# Mutual Information measures as a connectivity indicator

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Introduction. Dataset

- Which data?
  - Mice with 2 genotypes, **wild type** (eu) and **trisomic** (ts)

- How?
  - **Neuropixel** high density probes

- Where? **Prefrontal cortex**, with neurons from:
  - Supplementary Motor Cortex (M2)
  - Anterior Cingulate Cortex (AC)
 - PreLimbic Cortex (PrL)
  - InfraLimbic Cortex (IL)
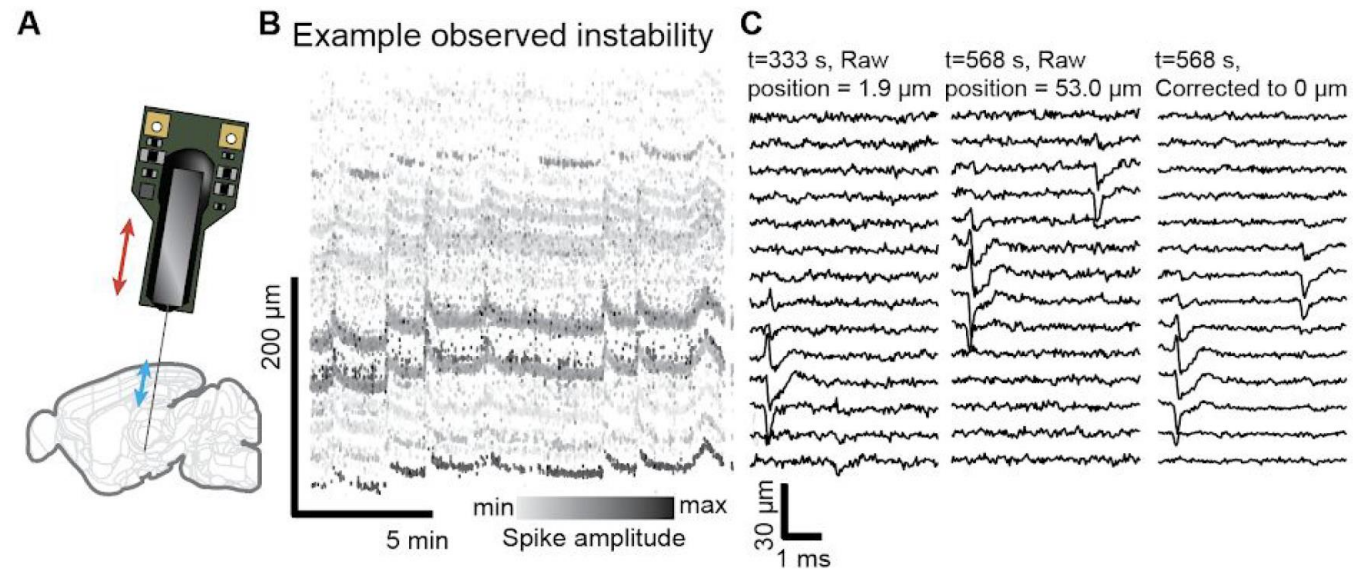
Extracted from **Figure 3** of *Nicholas A. Steinmetz et al.* **, Neuropixels 2.0: A miniaturized high-density probe for stable, long-term brain recordings**.Science, 372,eabf4588(2021).DOI:10.1126/science.abf4588

