

Feature Engineering for Graph-based Analysis of Recurrent Behavior in Biosignal Ensembles

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*“More data beats clever algorithms,
but **better data** beats more data”*

Peter Norvig
Director of Research @ Google

*“Coming up with features is difficult, time-consuming
requires **expert knowledge**.
“Applied ML” is basically feature engineering”*

Andrew Ng
Founder of DeepLearning.AI



Outline

- Machine Learning workflow
- Feature Engineering
- Biosignal Analysis: Domain knowledge
 - Graph representations
- Target Application #1: Detection of epileptic seizures (:: exploit statistics)
 - Alpha-stable models
 - Graph filtering
- Target Application #2: Classification of NPSLE patients (:: exploit recurrence)
 - Recurrence quantification analysis
- Conclusions

ML workflow

The dream...



Raw data



Dataset



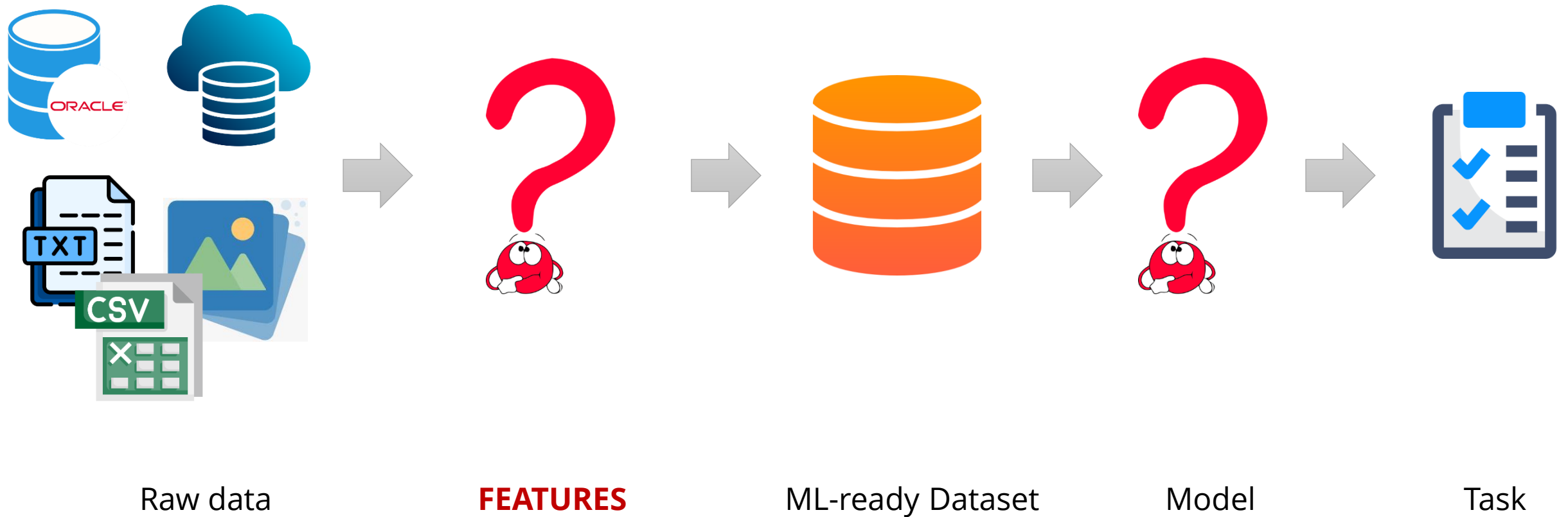
Model



Task



ML workflow

The reality...



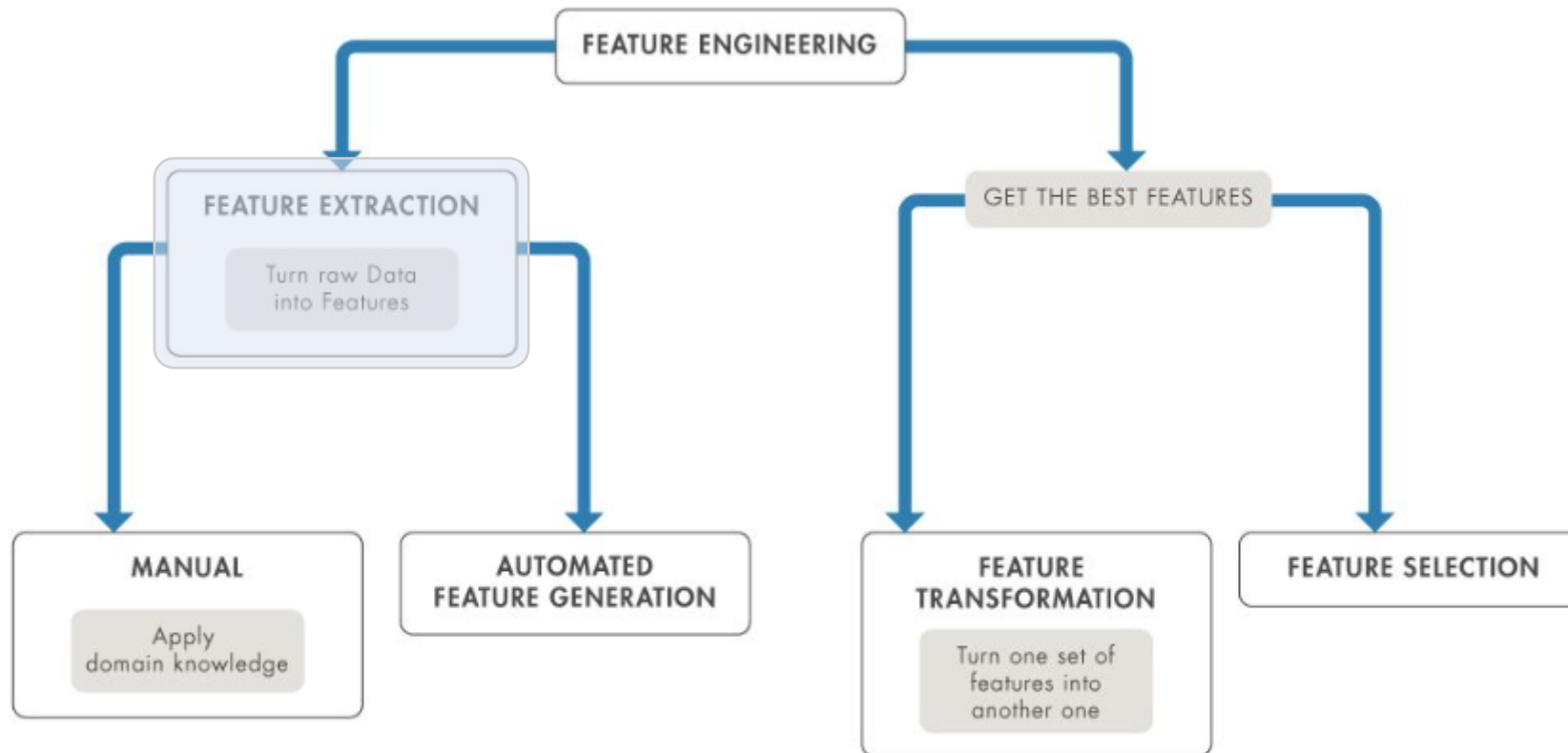
Feature engineering (FE)

