Gaussian Partial Information Decomposition: Quantifying Inter-areal Interactions in High Dimensional Neural Data

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Partial Information Decomposition

PID explains how information about a *message*, M, is represented by two other variables X and Y

$$I\big(M:(X,Y)\big) = \underbrace{UI(M:X\setminus Y)}_{\text{Unique to } X} + \underbrace{UI(M:Y\setminus X)}_{\text{Unique to } Y} + \underbrace{RI(M:X;Y)}_{\text{Redundant}} + \underbrace{SI(M:X;Y)}_{\text{Synergistic}}$$

Note: $UI, SI, RI \geq 0$

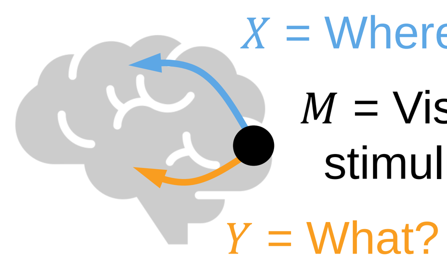
(Williams & Beer 2010; Bertschinger et al. 2014)

Motivating Example

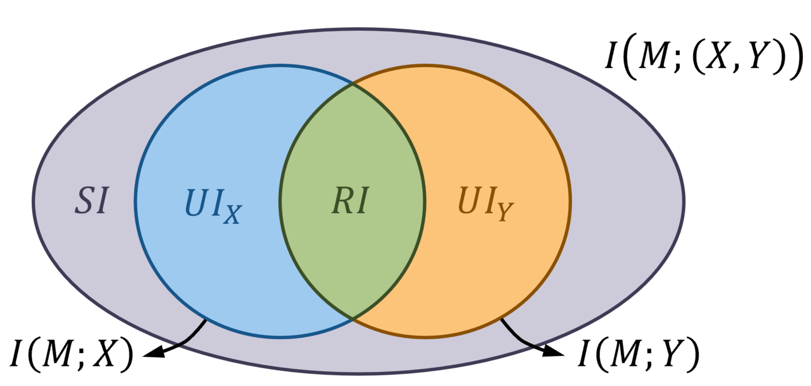
$M = [M_1, M_2, M_3]$

$X = [M_1, M_2, M_3 + Z]$

$Y = [M_2, Z]$



1 bit each of UI in X, RI and SI; 0 bits of UI in Y



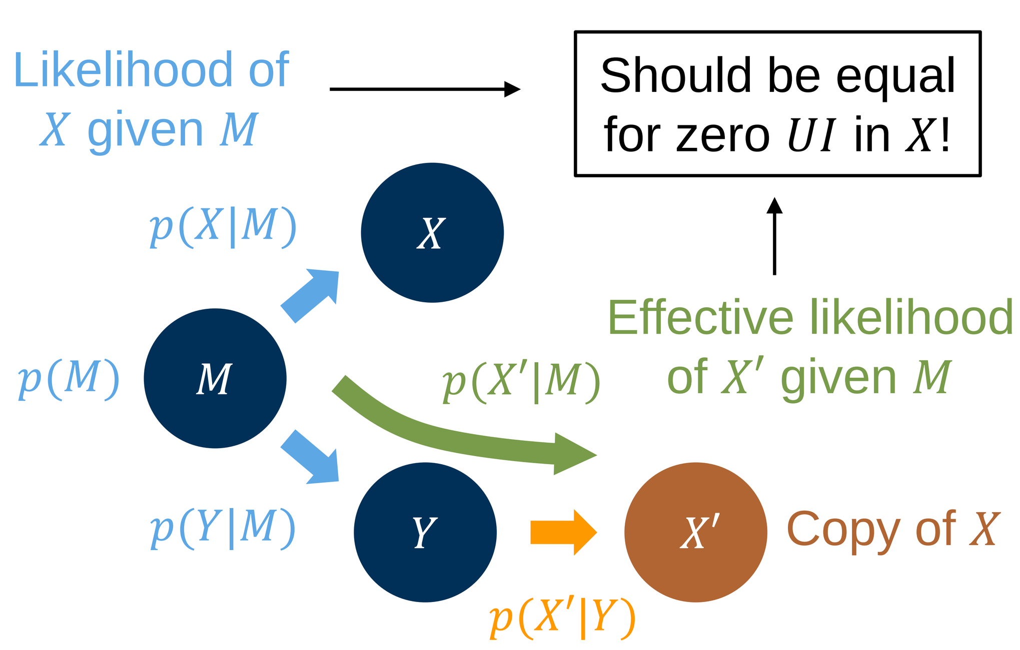
Why use PID? (Schneidman et al. 2003; Pica et al. 2017)