Introduction. Problem

From the Neuropixels, we can extract the individual neural activity of ~200 recorded neurons and compare it to behavioral variables (locomotion)
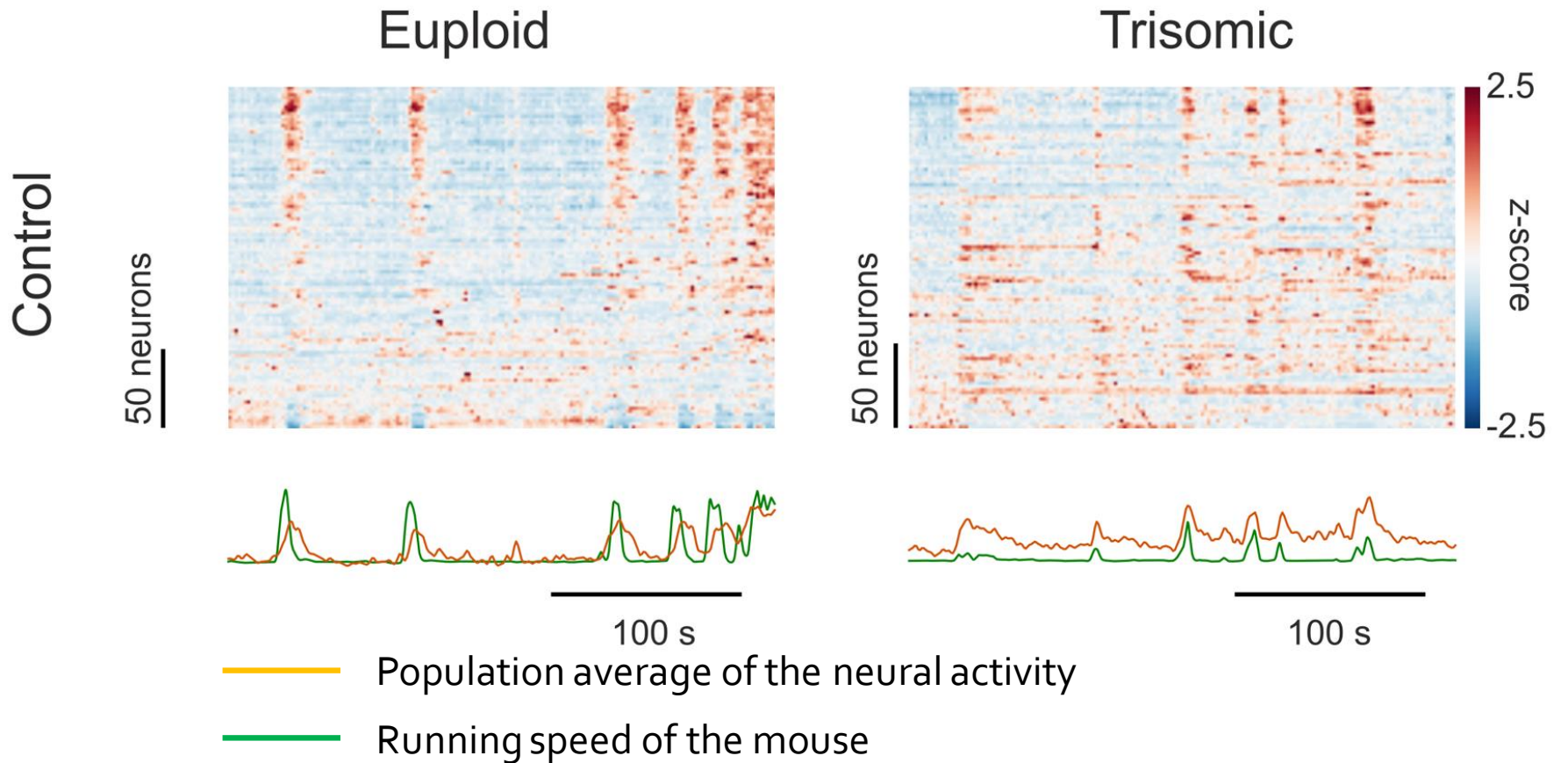

