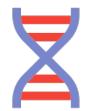




JUNE 18-22, 2023
CVPR VANCOUVER, CANADA



Visual DNA: Representing and Comparing Images using Distributions of Neuron Activations

Benjamin Ramtoula



Matthew Gadd



Paul Newman



Daniele De Martini



Poster session

WED-AM-274

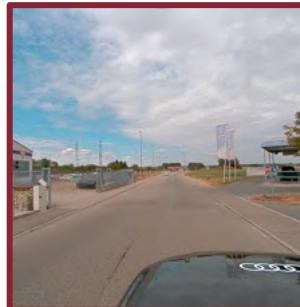
Mobile Robotics Group
University of Oxford



bramtoula.github.io/vdna

We lack good ways to compare datasets

Metadata is not enough, we need to rely on images themselves



Cityscapes, A2D2, and KITTI have strong similarities on paper but have distinct looks

Current solutions are not sensitive to many variation types

Cityscapes version



Original



Brighter



Darker

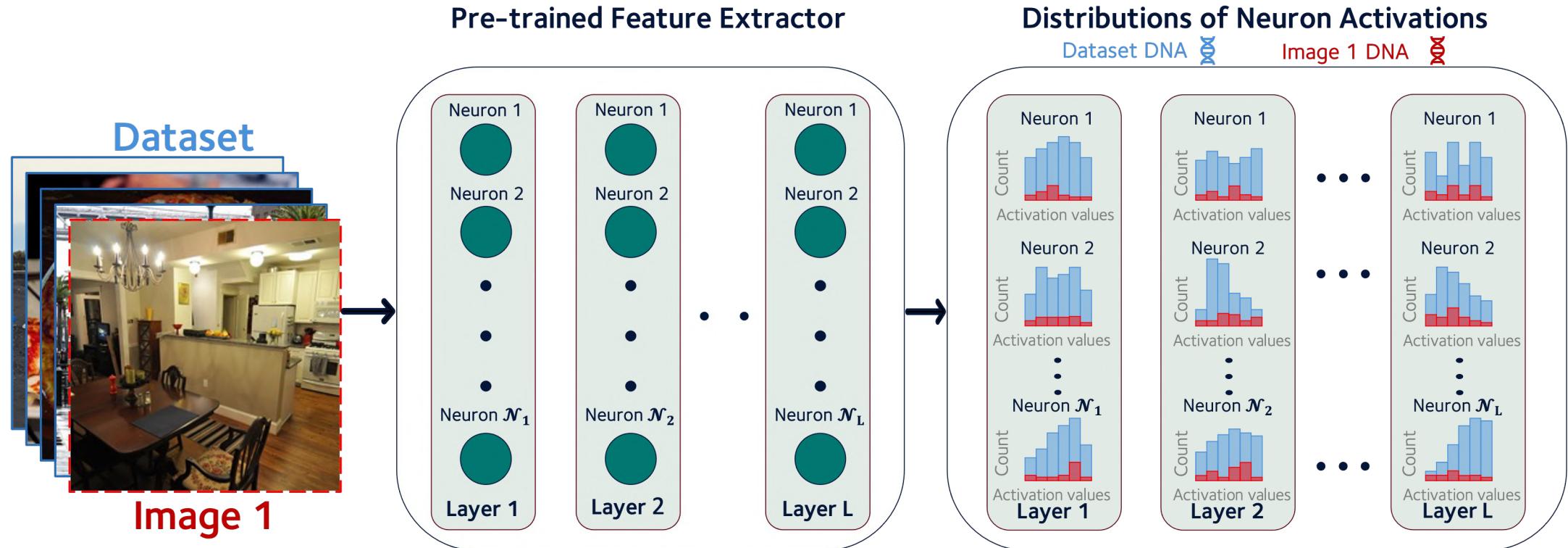


More contrast



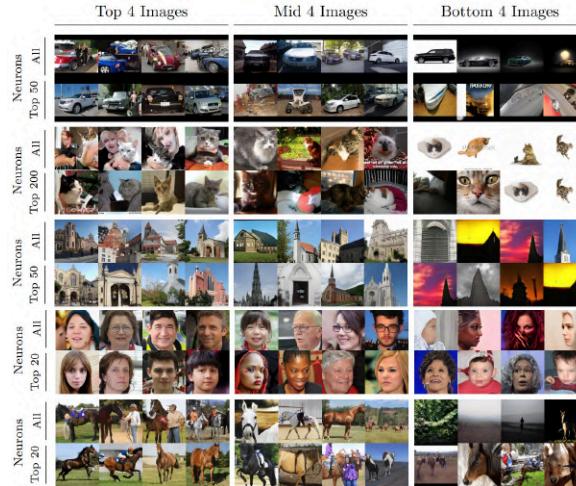
All lead to similar
embeddings usually used
for existing approaches

Distributions of Neuron Activations



- 👉 **Granularity** from individual neurons that react to different levels of patterns
- 👉 **Compact** size for any number of images
- 👉 Can be compared with **custom distances**