*“FE is the process of turning raw data into features that **better represent** the underlying problem to the models, resulting in improved model accuracy on unseen data”*

-  FE is difficult since extracting features from signals requires **deep domain knowledge**
-  Finding the best features fundamentally remains an **iterative process**, even if we apply automated methods

Feature engineering (FE)

FE encompasses one or more of the following steps:



Feature engineering (FE)

Manual vs Automated Feature Extraction

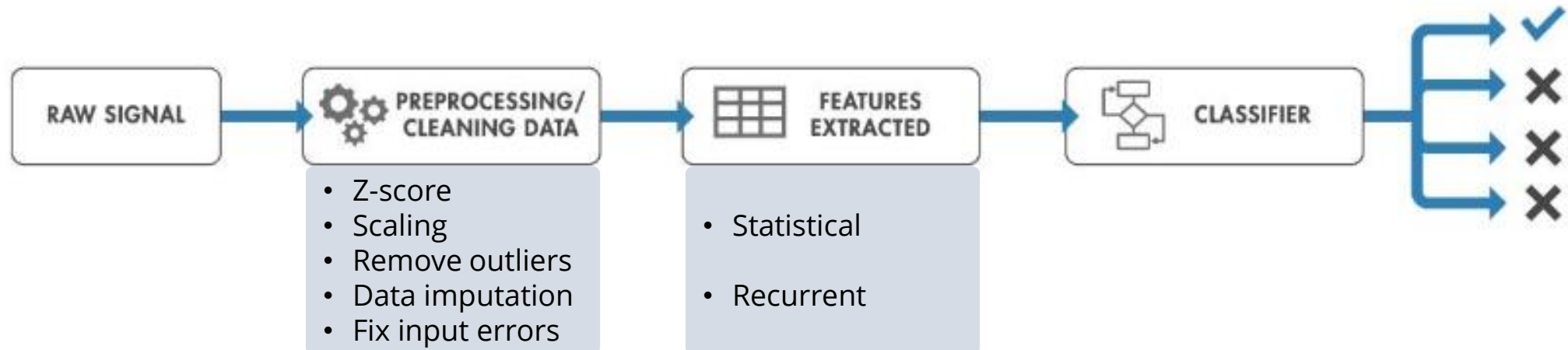
- **Manual:** generate features that are relevant for a given problem (e.g. mean of a signal window); Good understanding of the background or **domain** is a big plus
- **Automated:** use specialized algorithms or deep networks to extract features automatically from signals; Useful to move quickly from raw data to developing ML algorithms

Images vs Time Series Feature Extraction

- **Images:** it has been largely replaced by the first layers of deep networks
- **Time series:** it remains the first **challenge** that requires significant expertise

Feature extraction for time series

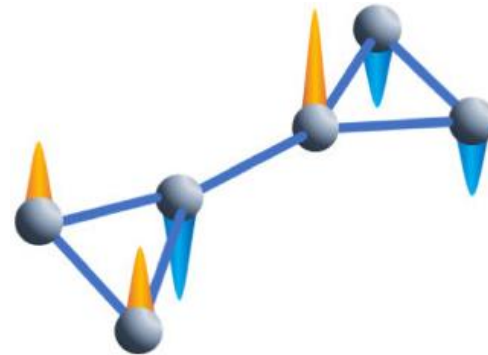
- Feature extraction identifies the most **discriminating characteristics** in signals, which a ML/DL algorithm can more easily consume
- ML/DL training directly with raw signals often yields poor results because of the **high data rate** and **information redundancy**



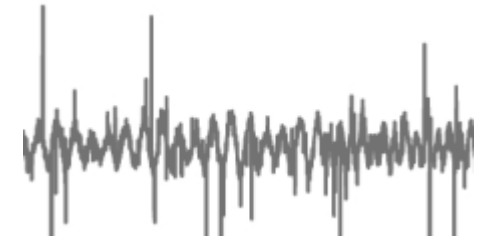
Biosignal Analysis: Domain knowledge



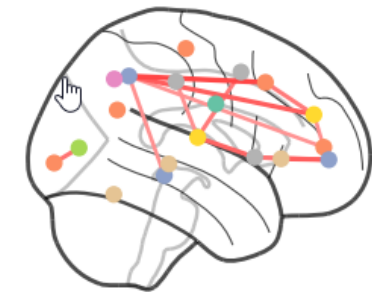
EEG signal ensembles



Graph representation

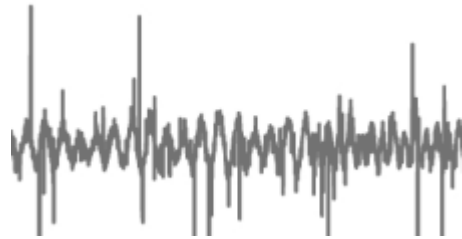


Impulsive noise

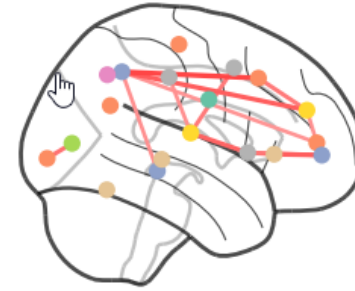


Dynamic connectivity

Biosignal Analysis: Domain knowledge



Impulsive noise



Dynamic connectivity

Alpha-Stable
Graph Filtering

Recurrence
Quantification
Analysis

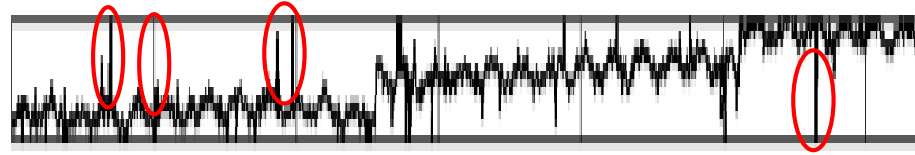
Target App #1

Detection of epileptic seizures

[Joint work w/ Dr. Anastasia Pentari]