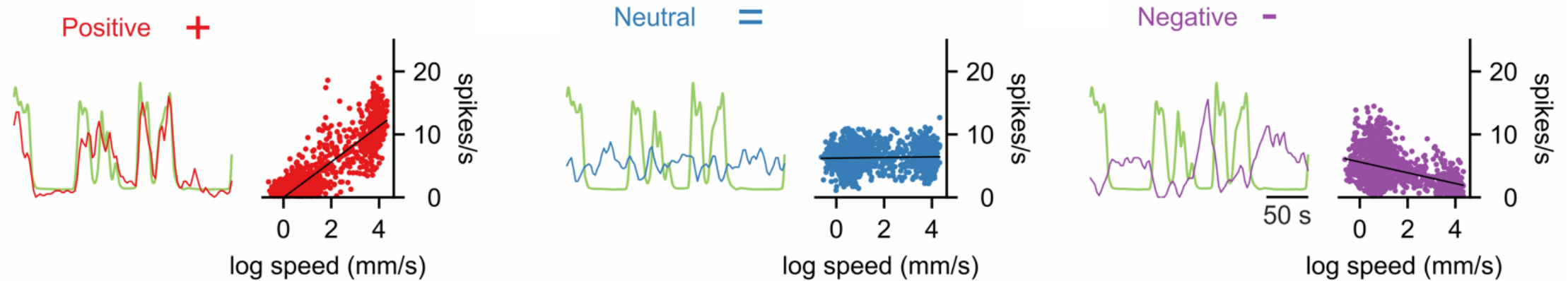Population average of the neural activity

Running speed of the mouse
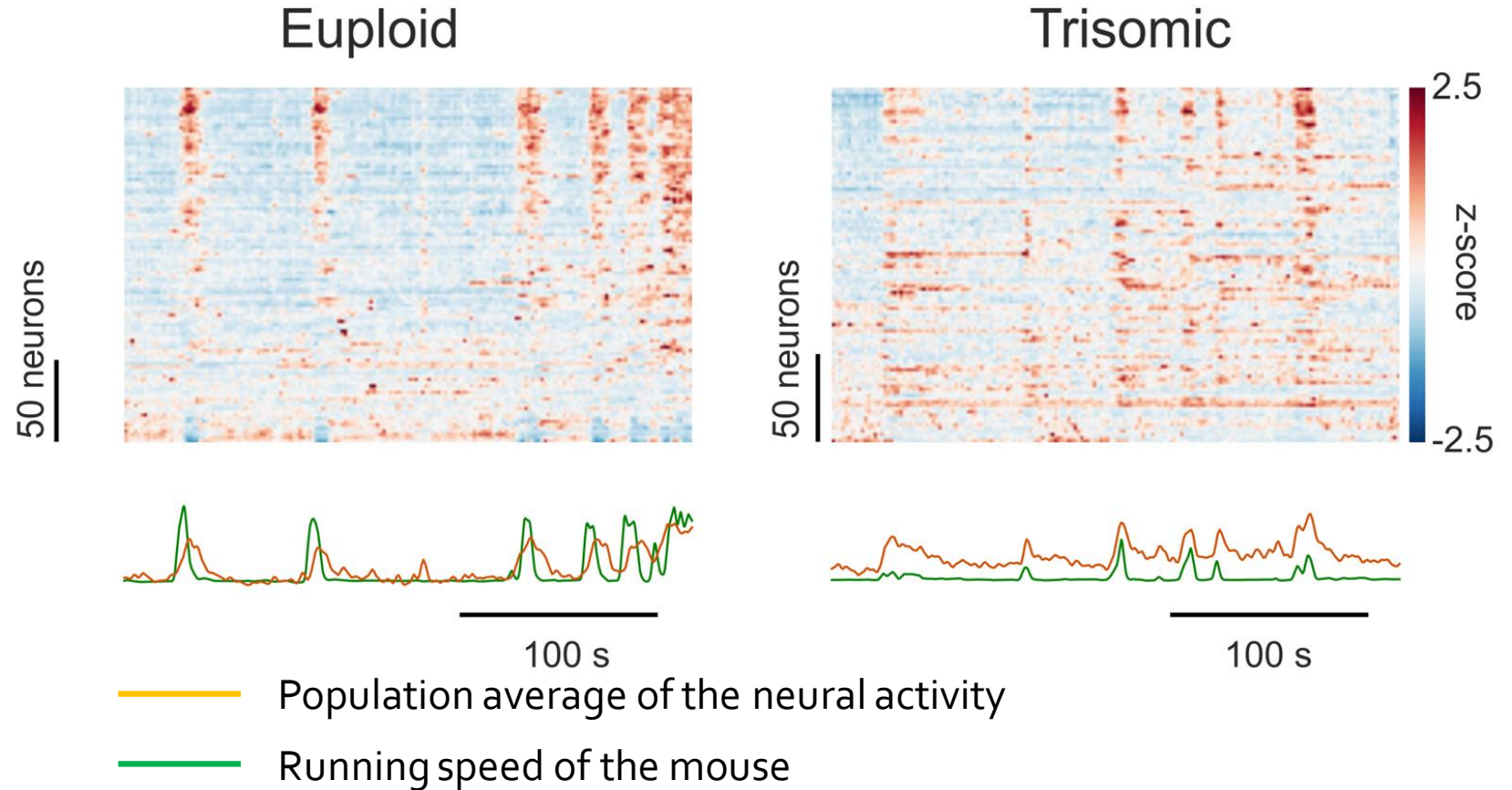
Introduction. Problem

