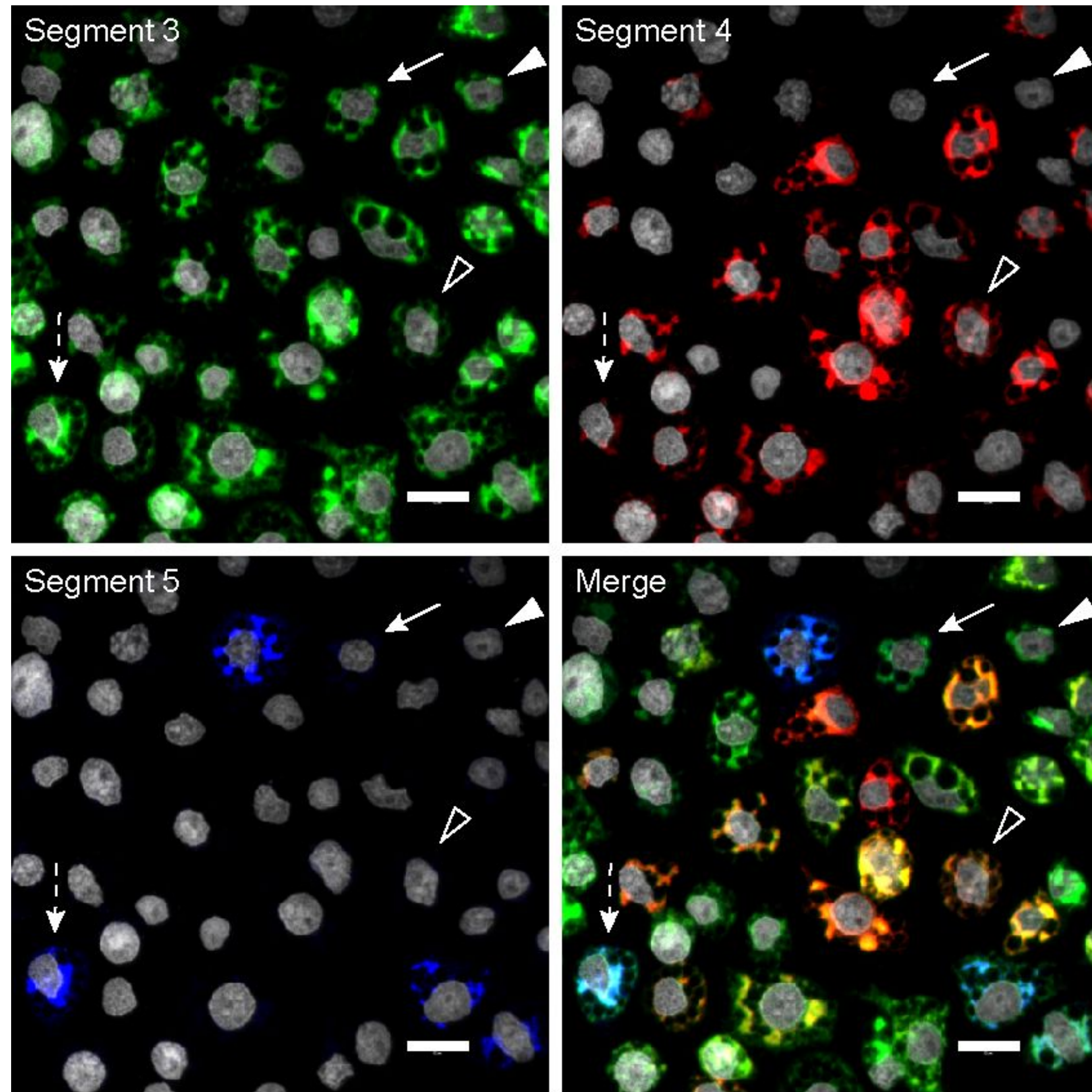
2nd exception = complex figures
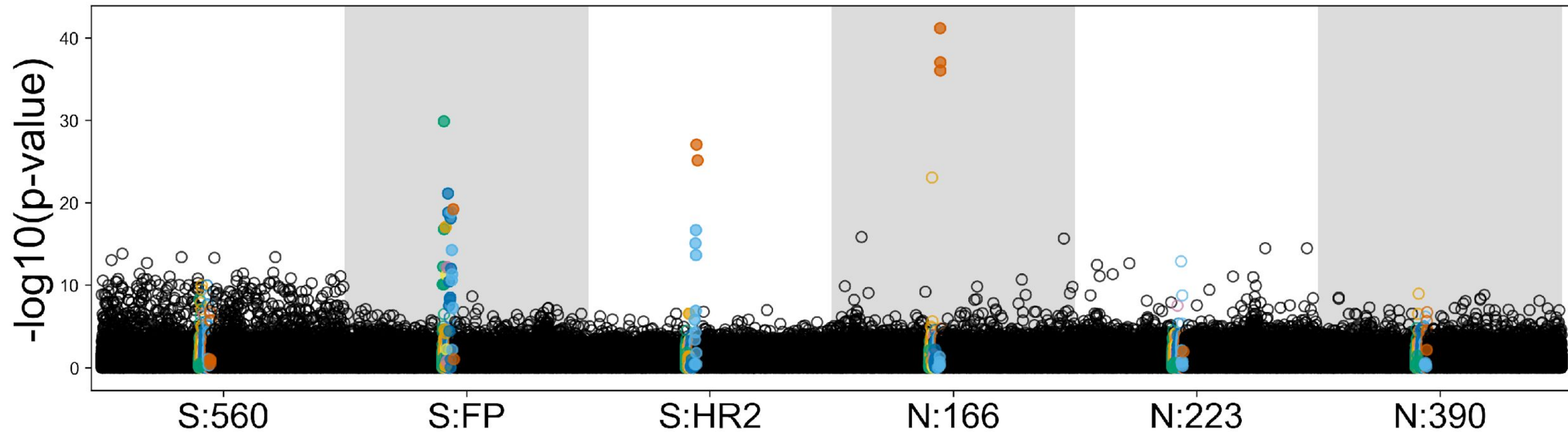
How to generate vector images