Impulsive noise

- EEG signals are often corrupted by **impulsive** noise (e.g. electronic equipment, subject motion, etc.) (ref. [1])



- Denoising is a critical issue; significant “peaky” patterns must be preserved
- Noise part is often characterized by non-Gaussian (**heavy-tailed**) statistics
- Existing methods:
 - Per-signal filtering (Wavelet-based, ICA-based, etc.)
 - Better adapt to Gaussian noise statistics
- Exploit graph structure of EEG signal to account for intra-/inter-channel dependencies \Rightarrow **Graph filters**
 - L2-based formulation (2nd order moments)

Graph representation of EEG signals

- Signal model w/ additive observation noise

Data matrix

$$\mathbf{X} = [\mathbf{x}_1, \dots, \mathbf{x}_N] \in \mathbb{R}^{N \times K}$$

i-th electrode's signal

samples/electrode

electrodes

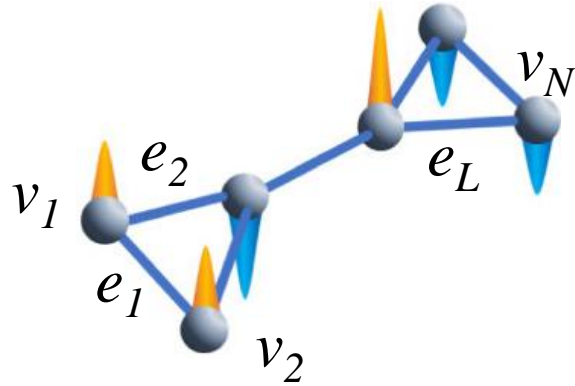
$$\mathbf{X} = \mathbf{S} + \mathbf{W}$$

Noiseless data matrix

Noise term

Graph representation of EEG signals

- Graph representation



$$\mathbf{X} = \mathbf{S} + \mathbf{W}$$



$$G = (V, E)$$

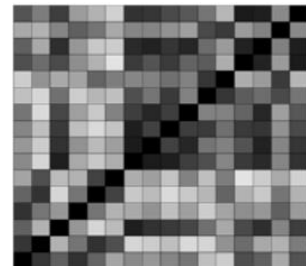
Adjacency matrix

(capture interrelations among the nodes)

$$\mathbf{A} \in \mathbb{R}^{N \times N}$$

- Correlation matrix \mathbf{A} (descriptor of brain's functional connectivity)

Weighted undirected
network



Thresholding



Unweighted undirected
network



Alpha-stable models

- Powerful tool in accurately modelling impulsive phenomena (e.g. medical imaging, communications, finance, etc.)
- Lack of closed-form expressions for the pdf (except for Gaussian, Cauchy and Lévy)
- Modelling signal statistics via **symmetric alpha-stable** (SaS) distributions

$\mathbf{X} = \mathbf{S} + \mathbf{W}$

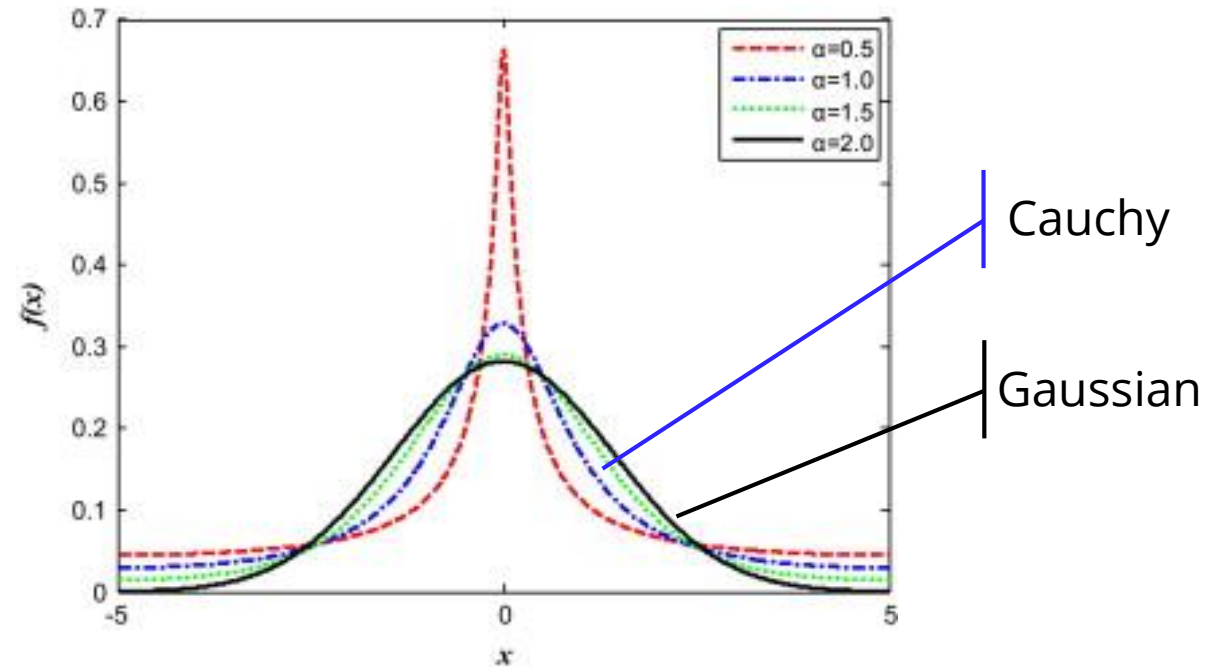
$f_{\alpha}(x; \gamma, \delta) = \frac{1}{\gamma} h\left(\frac{x - \delta}{\gamma}; \alpha\right)$

$h(x; \alpha) = \frac{1}{\pi} \int_0^{\infty} \cos(xt) e^{-t^{\alpha}} dt$

Model parameters	
$\alpha \in (0, 2]$	characteristic exponent
$\gamma > 0$	dispersion
$\delta \in \mathbb{R}$	location

Alpha-stable models

- Examples of SaS distributions



- Max Likelihood estimation of model parameters; reliable, tightest possible confidence intervals (ref. [2])

Alpha-stable models

- All moments of order $p < \alpha$ exist; **Fractional lower order moments** (FLOMs)

$$X \sim f_\alpha(\gamma, \delta = 0) \quad \Rightarrow \quad \mathbb{E}\{|X|^p\} = (C(p, \alpha) \cdot \gamma)^p, \quad 0 < p < \alpha$$

$$(C(p, \alpha))^p = \frac{\Gamma\left(1 - \frac{p}{\alpha}\right)}{\cos\left(\frac{\pi}{2}p\right)\Gamma(1-p)}$$

