

Radboud University Nijmegen





General Recipe for Recurrence Quantification with tdb

- Decide which **lag** to use:

Calculate the Average Mutual Information for a range of lags (*crqa_parameters*).

Take the lag where AMI reaches its first minimum. This is the lag at which least is known about $X(t+\tau)$ given $X(t)$, so we can create surrogate dimensions which give most new information about the system.

- Decide which embedding dimension to use:

Calculate how many False Nearest Neighbours you loose by adding a dimension (*crqa_parameters*). Take the embedding dimension with the lowest % of nearest neighbours (or start with the dimension which gives the greatest decrease of neighbours).

- Decide which type of **rescaling** you want to use:

Plot your timeseries: Lots of outliers? Use Mean Distance. Otherwise: Max Distance.

Calculate the max distance in reconstructed phasespace, after lag and embedding are known using $\max(\text{repmat}(y, \text{emDim}, \text{emLag}))$, divide by this value.

-Decide which individuals/thirds to use:

- Use `rp_plot` to show unthresholded (without radius) plots use `crqa_radius` to find a radius

-Run RQA(crqa) with these parameters! Or use crqa

-Compare to shuffled data (shuffle, surrogate)

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General Recipe for Recurrence Quantification with toolbox:

- Decide which **lag** to use:

Calculate the Average Mutual Information for a range of lags (*crqa_parameters*).

Take the lag where AMI reaches its first minimum. This is the lag at which least is known about $X(t+\tau)$ given $X(t)$, so we can create surrogate dimensions which give most new information about the system.

- Decide which **embedding dimension** to use:

Calculate how many False Nearest Neighbours you loose by adding a dimension (*crqa_parameters*). Take the embedding dimension with the lowest % of nearest neighbours (or start with the dimension which gives the greatest decrease of neighbours).

- Decide which type of **rescaling** you want to use:

Plot your timeseries: Lots of outliers? Use Mean Distance. Otherwise: Max Distance.

Calculate the max distance in reconstructed phasespace, after lag and embedding are known using *max(recmat(y,emDim,emLag)*, divide by this value.

- Decide which **radius / threshold** to use:

-Use *rp_plot* to show unthresholded (without radius) plots use *crqa_radius* to find a radius

- Run **RQA** (*crqa_cl*) with these parameters! Or use *crqa_rp*

- Compare to shuffled data (*shuffle*, *surrogates*)

Radius:

3.629

RP_N:

202508

RR:

0.05

DET:

0.999

MEAN_d1:

24.689

ENT_d1:

3.761

LAM_v1:

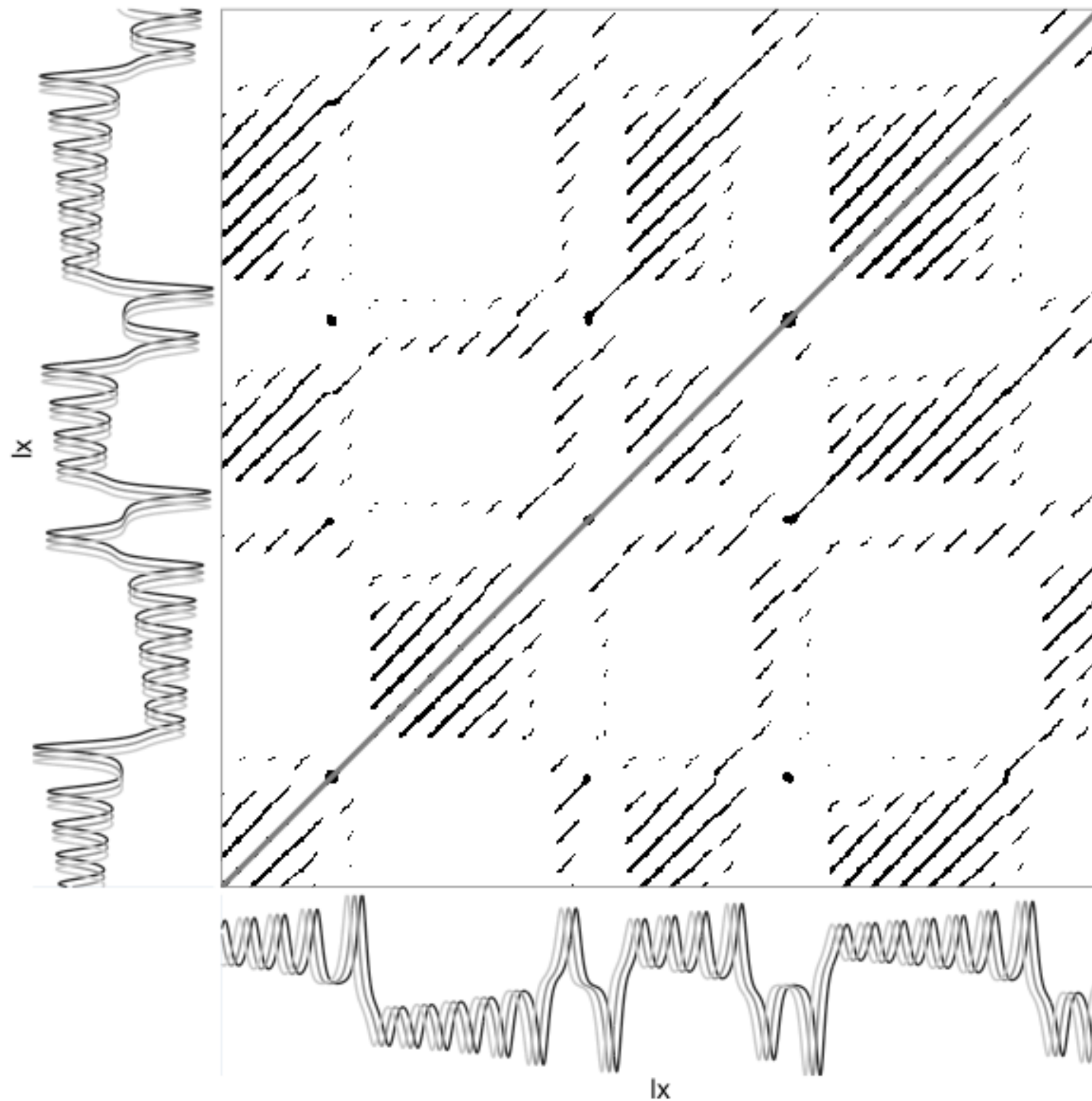
0.999

TT_v1:

9.212

ENT_v1:

2.761



e

n