- Draw images from scratch

- Trace a photograph

- Export from most programs

Know your file formats!

TIFF

PDF

PNG

AI

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
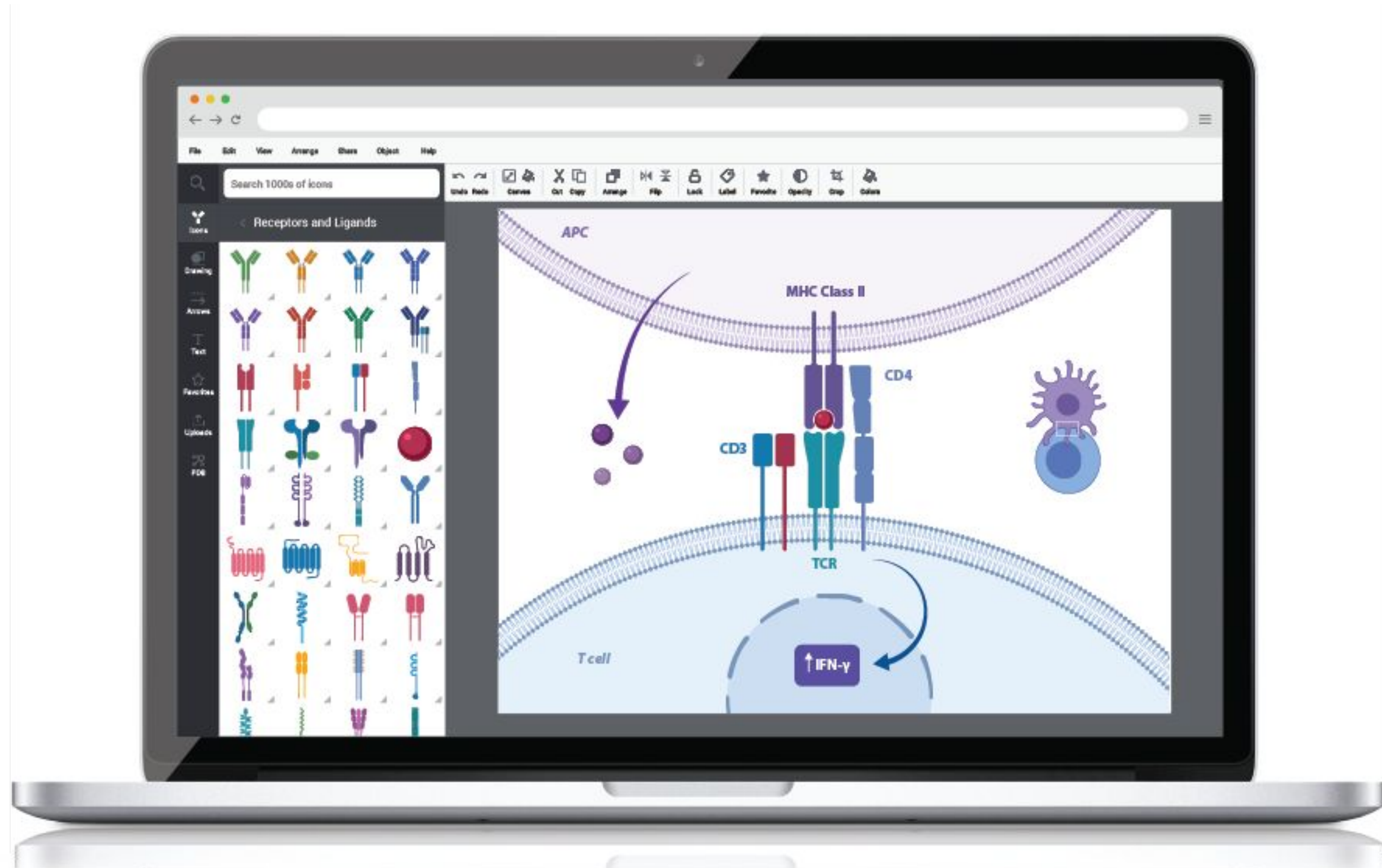
Tom Gallagher[1]*, Paul B. McCray, Jr[2]