- Quantify degree of dependence between two SaS variables X, Y , via the **covariation** (analogue of covariance)

$$[X, Y]_\alpha = \frac{\mathbb{E}\{XY^{\langle p-1 \rangle}\}}{\mathbb{E}\{|Y|^p\}} \gamma_Y^\alpha$$

$$z^{\langle a \rangle} = |z|^a \text{sign}(z)$$

Discrete case: FLOM-based covariation estimator

$$c_{ij}^{\text{FLOM}} = \frac{\sum_{k=1}^K x_{i,k} |x_{j,k}|^{p-1} \text{sign}(x_{j,k})}{\sum_{k=1}^K |x_{j,k}|^p} \gamma_{\mathbf{x}_j}^\alpha, \quad \mathbf{x}_i, \mathbf{x}_j \in \mathbb{R}^K$$

Alpha-stable models

- FLOM-based adjacency matrix (non-negative, symmetric)

$$\mathbf{A}_i = \frac{|\mathbf{C}_{\text{FLOM}}| + |\mathbf{C}_{\text{FLOM}}^T|}{2}$$

- **Note:** selection of an appropriate FLOM order, p , is critical towards better adapting to the underlying degree of impulsiveness
- Calculate p as a function of α , by minimizing the std of the FLOM-based covariation estimator (ref. [3])
 - **Convention:** the optimal p value is the mean over all channels

α	1	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2
p_{opt}	0.52	0.56	0.58	0.61	0.64	0.69	0.72	0.76	0.81	0.88	0.98

$$p \lesssim \alpha/2$$

Graph filtering as Lp-regularized optimization

- Existing formulation: L2-optimization regularized by graph total variation (ref. [4])

$$\hat{\mathbf{S}} = \underset{\mathbf{S} \in \mathbb{R}^{N \times K}}{\operatorname{argmin}} \left\{ \underbrace{\frac{1}{2} \|\mathbf{S} - \mathbf{X}\|_2^2}_{\text{Data fidelity term}} + \frac{1}{2} b \underbrace{\|\mathbf{S} - \mathbf{A}\mathbf{S}\|_2^2}_{\text{Smoothness term}} \right\}$$

↓

$$\hat{\mathbf{S}} = (\mathbf{I} + b(\mathbf{I} - \mathbf{A})^H(\mathbf{I} - \mathbf{A}))^{-1} \mathbf{X}$$

- Limitation:** 2nd order moments inappropriate for SaS models

Graph filtering as L_p-regularized optimization

- **Our scope:** Suppress the effects of heavy-tailed impulsive noise \Rightarrow Employ L_p (quasi)norms ($p < 2$); direct relation with FLOMs

$$\mathbb{E} \{|X|^p\} \simeq \lim_{N \rightarrow \infty} \frac{1}{N} \sum_{t=1}^N |x_t|^p = \lim_{N \rightarrow \infty} \frac{1}{N} \|\mathbf{x}\|_p^p$$

$$\hat{\mathbf{S}} = \operatorname{argmin}_{\mathbf{S} \in \mathbb{R}^{N \times K}} \left\{ \frac{1}{2} \|\mathbf{S} - \mathbf{X}\|_p^p + \frac{1}{2} b \|\mathbf{S} - \mathbf{A}\mathbf{S}\|_p^p \right\}$$

Data fidelity term

Smoothness term

- **Challenge:** Highly non-convex problem; singularity of gradient

Graph filtering as Lp-regularized optimization

- Use Lp,ε approximation of Lp (quasi)norm $\|\mathbf{x}\|_{p,\epsilon}^p = \sum_{j=1}^N (|x_j|^2 + \epsilon)^{p/2}$

$$\hat{\mathbf{S}} = \underset{\mathbf{S} \in \mathbb{R}^{N \times K}}{\operatorname{argmin}} \underbrace{\left\{ \frac{1}{2} \|\mathbf{S} - \mathbf{X}\|_{p,\epsilon}^p + \frac{1}{2} b \|\mathbf{S} - \mathbf{A}\mathbf{S}\|_{p,\epsilon}^p \right\}}_{Q_3}$$

- **Final implementation:** joint iterative reweighted least squares (IRLS) & Lp,ε
 - Better preserves both low- and high-amplitude EEG samples

Graph filtering as Lp-regularized optimization

- 1: **Inputs:** \mathbf{X} , \mathbf{A} , I_{max} , b , ε
- 2: **Outputs:** $\hat{\mathbf{S}}$
- 3: **Initialization:** $\mathbf{S}^{(0)} = \mathbf{X} + \varepsilon$

- 4: **for** $t = 1:I_{max}$ **do**
- 5: **for** $k = 1:K$ **do**
- 6: $\mathbf{r} = \mathbf{S}(:, k)^{(t)} - \mathbf{X}(:, k)$
- 7: $\mathbf{w} = |\mathbf{r} + \varepsilon|^{(p-2)/2}$
- 8: $\mathbf{D} = \text{diag}(\mathbf{w})$
- 9: $\mathbf{S}(:, k)^{(t)} = ((\mathbf{D}^2 + b(\mathbf{I} - \mathbf{A})^H(\mathbf{I} - \mathbf{A}))^{-1}\mathbf{D}^2) \mathbf{X}(:, k)$
- 10: **end for**
- 11: $\mathbf{S}^{(t+1)} = \mathbf{S}^{(t)} + \left(\nabla^2 Q_3(\mathbf{S}^{(t)})\right)^{-1} \nabla Q_3(\mathbf{S}^{(t)})$
- 12: **end for**
- 13: $\hat{\mathbf{S}} = \mathbf{S}^{(I_{max})}$

Experimental evaluation

- **Test case 1:** Synthetic noise of varying impulsiveness added to “noise-free” EEG ensembles
 - 32-channel EEGs
 - $\alpha \in \{1.1:0.3:2\}$, $\gamma = 1$
 - 100 Monte Carlo runs; results averaged over all channels and MC runs
 - Performance metrics

$$\text{SER}(\mathbf{s}, \hat{\mathbf{s}}) = 10 \log_{10} \left(\frac{\|\mathbf{s}\|_2^2}{\|\mathbf{s} - \hat{\mathbf{s}}\|_2^2} \right)$$

$$\text{SSIM}(x, y) = \frac{(2\mu_x\mu_y + c_1)(2\sigma_{xy} + c_2)}{(\mu_x^2 + \mu_y^2 + c_1)(\sigma_x^2 + \sigma_y^2 + c_2)}$$