- Measuring redundancy between two brain regions (e.g., testing efficiency of a neural code)
- Can help understand functional organization
- Can help distinguish between different hypotheses about encoding/computation

Quantifying Unique Information

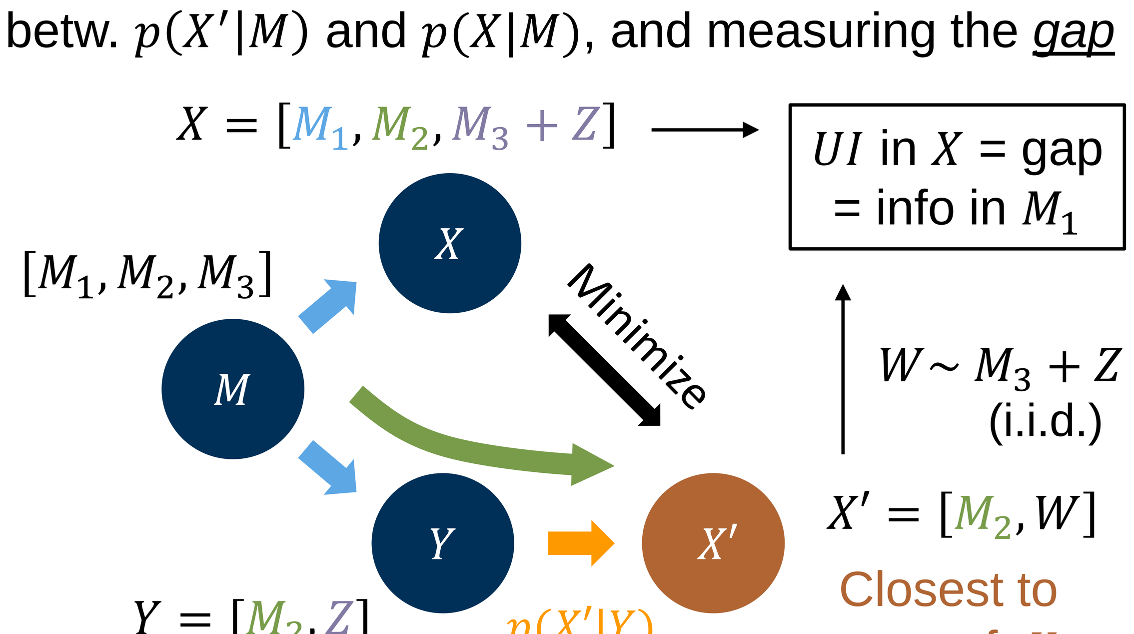
When is Unique Information in X w.r.t. Y zero?