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. ALI, air–liquid interface; SARS-CoV-2, Severe Acute Respiratory Syndrome Coronavirus 2; t-SNE, t-distributed stochastic neighbor embedding.
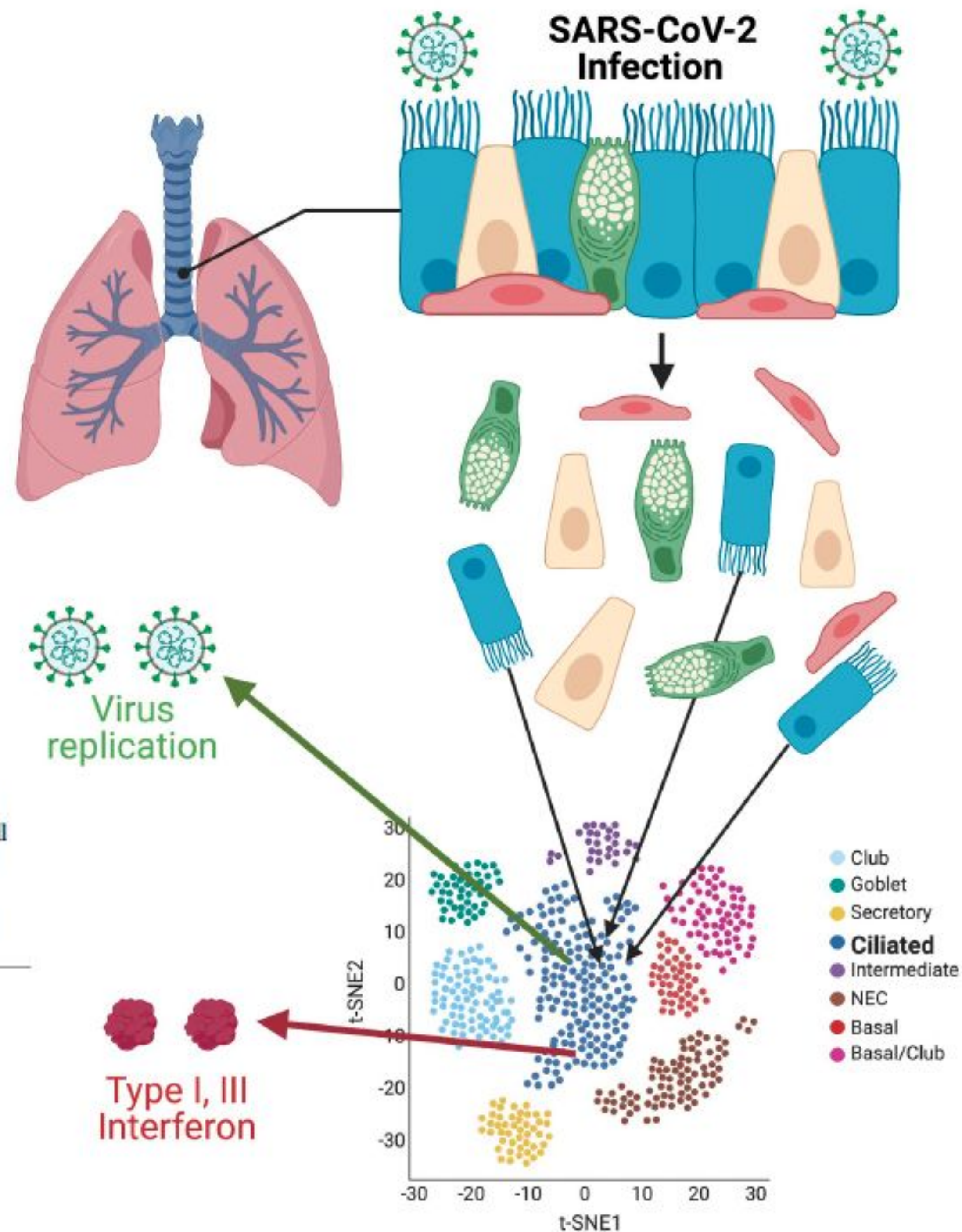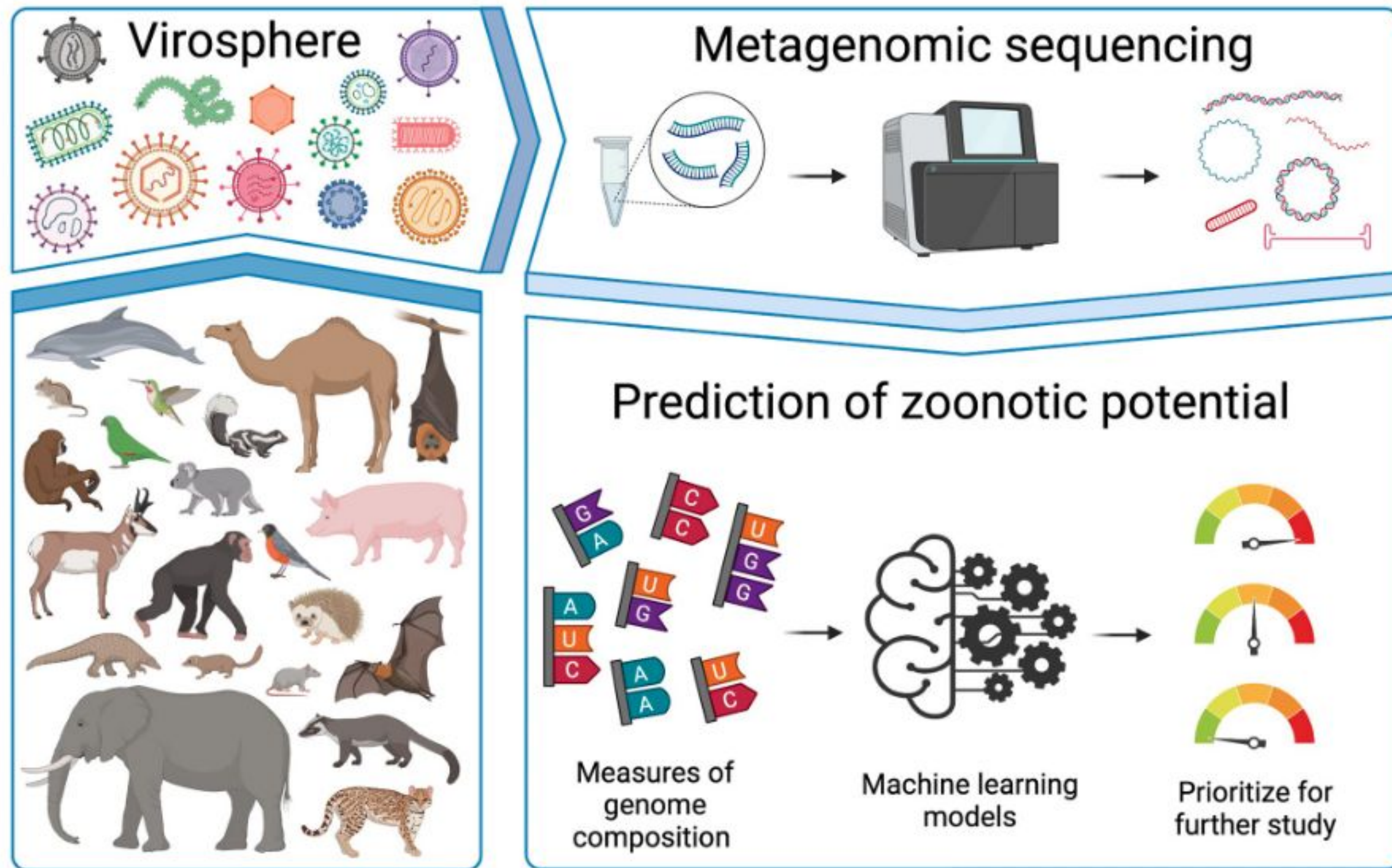
Fig 1. Predicting zoonotic potential using genomic signatures. Characterizing the diversity of viruses infecting non-human animals (i.e., the animal 'virosphere') is a critical component of pandemic prevention. However, current approaches for in-depth characterization cannot keep pace with the rate of 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.