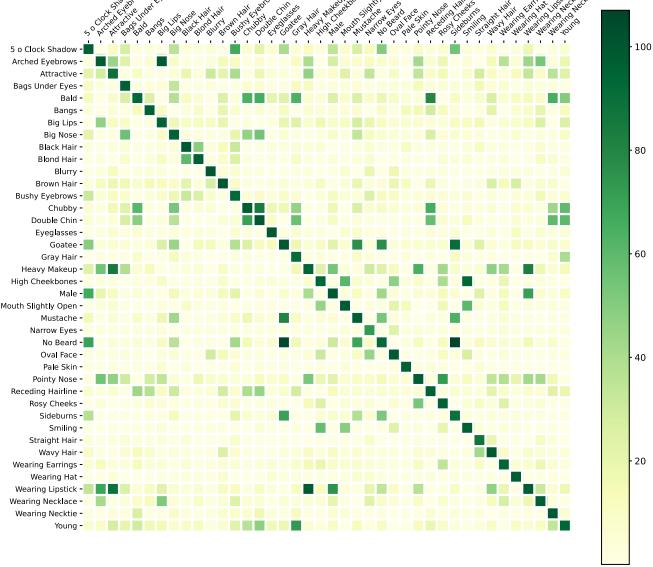
Many applications!



Evaluating **realism** of **synthetic** images



Retrieving most **similar images** to a dataset



Comparing datasets while **ignoring selected factors**

MSeg: A Composite Dataset for Multi-domain Semantic Segmentation

John Lambert^{1,3}, Zhuang Liu^{1,2}, Ozan Sener¹, James Hays^{3,4}, and Vladlen Koltun¹

¹Intel Labs, ²University of California, Berkeley, ³Georgia Institute of Technology, ⁴Argo AI

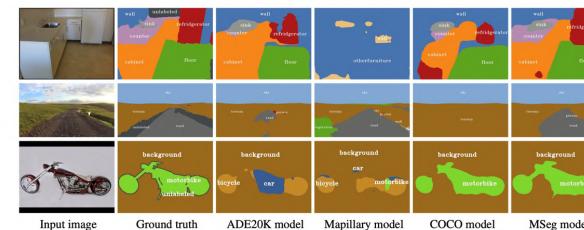


Figure 1: MSeg unifies multiple semantic segmentation datasets by reconciling their taxonomies and resolving incompatible annotations. This enables training models that perform consistently across domains and generalize better. Input images in this figure were taken (top to bottom) from the ScanNet [8], WildDash [44], and Pascal VOC [10] datasets, none of which were seen during training.

Predicting transfer learning performance

Try it yourself!

No tuning or training necessary for holistic comparisons!

```
pip install vdna
```

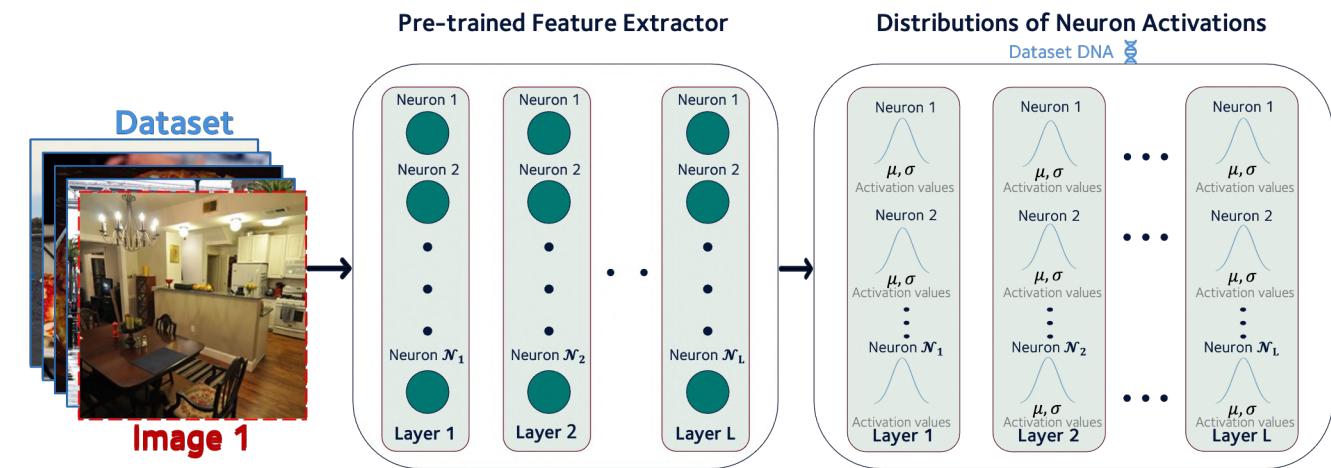
```
from vdna import VDNAProcessor, EMD  
  
vdna_proc = VDNAProcessor()  
  
vdna1 = vdna_proc.make_vdna(source="/path/to/dataset1")  
vdna2 = vdna_proc.make_vdna(source="/path/to/dataset2")  
  
emd = EMD(vdna1, vdna2)
```

More specifically, what is a Visual DNA?