From the Neuropixels, we can extract the individual neural activity of ~200 recorded neurons and compare it to behavioral variables (locomotion)

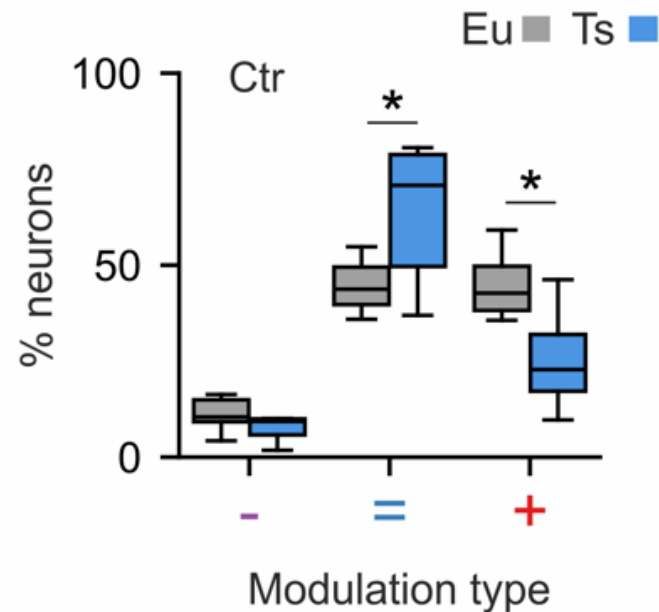Why do the neural activity and locomotion decorrelate in the trisomic mice?

Euploid — Trisomic — Control — 50 neurons — z-score 2.5 to -2.5 — 100 s

— Population average of the neural activity
— Running speed of the mouse

Preliminar results

Attending to this classification, we see the following…

… but can we learn something in this dataset from the network point of view?

Coherence measures

Entropy & Mutual Information

Shannon Entropy

$$H(X) = -\sum p(x) \log_2 p(x) dx$$

$p(x) \equiv$ probability distribution of variable X

- Measures the **uncertainty** in the probability distribution, the more random (uniform) the higher the entropy