Insert Content

Drag and drop add sections and content to your poster.

Layout

Title Section

Content

Text Image Padding

Header Caption

#1125 Highly-multiplexed serology for studying the virosphere

NAU NORTHERN ARIZONA UNIVERSITY

Jason Ladner - jason.ladner@nau.edu
The Pathogen and Microbiome Institute - Northern Arizona University

Abstract

Emerging and re-emerging infectious diseases represent a serious and ongoing threat to the human population. However, we do not know which viruses pose the greatest future risk, which complicates efforts aimed at prevention and mitigation. One thing we do know is that the vast majority of emerging viruses are maintained in stable relationships with other species of animals, and emergence within the human population results from cross-species transmission. Therefore, if we want to be prepared for the next emerging virus, we need to broadly characterize the diversity and ecology of the viruses currently infecting other animals (the animal virosphere). High-throughput metagenomic sequencing has accelerated the pace of virus discovery. However, molecular assays can only detect active viral infections and only if virus is present within the sampled fluid or tissue at the time of collection. In contrast, serological assays measure long-lived antibody responses to infections, which can be detected within the blood, regardless of the infected tissues. Therefore, serological assays can provide a complementary approach to understanding the circulation of viruses within captive and wild animal populations, and while serological assays have historically been limited in scope, recent advancements now allow 1000s to 100,000s of antigens to be assessed simultaneously using <1 µl of blood (highly-multiplexed serology).
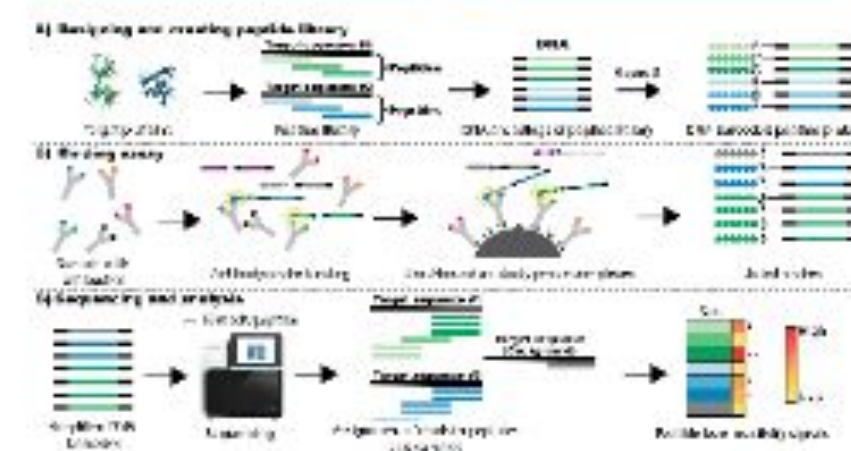
Highly-multiplexed serology