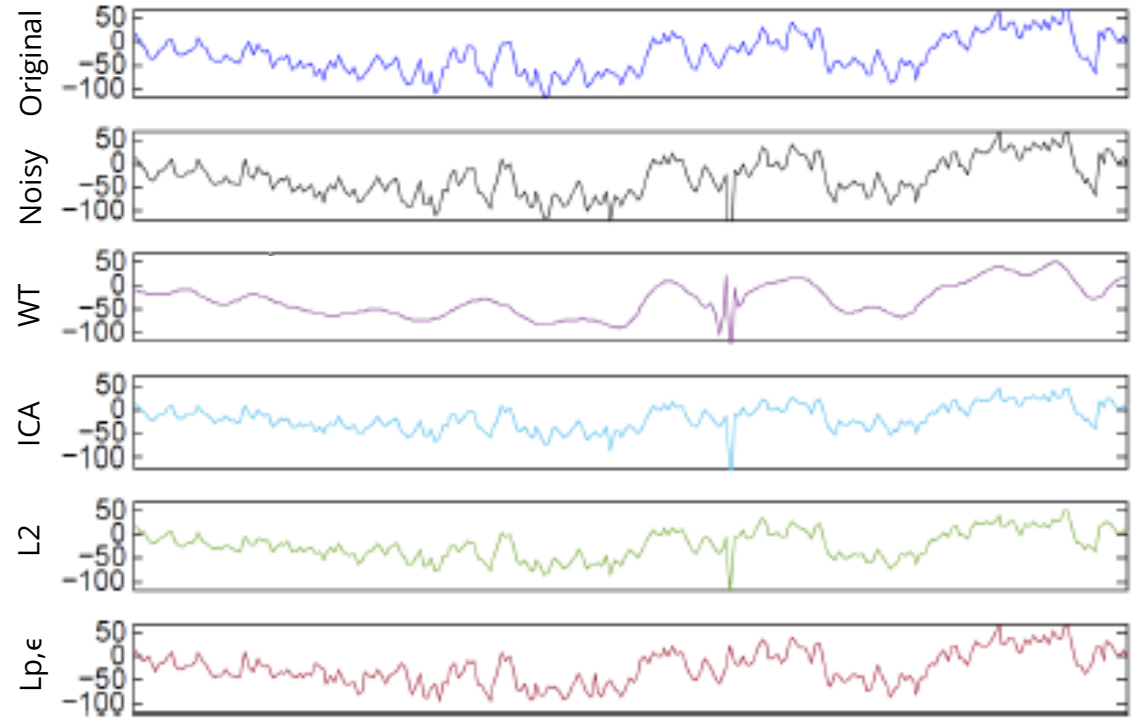
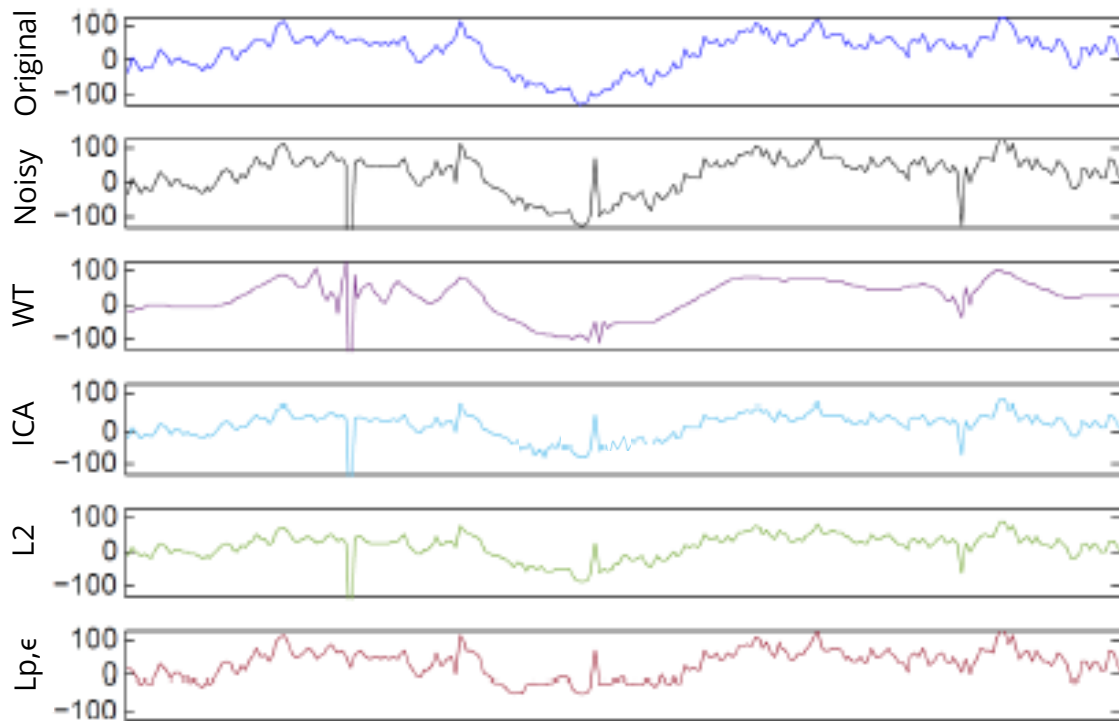
$$c_1 = (k_1 L)^2$$

$$c_2 = (k_2 L)^2$$

$$L = 100, \quad k_1 = k_2 = 0.05$$

Experimental evaluation

- **Test case 1:** Synthetic noise of varying impulsiveness added to “noise-free” EEG ensembles



Experimental evaluation

- **Test case 2:** Filtering of raw data followed by a **classification** task
 - 32-channel EEGs; ground truth (noise-free) signals are unknown
 - 15 “normal” subjects (non-epileptic), 15 “abnormal” subjects (epileptic)
 - Non-overlapping windows of length 256 are selected for each subject
 - 3 filtering methods: “WT”, “L2”, “Lp,ε”
 - 5 features: {mean, std, mean($\pm 10\%$ · max_ampl), min_ampl, max_ampl}
 - kNN classifier (2/3 training, 1/3 testing subjects); majority voting to identify the dominant class of each testing subject’s windows

Model parameters

WT	L2	Lp,ε
db8	$b = 0.01$	$b = 0.1$
2-level		$\varepsilon = 0.01$
		$I_{max} = 10$