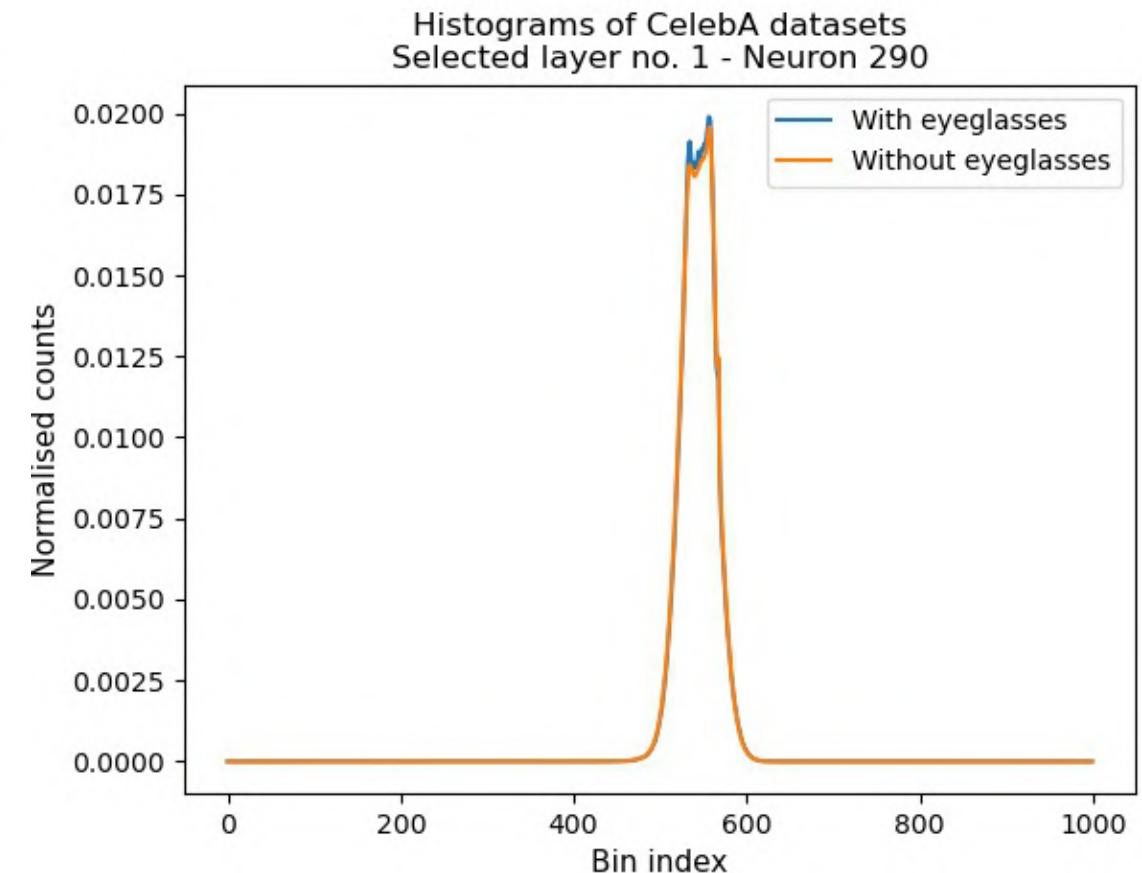
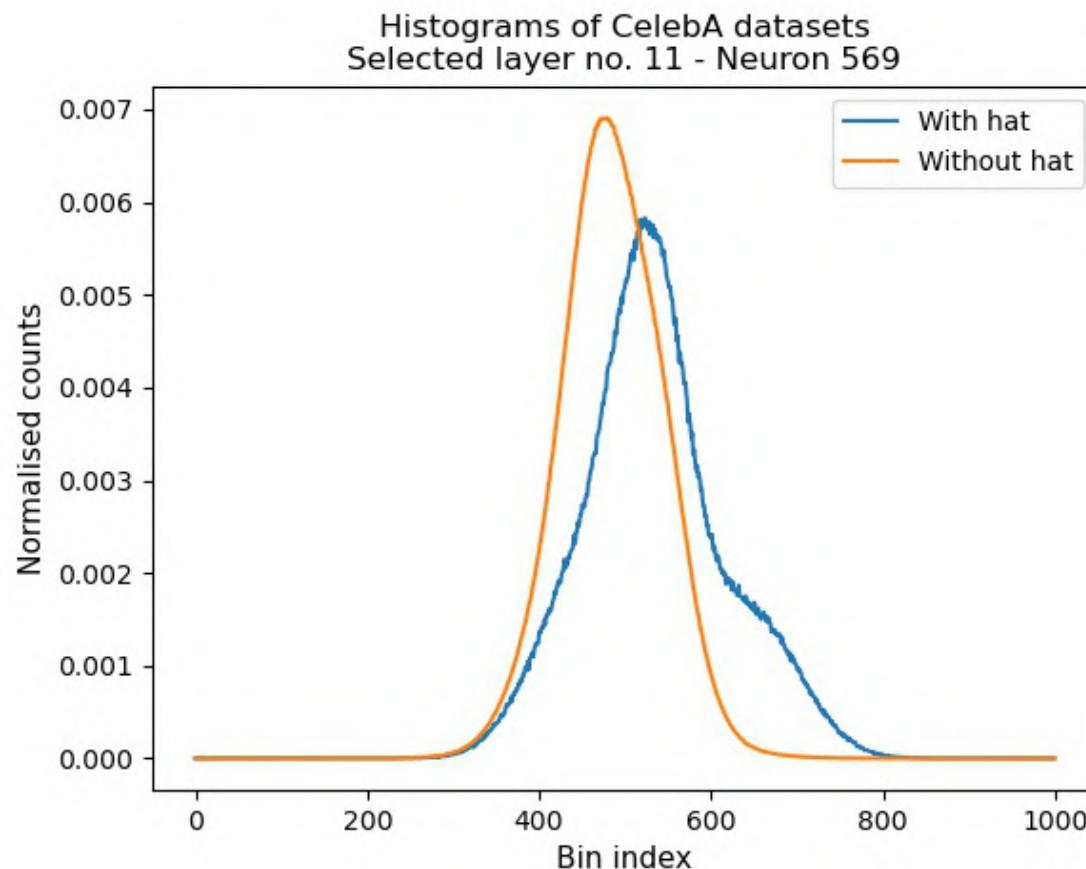
Given images to represent...