Singleplex vs. Highly multiplex

Measure reactivity against a single antigen

Measure reactivity against 100,000s of antigens

PepSeq protocol for highly-multiplexed serology

A) Design/synthesis of diverse libraries of DNA-barcoded peptides
B) Assay enriches peptides recognized by antibodies
C) Amplification and sequencing of DNA tags to estimate relative abundance of each peptide (i.e., enrichment)
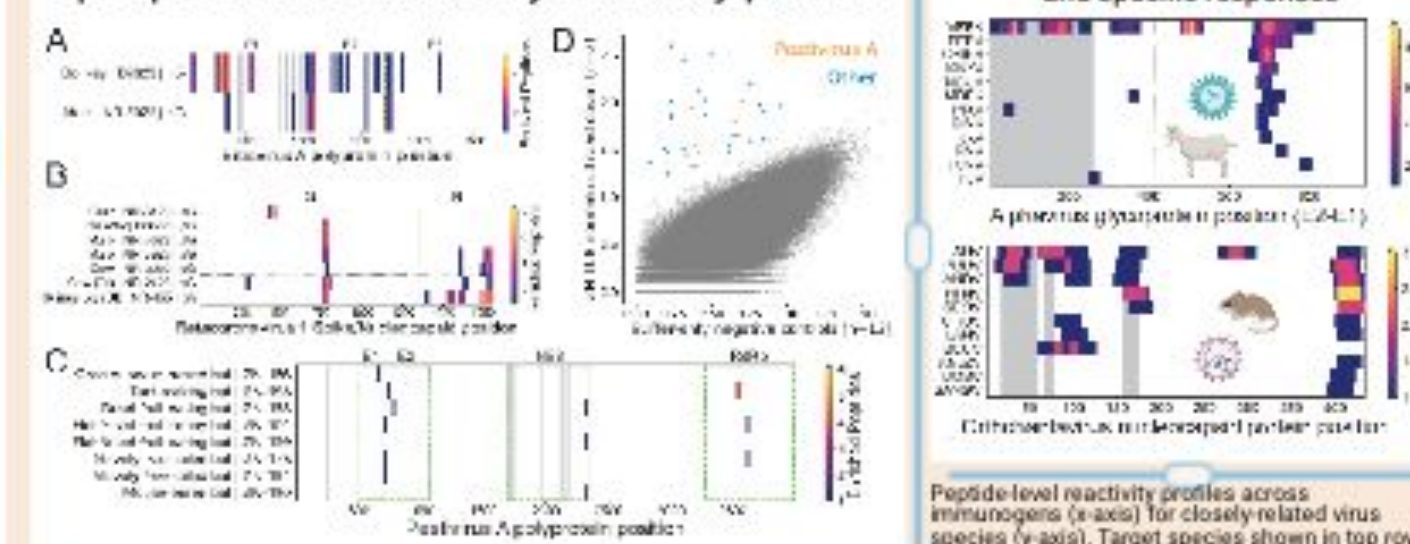
RESULTS

