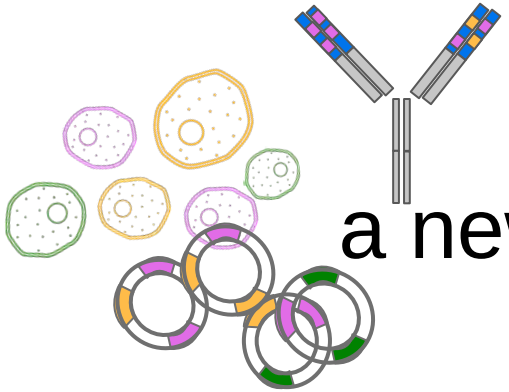
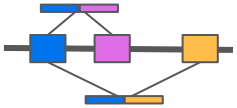
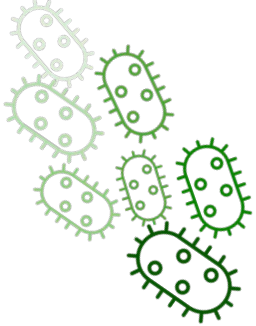
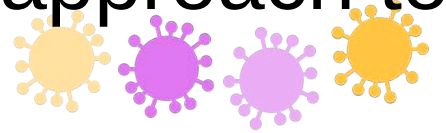

NOMAD:
a new approach to ‘omics

Genomics today: alignment first to a database of genomes/genes/proteins/+

- Does this “work”?
  - Ad hoc heuristics, cannot scale
  - In humans, biased towards individuals of European descent
  - Does not discovery novelty
    - Detect emergence of antimicrobial resistance or virus’
  - Poor statistical properties

NOMAD:
Reference-free, RNA editing, splicing, Single cell discovery
At scale for genomics
NOMAD is disseminated (Aim 1) and outputs for discovery published (Aim 2)
https://www.biorxiv.org/content/10.1101/2022.06.24.497555v2

A statistical reference-free genomic algorithm subsumes common workflows and enables novel discovery

Kaitlin Chaung, Tavor Z. Baharav, Ivan N. Zheludev, Julia Salzman

doi: https://doi.org/10.1101/2022.06.24.497555