We rely on features learned by a neural network

We keep track of distributions fitted to activations at selected neurons



But... Histograms allow better fit



DNAs are compact

Representing the Flickr-Faces-HQ Dataset (FFHQ) dataset

70 000 images



89.1 GB

Raw feat. extractor activations

1.10 TB

DNA (histograms)



14.8 MB

DNA (Gaussians)



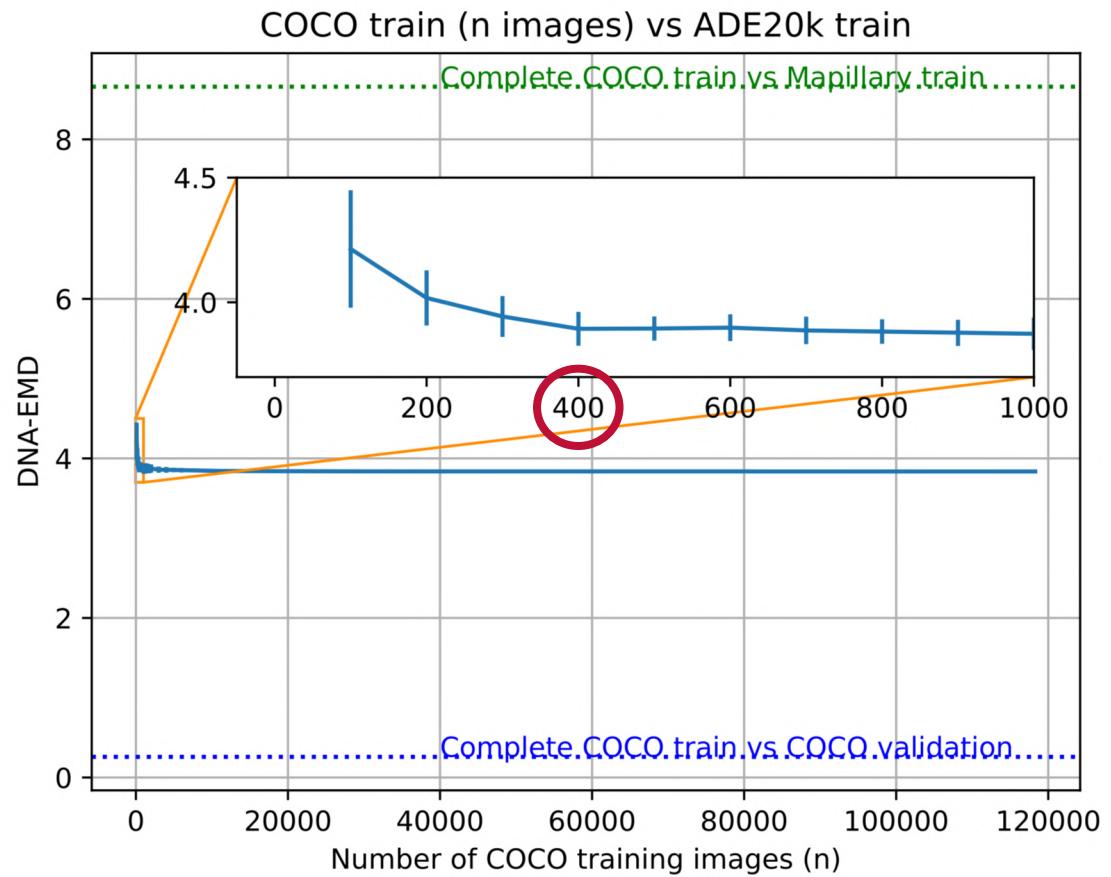
84.7 kB



DNAs don't need that many images

400 images

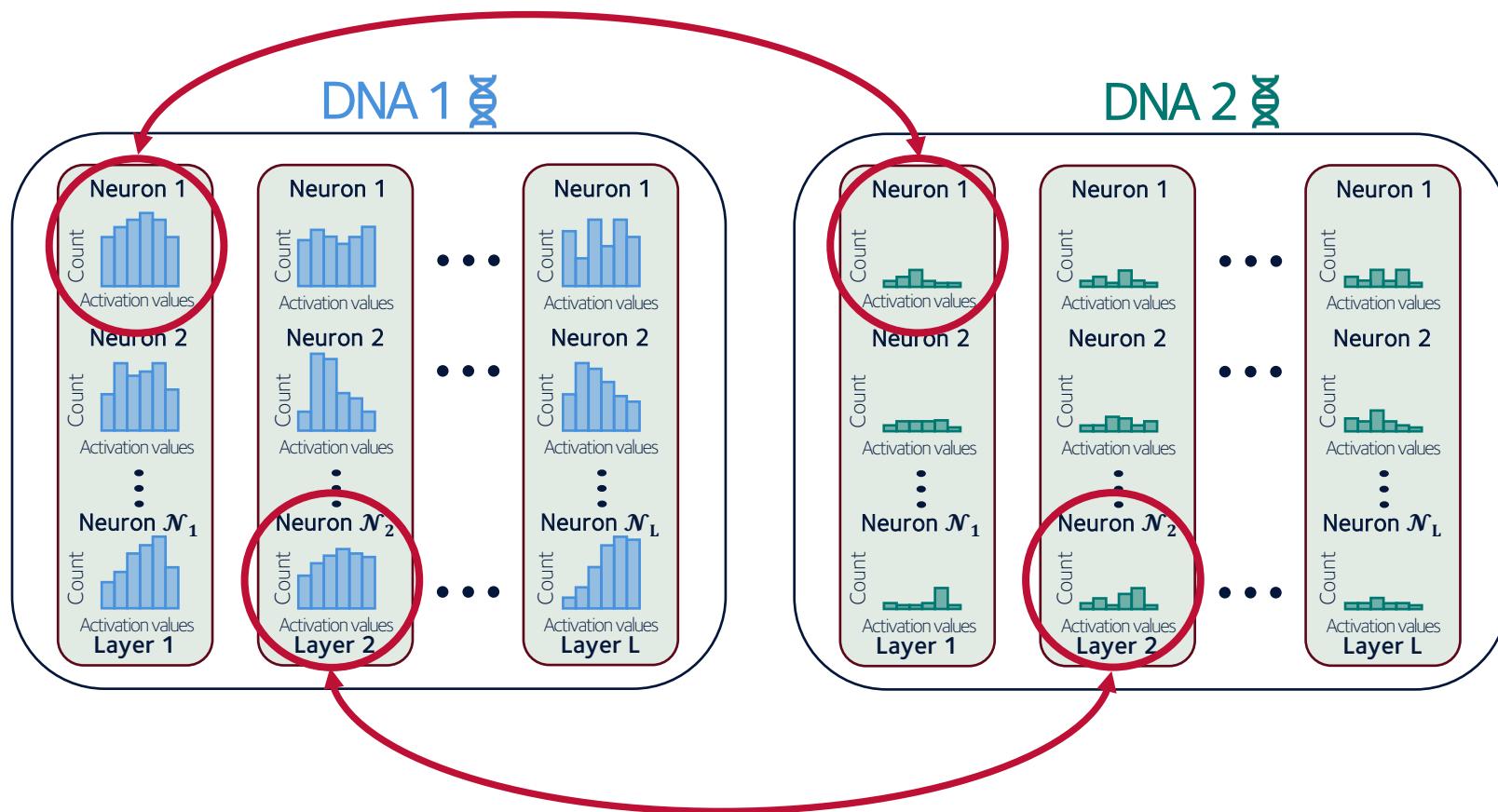
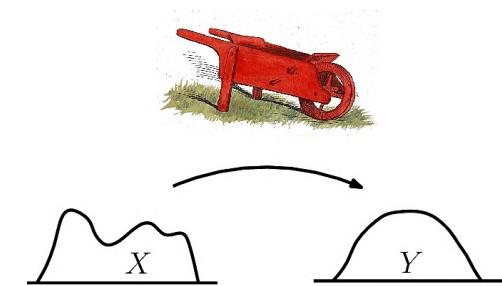
can be sufficient to create a representative DNA