If you can create a "copy" of X (call it X') using Y alone: X' and M should have the same joint statistics as X and M



Transform to create the copy X' from Y

If you cannot create an exact copy, then X has UI w.r.t. Y: quantify it by minimizing the "distance" betw. $p(X'|M)$ and $p(X|M)$, and measuring the *gap*



Gaussian Partial Info Decomposition

Unique information in X:

$$\delta(M : X \setminus Y) = \min_{p(x'|y)} \mathbb{E}_M\big[D_{KL}\big(p(x|M) \,\|\, p(x'|M)\big)\big]$$

Taking M, X and Y to be jointly Gaussian, and parameterizing $p(x'|y)$ using a Gaussian transform:

$$M \sim \mathcal{N}(0, I) \qquad X \mid M \sim \mathcal{N}\big(H_X M, \Sigma_{X|M}\big)$$
$$p(x'|y) = \mathcal{N}(T \cdot y,\ \Sigma_T) \qquad Y \mid M \sim \mathcal{N}\big(H_Y M, \Sigma_{Y|M}\big)$$

$$\delta_G(M : X \setminus Y) = \min_{T, \Sigma_T \succcurlyeq 0} \mathbb{E}_M \,\|(H_X - TH_Y)M\|^2_{TT^T + \Sigma_T} + \mathrm{Tr}\big((TT^T + \Sigma_T)^{-1}\big) + \log\det(TT^T + \Sigma_T) - d_X$$

Approximate solution: (Schamberg & Venkatesh, 2021)

$$\hat{T} = \arg\min_T \mathbb{E}_M \,\|(H_X - TH_Y)M\|^2_{I + H_X H_X^T}$$
$$\text{s.t.} \quad I + H_X H_X^T - T(I + H_Y H_Y^T)T^T \succcurlyeq 0$$

PID vs. Other Techniques

Techniques for measuring "unique explained variance" typically conflate unique and synergistic information:

$$M = \alpha_1 Y + \epsilon_1 \qquad UEV = \mathrm{Var}(\epsilon_2) - \mathrm{Var}(\epsilon_1)$$
$$M = \alpha_2 Y + \beta_2 X + \epsilon_2 \qquad \text{(Conditional info in } X\text{)}$$

PID captures *unique*, not *conditional* information:

$$I(M;X) = UI(M:X\setminus Y) + RI(M:X\,;Y)$$
$$I(M\,;X \mid Y) = UI(M:X\setminus Y) + SI(M:X\,;Y)$$

Accuracy & Speed of Gaussian PID

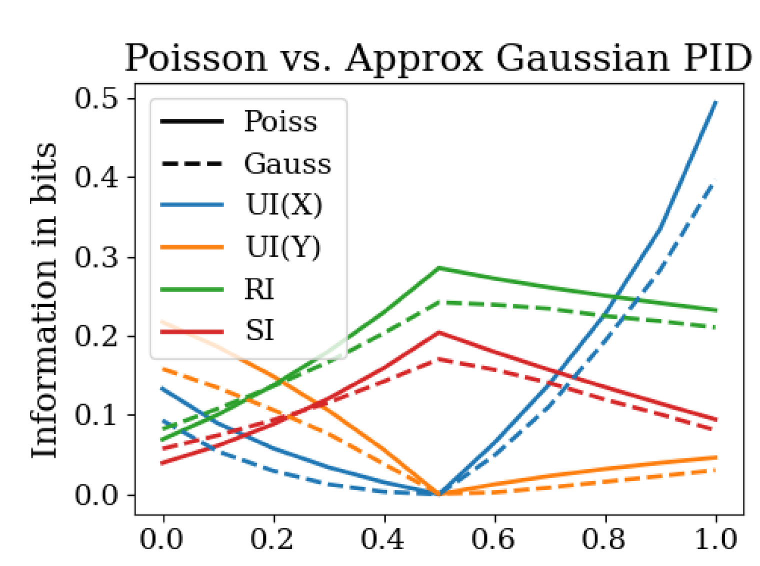
- First available method for computing this definition: how do you evaluate?
- Relatively few estimators / computation methods of other "good" PID definitions

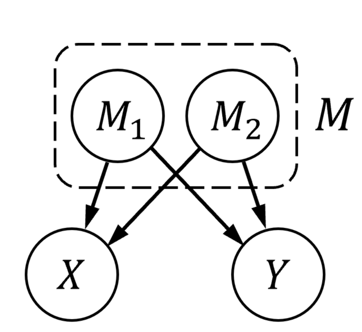
(Bertschinger et al. 2014; Banerjee et al. 2018)