Experimental evaluation

- **Test case 2:** Filtering of raw data followed by a **classification** task

Classification accuracy

A	Original	WT	L2	Lp,ε
-	50%	50%		
Correlation			60%	
Covariation				90%

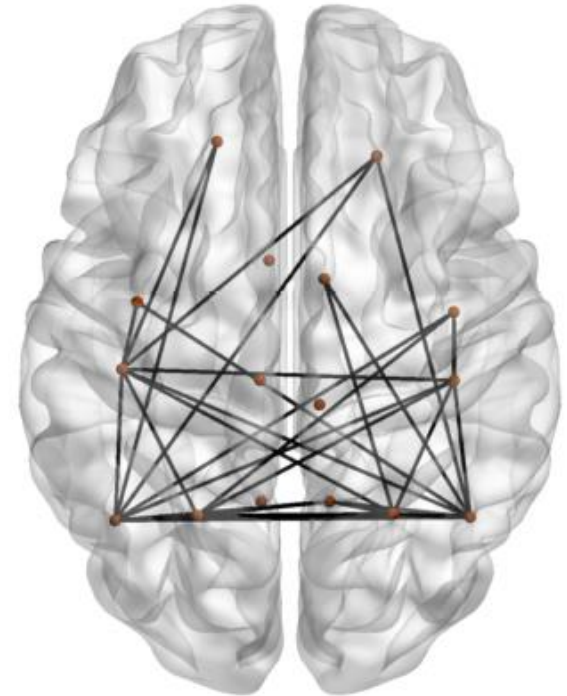
Target App #2

Classification of NPSLE patients

[Joint work w/ Prof. Akis Simos (Evolutionary Neuropsychology) and Dr. Anastasia Pentari]

Brain functional connectivity

- Brain function is highly dynamic \Rightarrow Assessing functional associations in neurophysiological activity between two or more brain regions is challenging
- Associations as evidence of **functional connectivity** (FC) between regions
- fMRI studies: measure temporal variations in brain activity
- **Limitations:** non-stationary behavior of brain signals is not accounted for; predictability of the signal recorded in one brain region is not captured from the signal recorded in other regions
- **Hypothesis:** brain signals are characterized by the phenomenon of **recurrence**, i.e., similar situations of a dynamic system should evolve in a similar manner



Clinical test case

- Neuropsychiatric systemic lupus erythematosus (NPSLE): disorder that is characterized by a variety of neuropsychiatric symptoms in the absence of remarkable brain injuries
- **Idea:** capture **recurrent** dynamic characteristics of rs-fMRI time series, which could serve as complementary indices of functional connectivity
- We adopt a Region-of-Interest (ROI) approach focusing on abnormal dynamic connectivity between 16 frontoparietal regions (eight in each hemisphere)
- Participants: 45 patients diagnosed with NPSLE (Rheumatology outpatient clinic, University Hospital of Heraklion), 35 age-matched and gender-matched healthy volunteers

Recurrence quantification analysis



Develop advanced techniques for extracting and characterizing the inherent **complex dynamic structures** apparent in scientific data



Recurrence is a fundamental feature of nonlinear dynamical systems
It is a time the trajectory returns to a location it has visited before

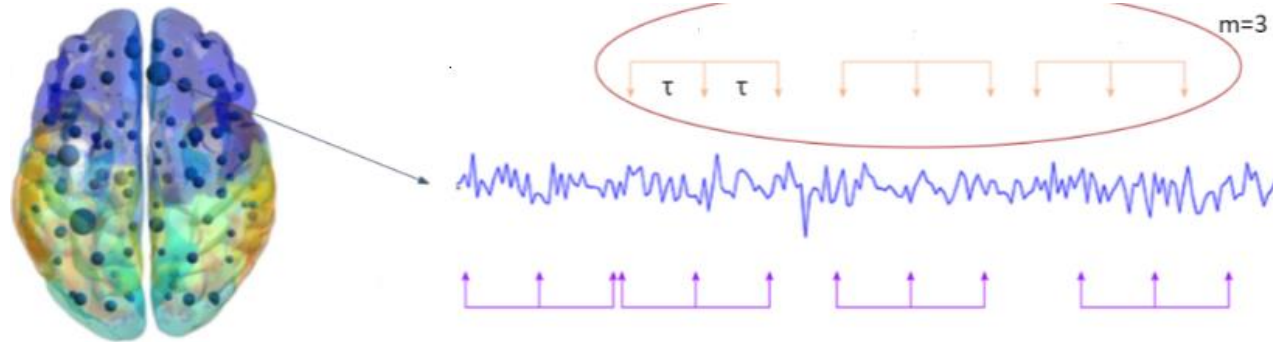


Visualize and **analyze recurrences** to understand and characterize the dynamics of complex nonlinear systems

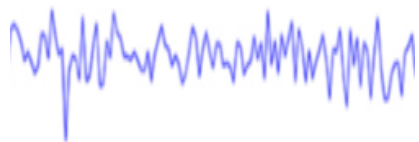
Recurrence quantification analysis

- **Recurrence Plot (RP)**

- Depicts the (local) neighborhood structure
- Captures time indices at which phase space trajectories return to a neighborhood
- Visualize recurrences based on a binary recurrence matrix



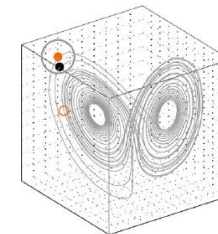
Original time series



$$\mathbf{r} = \{r_i\}_{i=1}^n$$

Time-Delay
Embedding

States (Phase Space)

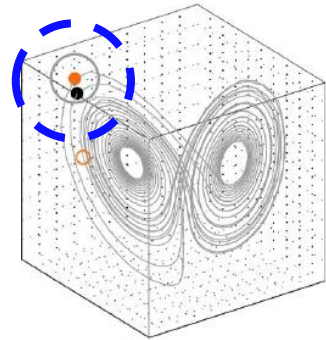


$$\mathbf{x}_i = [r_i, r_{i+\tau}, \dots, r_{i+(m-1)\tau}] \quad i = 1, \dots, N$$