- If measured in bits, it also correspond to the number of **yes/no questions** we need to characterize the distribution
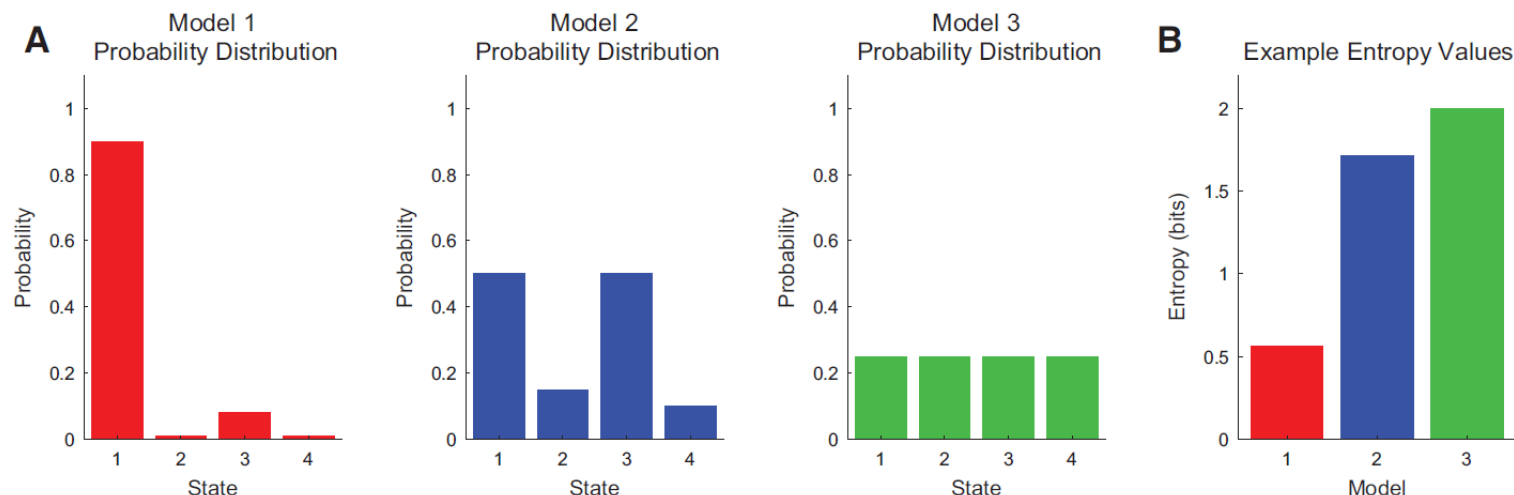
Figure 3. Example entropy calculations. A, Example probability distributions for three models (red, blue, and green); B, their associated entropy values. Model 1 was most likely to be in state 1, so it had low entropy. Model 3 was equally likely to be in all four states, so it had maximum entropy. Uniform count binning (see *Data Binning*) will produce equally likely states and maximize entropy, similar to Model 3.

Entropy & Mutual Information

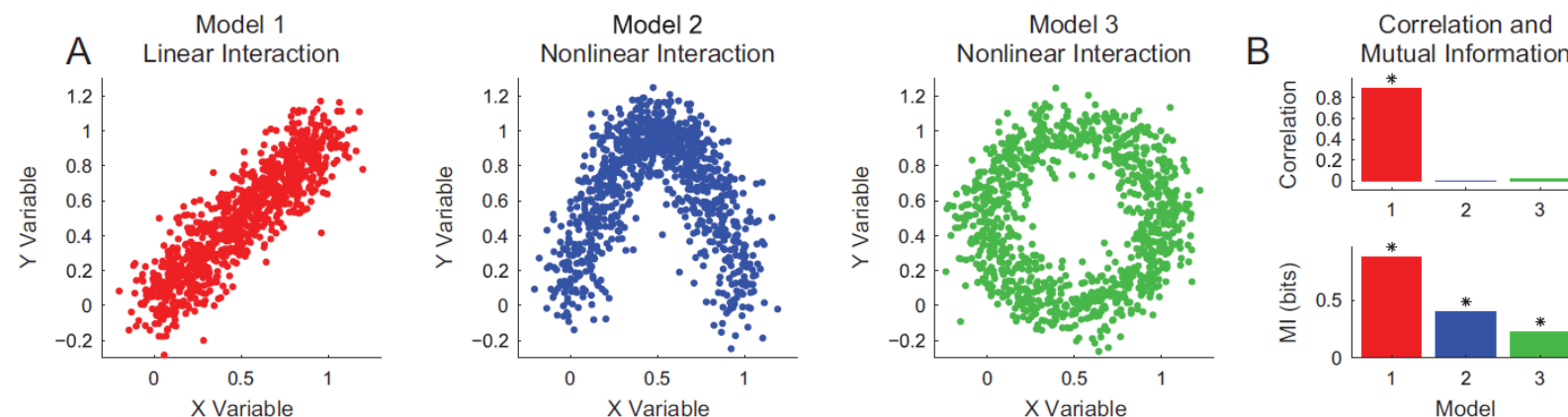**Shannon Entropy**

$$H(X) = -\sum p(x) \log_2 p(x) dx$$

$p(x) \equiv$ probability distribution of variable X

Mutual Information

$$I(X,Y) = H(X) + H(Y) - H(X,Y)$$

$H(X,Y) \equiv$ joint entropy (shared)