Accuracy

Compare with Bertschinger et al. PID for discrete variables: approximate a multivariate Poisson as Gaussian using its joint covariance matrix

$$M_1, M_2 \sim \mathrm{Poiss}(\lambda_M)$$
$$X \sim \mathrm{Bin}(M_1, w_{X1}) + \mathrm{Bin}(M_2, w_{X2}) + \mathrm{Poiss}(\lambda_X)$$
$$Y \sim \mathrm{Bin}(M_1, w_{Y1}) + \mathrm{Bin}(M_2, w_{Y2}) + \mathrm{Poiss}(\lambda_Y)$$





Values and trends of the two methods are consistent

Speed

No. of convex optimization variables (complexity):

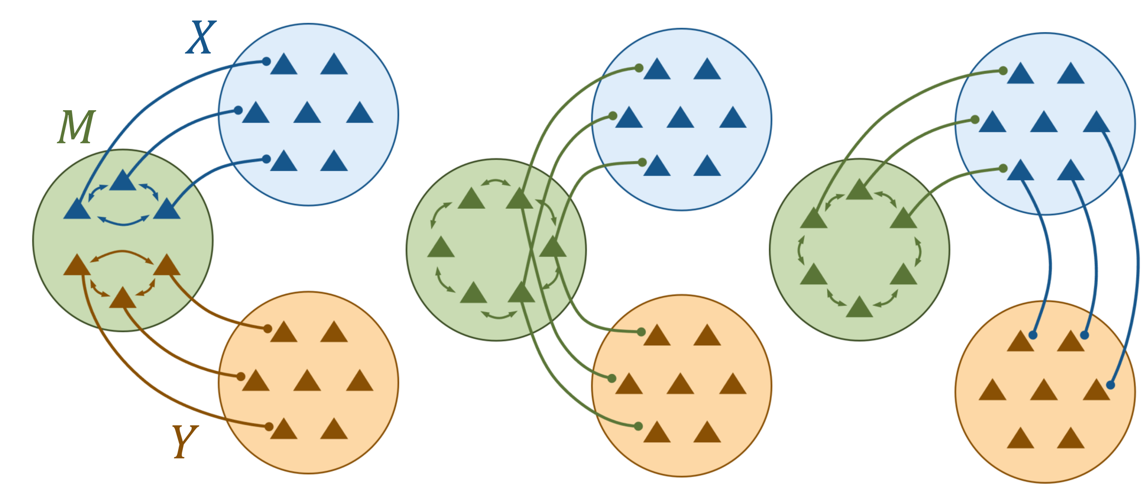
Bertschinger et al.: $O(K^d)$ $\quad d$ = Dimensionality

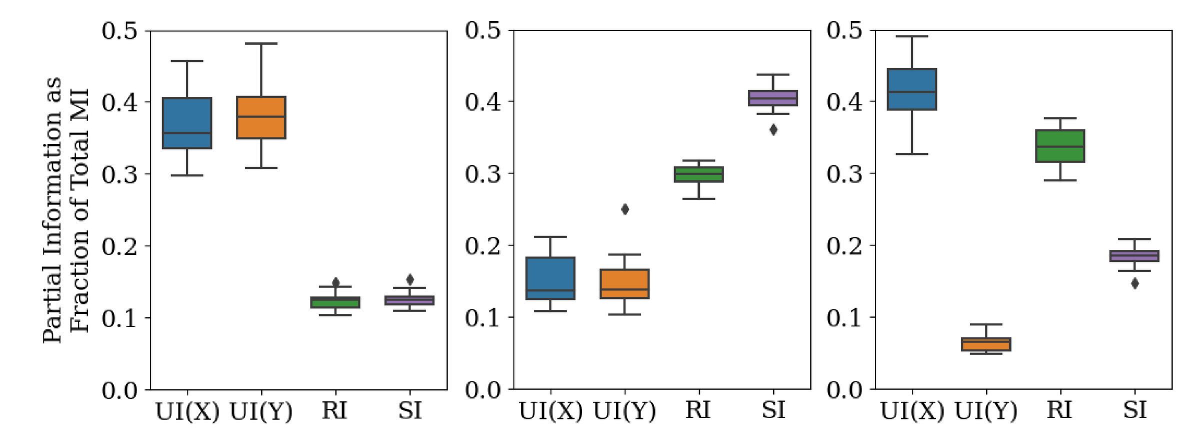
Ours: $O(d^2)$ $\quad K$ = support of p_{MXY}