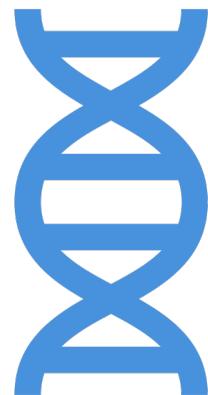
Comparing DNAs

Comparing DNAs → Comparing distributions for all neurons

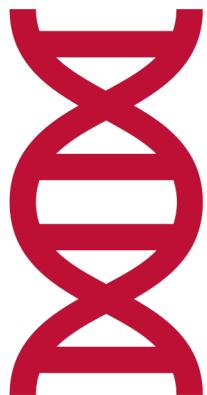
- 👉 e.g., Earth Mover's Distance for histograms
- 👉 e.g., Fréchet Distance for Gaussians



Finding neurons sensitive to an attribute



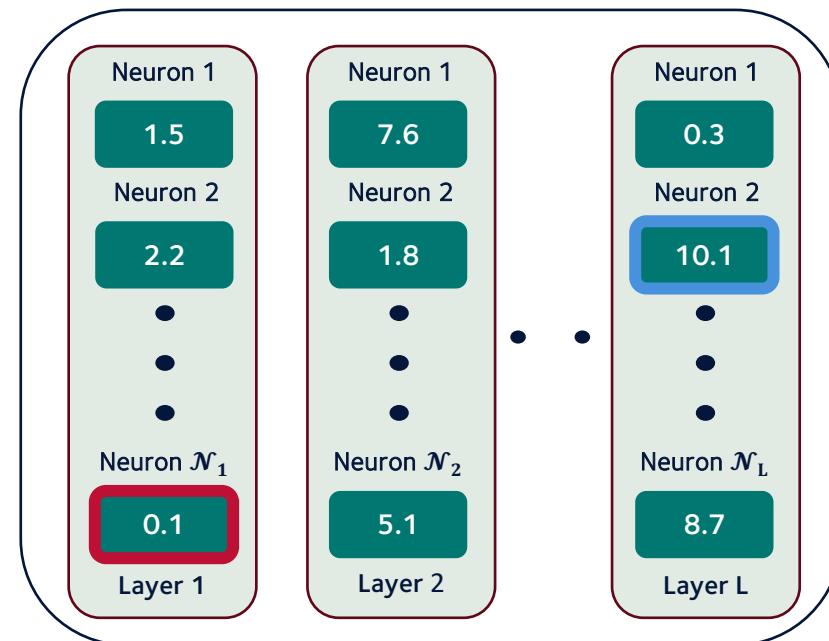
VS



With attribute

Without attribute

Earth Mover's Distances



- 👉 Small EMD → Neuron **not sensitive** to difference in images
- 👉 High EMD → Neuron **sensitive** to differences

We can order neurons by their sensitivity to the attribute

Few neurons are sufficient to focus on high-level concepts

Reference
image



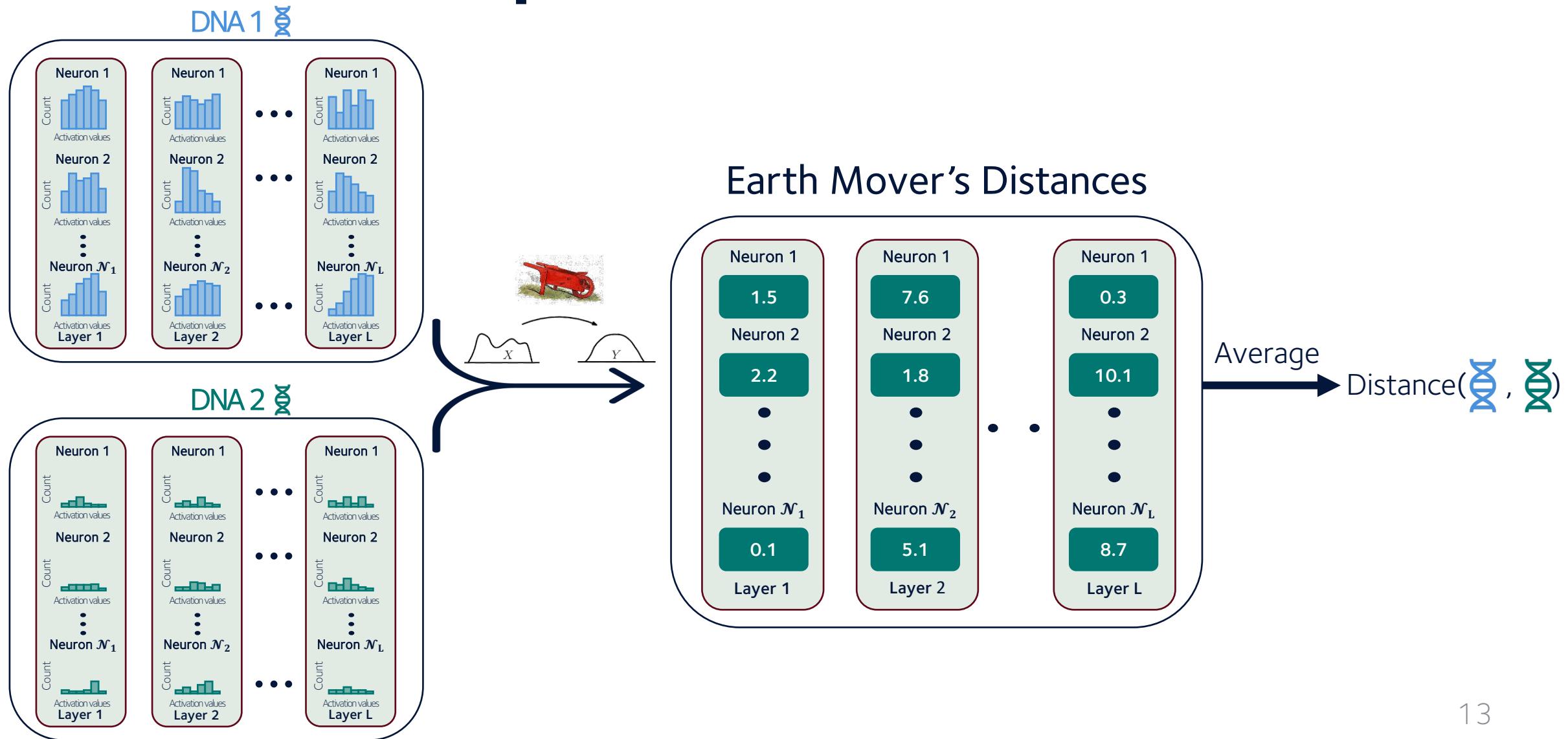
Images reacting most to the
top 1 “eyeglasses” neuron