Recurrence quantification analysis

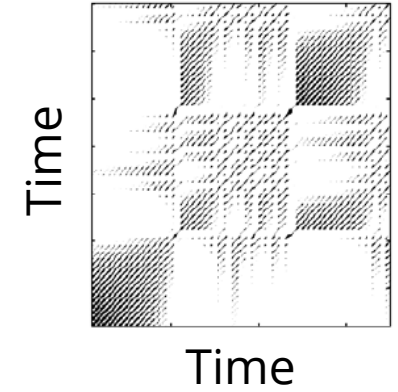
- **Recurrence Plot (RP)**

States (Phase Space)



$$\mathbf{x}_i = [r_i, r_{i+\tau}, \dots, r_{i+(m-1)\tau}]$$

Binary
Recurrence
Matrix



$$\mathbf{R}_{i,j} = \Theta(\varepsilon - d(\mathbf{x}_i, \mathbf{x}_j)) \quad i, j = 1, \dots, N$$

$$\Theta(n) = \begin{cases} 1, & \text{if } n \geq 0 \\ 0, & \text{if } n < 0 \end{cases} \longrightarrow \mathbf{R}_{i,j}(\varepsilon) = \begin{cases} 1, & d(\mathbf{x}_i, \mathbf{x}_j) \leq \varepsilon \quad \bullet \\ 0, & \text{otherwise} \quad \circ \end{cases}$$

Critical Parameters

m Embedding dimension

τ Delay

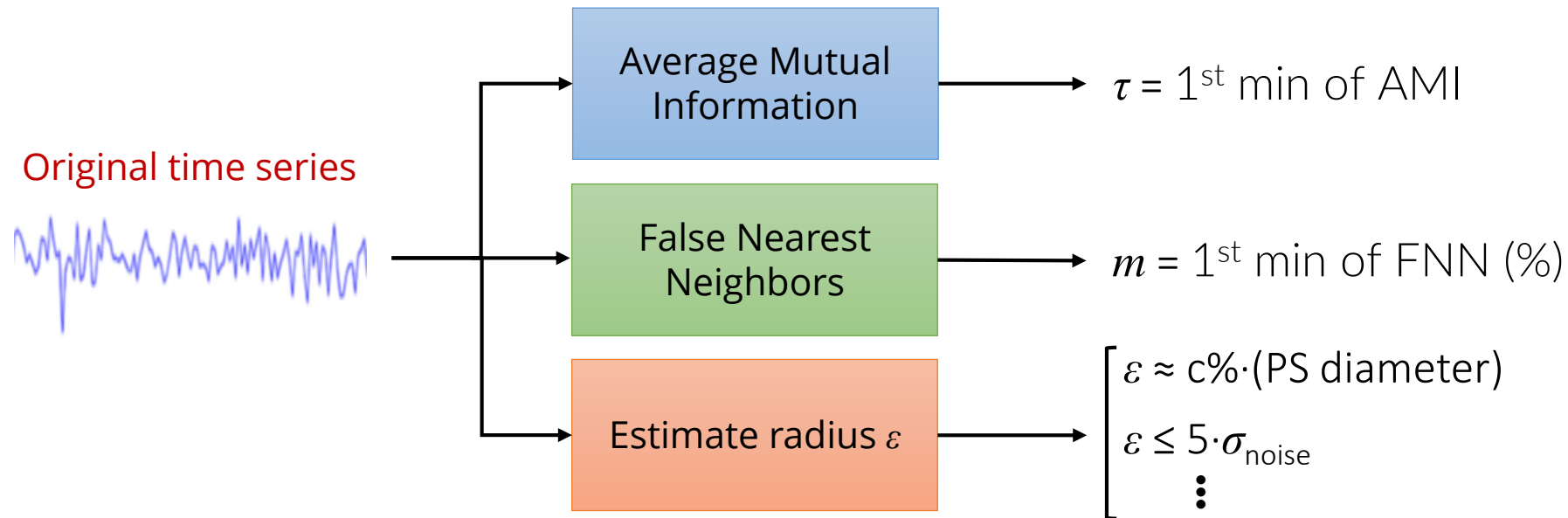
$N (= n - (m-1)\tau)$ Number of states

Recurrence quantification analysis

- Selection of embedding parameters

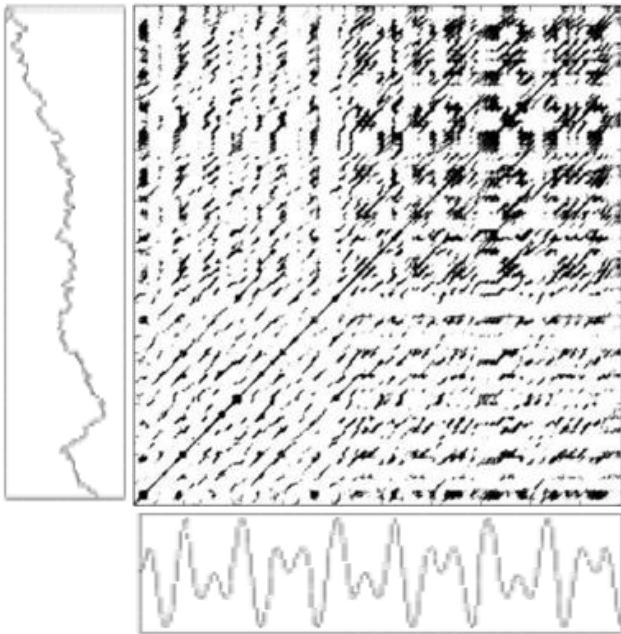


Inaccurate choice of m , τ , ε can hinder the discovery of low-dimensional dynamics or produce false positive indication of chaotic structure



Cross recurrence plot (CRP)

- Study and quantify the **interaction** of two distinct systems due to coupling
- Estimate **time-synchronization** profiles and detect **co-movements**
- Analyze **dependencies** between two distinct systems using CRP; Visualize times at which a state in one system occurs simultaneously in the second



$$\text{CR}_{i,j}(\varepsilon) = \Theta(\varepsilon - \|\mathbf{x}_i - \mathbf{y}_j\|_p) \quad i = 1, \dots, N, \quad j = 1, \dots, M$$

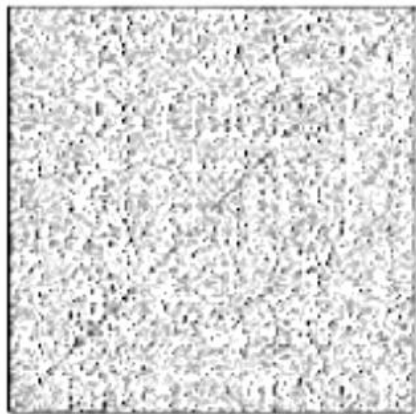


CR is not necessarily square (in general $N \neq M$)

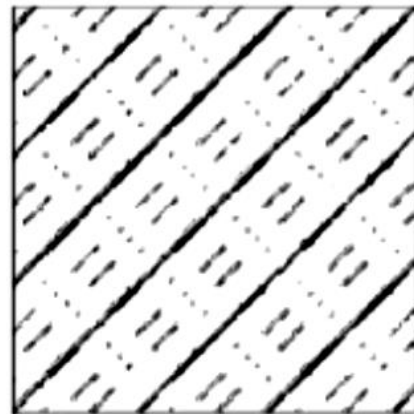
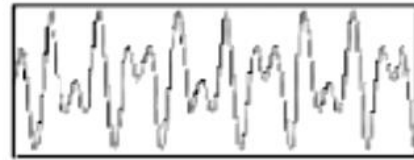
If embedding parameters differ, use the **higher embedding**