Simulation with Spiking Neurons

Simulate spiking neurons with different connectivity architectures and examine PID profiles

- Three groups of 20 neurons each, interconnected as shown below (Katselis et al. 2016)
- Covariance matrices computed on short windows of random spiking activity
- Approximate Gaussian PID values computed from covariances



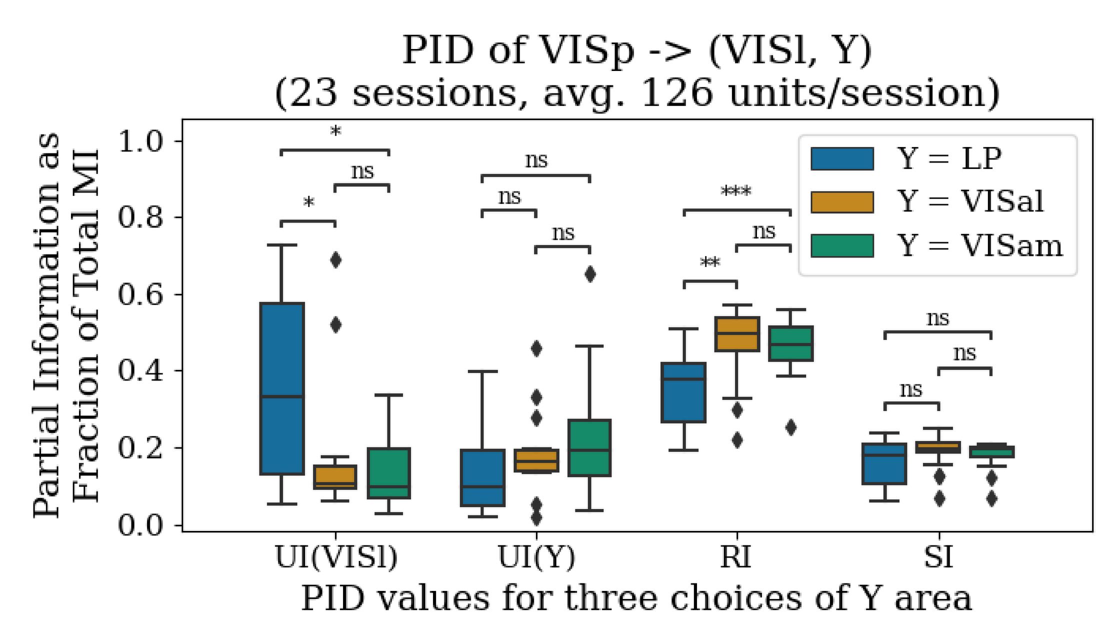


Interactions between Visual Areas

Allen Institute Visual Coding Neuropixels dataset

(Siegle et al. 2021: https://portal.brain-map.org/explore/circuits/visual-coding-neuropixels)

Measure PID profiles between three sets of mouse visual brain areas: 1. (VISp, VISl, LP), 2. (VISp, VISl, VISal) and 3. (VISp, VISl, VISam)



More unique info in VISl in (1); more redundant info between VISl and VISal/am in (2) and (3)

Hypothesis: VISp is less strongly connected with subdomains of LP targeted in this dataset, compared to connections between VISp and VISal or VISam.

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