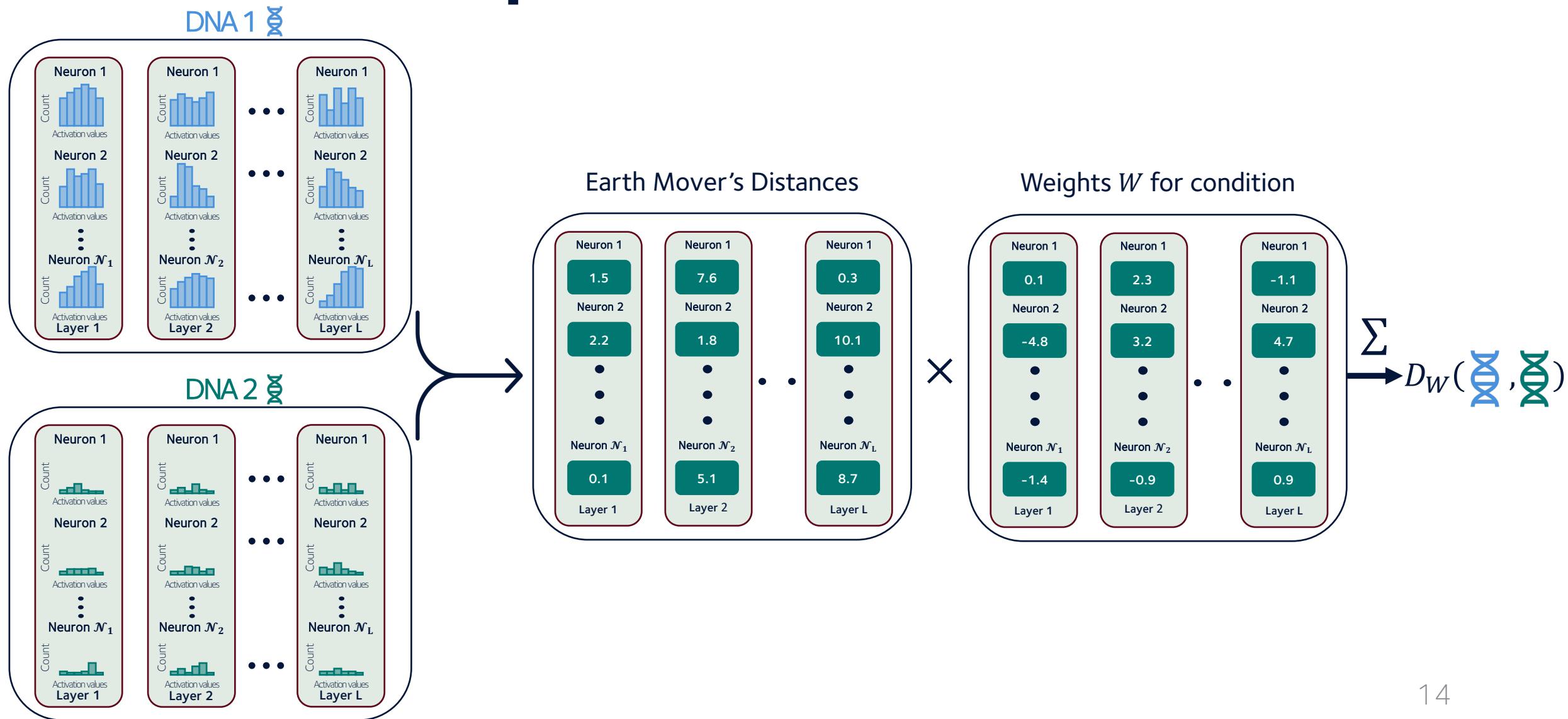
Images reacting most to the
top 20 “wearing hat” neurons