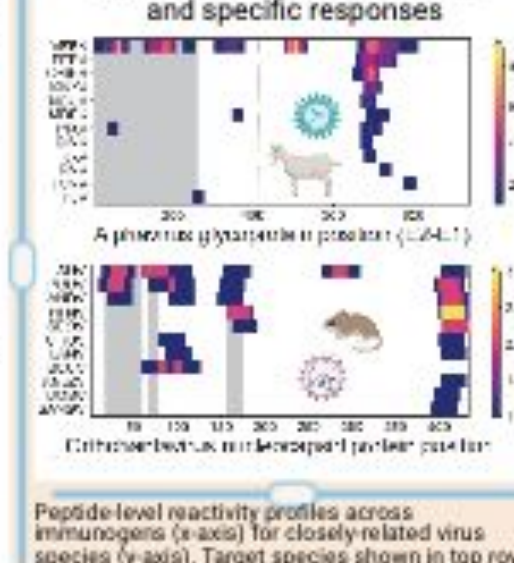Broad surveys of antibody reactivities against viruses
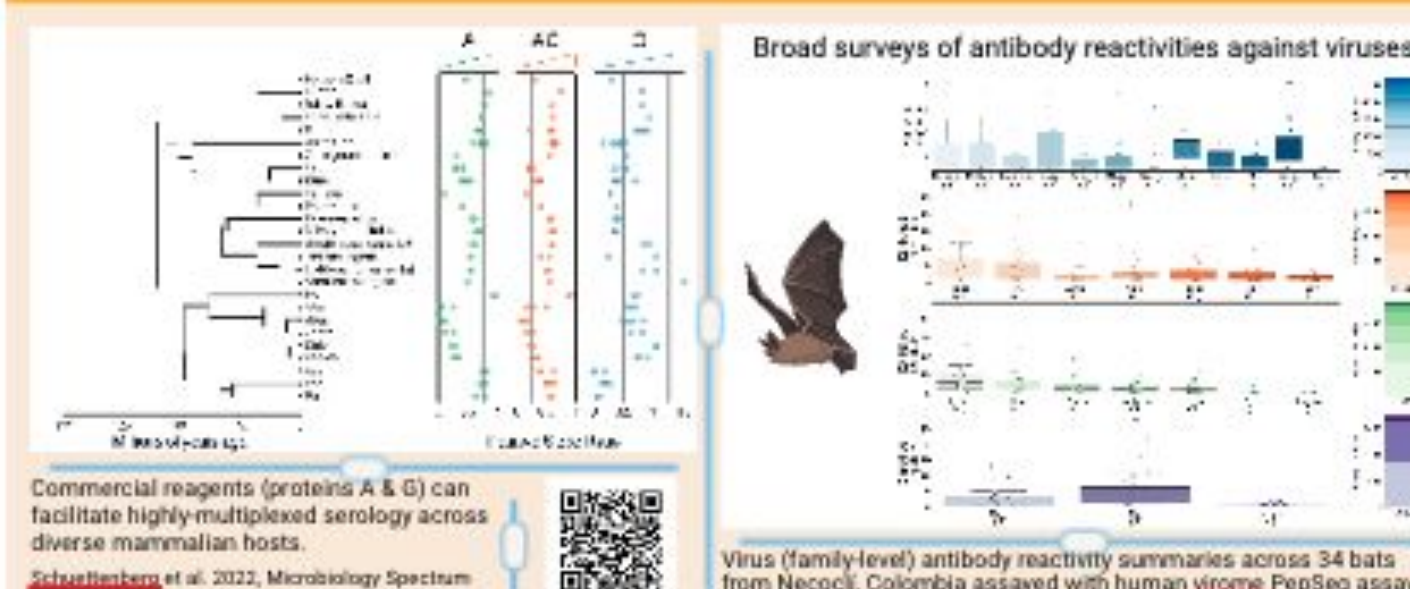
Commercial reagents (proteins A & G) can facilitate highly-multiplexed serology across diverse mammalian hosts.
Schuettenberg et al. 2022, Microbiology Spectrum

Virus (family-level) antibody reactivity summaries across 34 bats from Necocli, Colombia assayed with human virome PepSeq assay.

Epitope-resolved antibody reactivity profiles

Distinguishing cross-reactive and specific responses

Peptide-level reactivity profiles across immunogens (x-axis) for closely-related virus species (y-axis). Target species shown in top row.

Sample input options

Plasma, Serum
0.5 uL per assay

Dried blood spots
up to 24 assays per spot

In development
Saliva
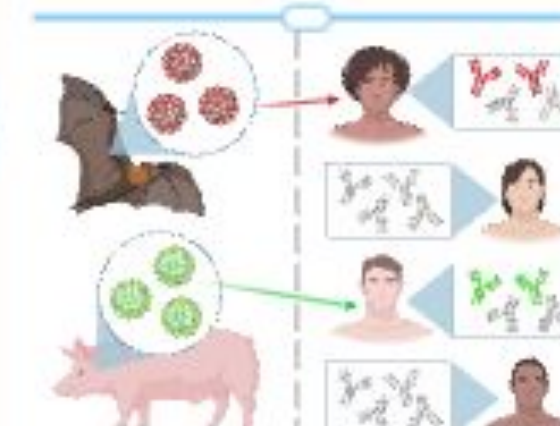Blood-fed arthropods

Applications

Exploration of the mammalian virosphere

Long-lived markers of past exposure
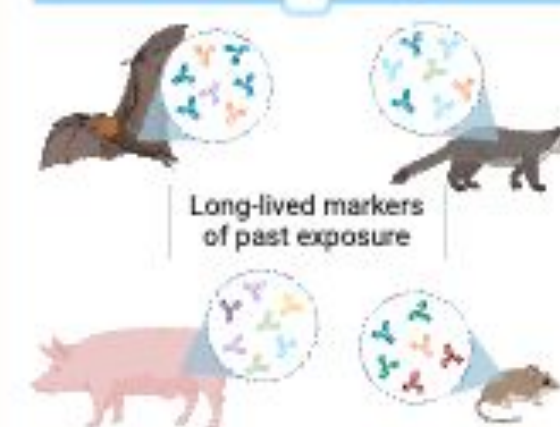
Broad sero-surveys for spillover events

Acknowledgements

48 x 36 in

Help

BioRender Demo