- MI tells us the **reduction in uncertainty** that we get in one variable by knowing the other

Figure 5. Example of linear versus nonlinear analysis methods. **A**, Example data for three models (red, blue, and green) with linear (red) and nonlinear (blue and green) interactions; **B**, the associated correlation coefficient and mutual information (MI) values for all three models (star: $p < 0.05$, correlation coefficient and p-value calculated via MATLAB, mutual information and p-value calculated via the Neuroscience Information Theory Toolbox; see *Data Binning and Significance Testing*, 4 bins and 1000 null data sets).

Results

Neuropixels → Spike trains → Continuous time series of spiking rates with time bin Δt → Mutual Information measure between neurons pairs
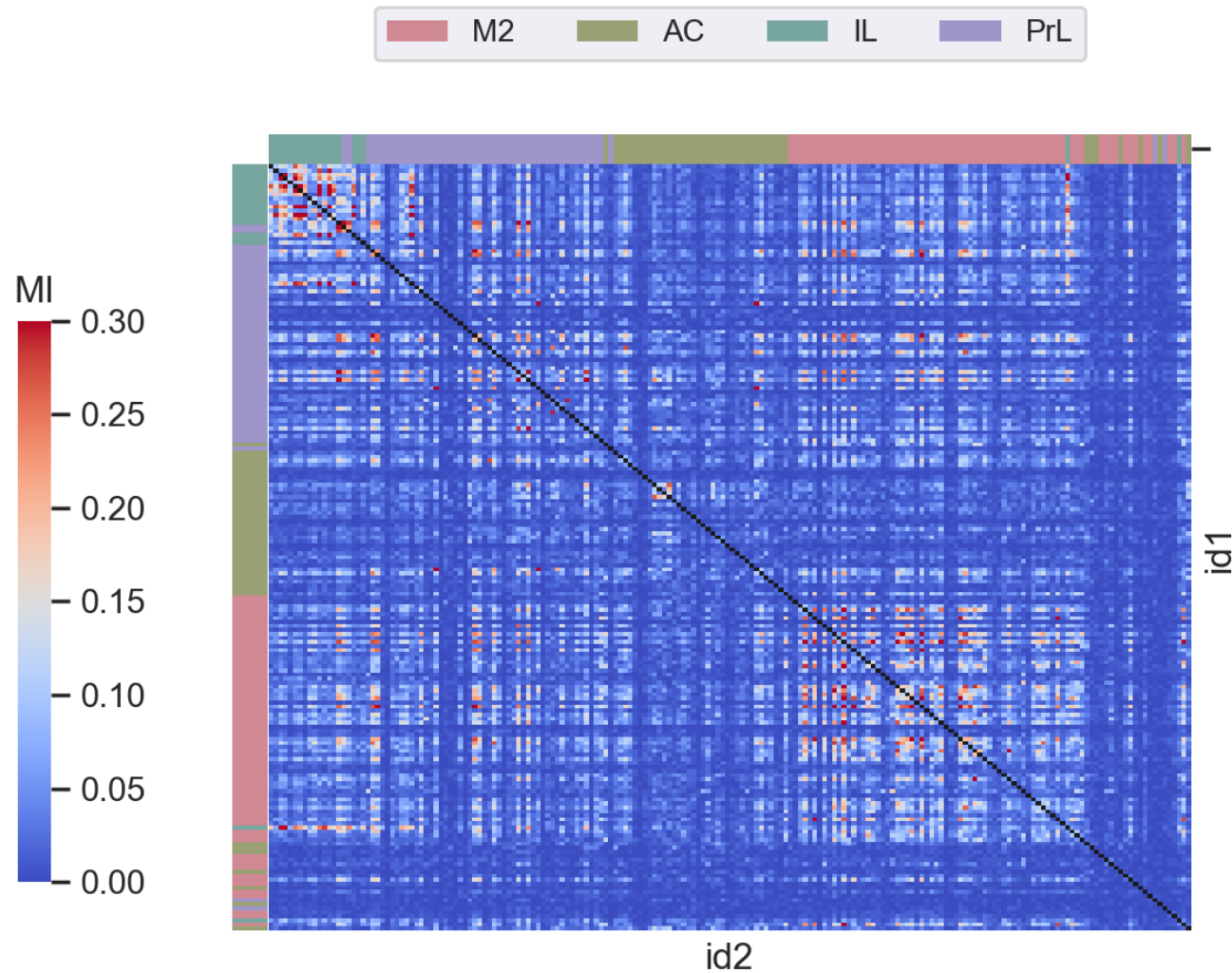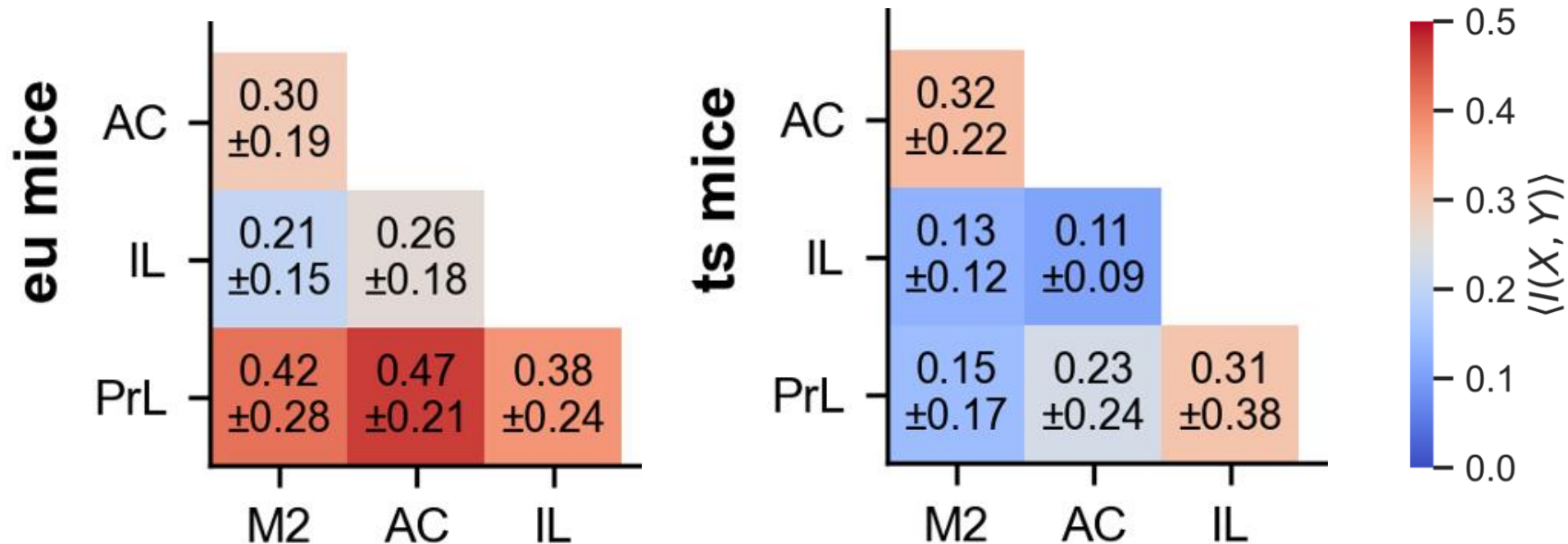
Results

Neuropixels → Spike trains → Continuous time series of spiking rates with time bin Δt → Mutual Information measure between neurons pairs   →   Average between populations and mice