Properties of (C)RP

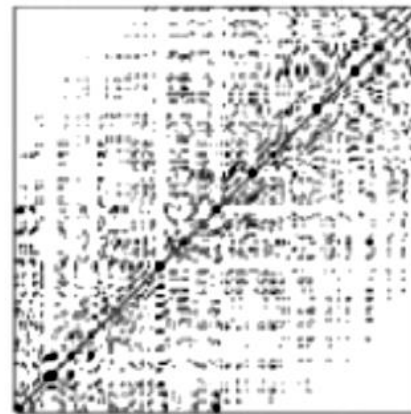
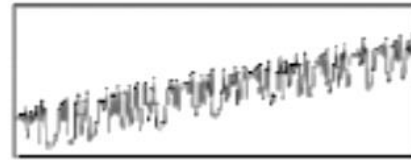
- Several **linear** and **curvilinear** structures appear in (C)RPs; Give hints about the time evolution of the high-dimensional phase space trajectories
- (C)RPs applied on **short** and **non-stationary** data
- Large-scale and small-scale structures



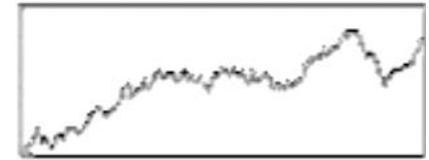
White noise
(uncorrelated data)



Harmonic oscillation
(2 frequencies)



Logistic map
(chaotic data + linear trend)



AR process

Recurrence quantification analysis (RQA)

- Enhance the visual interpretation of (C)RPs by quantifying small-scale patterns with appropriate **measures of complexity**
- (C)RQA: nonlinear data analysis method, which quantifies the **number** and **duration** of recurrences of a (pair of) dynamical system(s) occurring in its (their) phase space trajectory
- **(C)RQA measures**: categorized according to the structures they are based on (e.g. diagonal, vertical lines); depend on threshold ε

RQA measures

Based on recurrence density

Recurrence Rate (**RR**)

$$RR(\varepsilon) = \frac{1}{N^2} \sum_{i=1}^N \sum_{j=1}^N \mathbf{R}_{i,j}(\varepsilon)$$

RR for CRP (**CC**)

$$CC(\varepsilon) = \frac{1}{N^2} \sum_{i=1}^N \sum_{j=1}^N \mathbf{C}\mathbf{R}_{i,j}(\varepsilon)$$

RQA measures

Based on diagonal lines

Histogram of diagonal lines of length l :
$$P(\varepsilon, l) = \sum_{i=1}^N \sum_{j=1}^N (1 - \mathbf{R}_{i-1, j-1}(\varepsilon)) (1 - \mathbf{R}_{i+l, j+l}(\varepsilon)) \prod_{k=0}^{l-1} \mathbf{R}_{i+k, j+k}(\varepsilon)$$

Determinism (**DET**)

Avg diagonal length (**L**)

Longest diagonal (**L_{max}**)

Divergence (**DIV**)

$$DET = \frac{\sum_{l=l_{min}}^N l P(l)}{\sum_{l=1}^N l P(l)}$$

$$L = \frac{\sum_{l=l_{min}}^N l P(l)}{\sum_{l=l_{min}}^N P(l)}$$

$$L_{max} = \max_{i=1, \dots, N_l} \{l_i\}$$

$$DIV = \frac{1}{L_{max}}$$

Measure of determinism
(or predictability) of a
system

Measures average time
that two trajectory
segments are close (mean
prediction time)

The faster the trajectory
segments diverge, the
shorter are the diagonal
lines, thus L_{max}

The faster the trajectory
segments diverge, the
higher is the value of DIV

RQA measures

Based on diagonal lines

Histogram of diagonal lines of length l :
$$P(\varepsilon, l) = \sum_{i=1}^N \sum_{j=1}^N (1 - \mathbf{R}_{i-1, j-1}(\varepsilon)) (1 - \mathbf{R}_{i+l, j+l}(\varepsilon)) \prod_{k=0}^{l-1} \mathbf{R}_{i+k, j+k}(\varepsilon)$$

Entropy (**ENTR**)

$$ENTR = - \sum_{l=l_{min}}^N p(l) \ln(p(l))$$

$\left| = \frac{P(l)}{N_l} \right.$

Measure of RP complexity w.r.t. diagonal lines (e.g. ENTR is low for uncorrelated processes)

Trend (**TREND**)

$$TREND = \frac{\sum_{t=1}^{\tilde{N}} \left(t - \frac{\tilde{N}}{2}\right) (RR_t - \overline{RR_t})}{\sum_{t=1}^{\tilde{N}} \left(t - \frac{\tilde{N}}{2}\right)^2}$$

$RR_t = \frac{1}{N-t} \sum_{i=1}^{N-t} \mathbf{R}_{i, i+t}$

Measures non-stationarity in terms of recurrence point density of the diagonals parallel to LOI, as a function of time distance t between these diagonals and the LOI

CRQA-based feature extraction

- 6 CRQA measures (features) are selected: RR, DET, L, L_{max}, ENTR, V_{max}
- Relative sensitivity of CRQA features in differentiating NPSLE patients vs healthy volunteers is compared against:
 - Nodal RQA measures (per ROI)
 - Conventional static FC metric (zero-order Pearson correlation between two ROIs (total of 120 unique connections for 16 ROIs))

Classification performance

- SVM classifier

FE method	Precision	Recall	F1 score
CRQA-based FC	0.98	0.94	0.96
RQA-based FC	0.91	0.90	0.90
Static FC	0.74	0.78	0.76

Conclusions & Key remarks

- Feature Engineering unlocks **hidden insights**: most improvement will probably come from thinking carefully what we put into our models
- This can be (semi-)automated but still one of the true arts in Data Science
- No amount of complex modeling can compensate for poor-quality data; Feature engineering is the first line of defense to enhance **data quality**
- **Domain knowledge** is a powerful ally in practice
- Dimensionality reduction is vital; Feature engineering not only adds valuable attributes but also helps **reduce dimensionality** (it isn't just about computational efficiency; it's about reducing noise, overfitting, and making models more interpretable)

THANKS
FOR
WATCHING!

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<https://bit.ly/3VkuWYx>



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