Holistic comparison

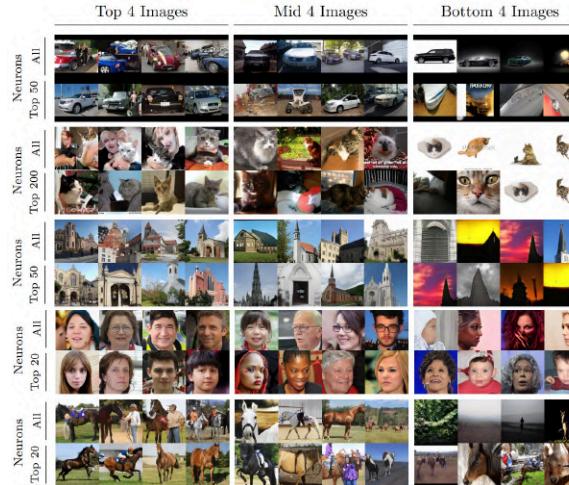


Custom comparison

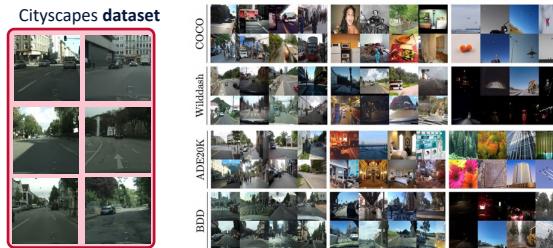


Many applications!

Use neurons focusing on general realism by measuring sensitivity of fake vs real data



Evaluating **realism** of **synthetic** images

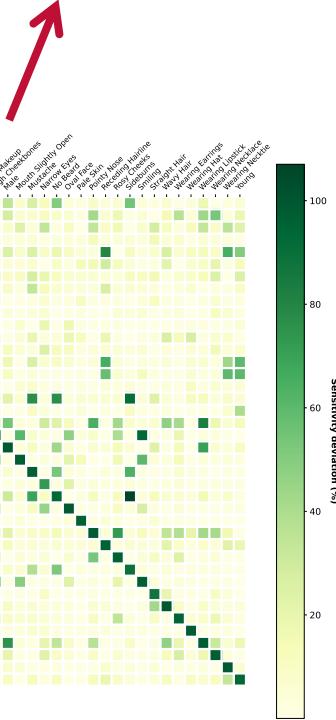


Use all neurons



Retrieving most similar images to a dataset

Optimise a loss to find weights to linearly combine neurons



Comparing datasets while **ignoring selected factors**

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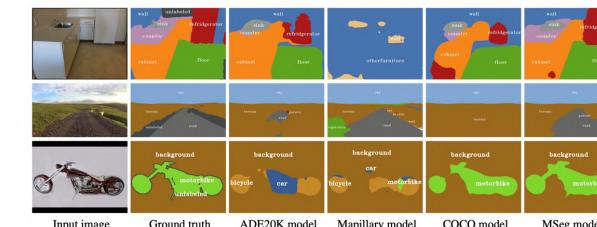


Figure 1: MSeg unifies multiple semantic segmentation datasets by reconciling their taxonomies and resolving incompatible annotations. This enables training models that perform consistently across domains and generalize better. Input images in this figure were taken (top to bottom) from the ScanNet [8], WildDash [44], and Pascal VOC [10] datasets, none of which were seen during training.

Compare DNAs using neurons of the last layer

Predicting transfer learning performance

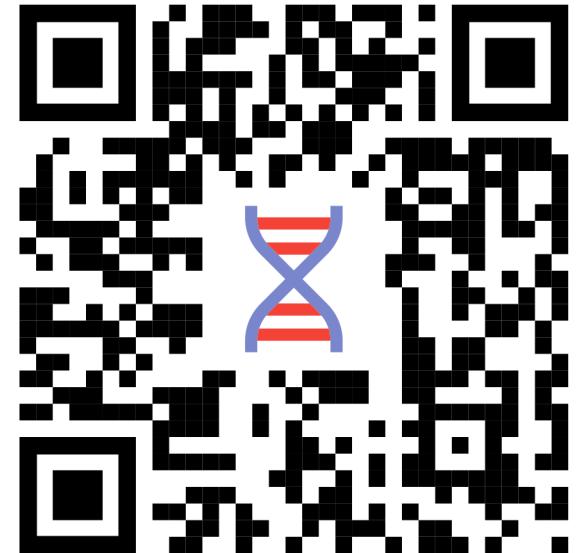
Thank you for your interest!

🔍 Many more details and results in the paper.

💻 Still many applications and extensions to explore!

🐍 If relevant to you, please try it!

```
pip install vdna
```



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Engineering and
Physical Sciences
Research Council