Results

What if we now consider the MI between each population rate instead of single neurons?
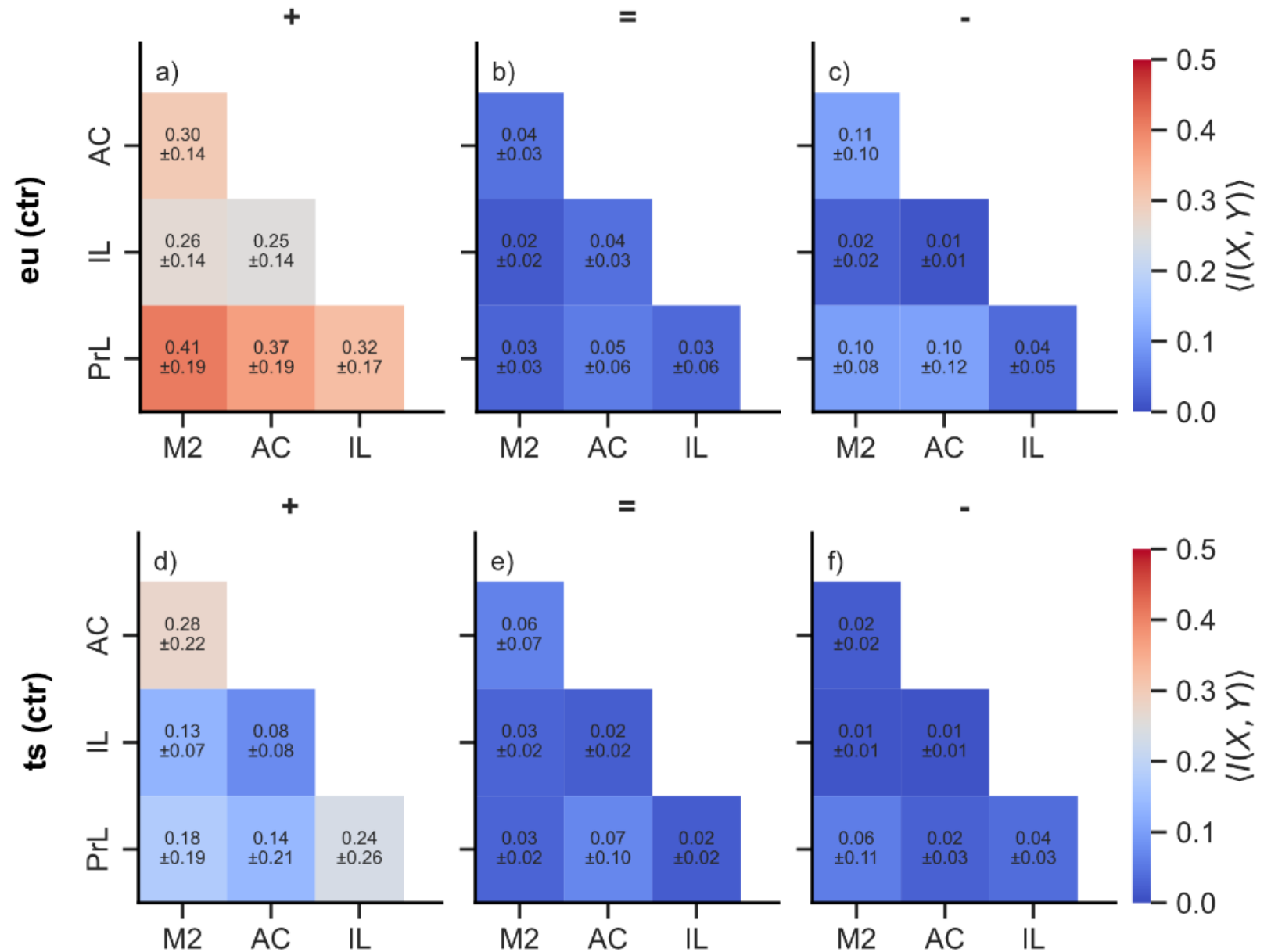

Again, each cell shows the average also across mice (n = 6 for eu, n = 5 for ts)... but still errors are very big, why?

Results

What if we also consider the classification attending to locomotion?

We see that the = and – guys are barely contributing to the encoding, while the + ones encode less

Take home ideas

- Mutual information makes **no assumption** about the data and can help us to reveal **non-linear correlations** and **intricate encoding patterns**

- In our case, it reveals specific connectivity patterns present only at network level and finding loss of coherence in the trisomic genotype

Thanks for your attention! Questions?

Special thanks to,

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