10-RR_intervals_phase_space_reconstruction_and_recurrence_plot

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1 R-R intervals time series

1.1 Facultad de Ciencias, UNAM

1.1.1 Ana Daniela del Río Pulido and Erin C. McKiernan

Functions used in previous notebooks will be used. To exemplify, we will use the meditation recordings as well as one recording in rest and after performing exercise.

The objective of this notebook is to visualize the techniques used in previous notebooks (phase space recontruction and recurrence plot), but only using the R/R intervals time series. Consider that there must be an adequate R peak detection in the recording.

2 Setting up the notebook

We begin by setting up the Jupyter notebook and importing the Python modules needed for plotting figures, create animations, etc. We include commands to view plots in the Jupyter notebook, and to create figures with good resolution and large labels. These commands can be customized to produce figures with other specifications.

[1]:

```python
# Imports python libraries
import numpy as np
import random as rd
import wave
import sys
import os
import matplotlib.pyplot as plt
from matplotlib.pyplot import figure
import matplotlib as mpl
from mpl_toolkits.axes_grid1.inset_locator import inset_axes
sys.path.insert(1, r'./../functions') # add to pythonpath

# commands to create high-resolution figures with large labels
%config InlineBackend.figure_formats = {'png', 'retina'}
plt.rcParams['figure.dpi'] = 50
plt.rcParams['axes.labelsize'] = 16 # fontsize for figure labels
plt.rcParams['axes.titlesize'] = 18 # fontsize for figure titles
plt.rcParams['font.size'] = 14 # fontsize for figure numbers
plt.rcParams['lines.linewidth'] = 1.4 # line width for plotting
```

2.1 Extracting data

ECG recordings were obtained using the Backyard Brains Heart and Brain Spiker Box. The recordings are saved as audio files in .wav format. The first thing we have to do is open the .wav files and extract the data. We can extract the number of recording channels, sampling rate, etc.

[2]:

```
#Function that extracts the number of recording channels, sampling rate, time␣
 ↪and signal
#variable is the path and filename of the .wav file
def ecg(variable):
    record = wave.open(variable, 'r') # load the data

    # Get the number of channels, sample rate, etc.
    numChannels = record.getnchannels() #number of channels
    numFrames = record.getnframes() #number of frames
    sampleRate = record.getframerate() #sampling rate
    sampleWidth = record.getsampwidth()

    # Get wave data
    dstr = record.readframes(numFrames * numChannels)
    waveData = np.frombuffer(dstr, np.int16)

    # Get time window
    timeECG = np.linspace(0, len(waveData)/sampleRate, num=len(waveData))

    return timeECG, waveData
```

3 R peaks

Function for detecting R peaks. We will be able to calculate the heart frequency and R-R intervals.

The following function creates an array of values which surpass a certain threshold. Afterwards, it determines the maximum value of this array and adds it in the R-vector. And this is repeated until the end of the time series.

[3]:

```
def detecta_maximos_locales(timeECG, waveData, threshold_ratio=0.7):
    # If not all the R peaks are detected, lower the threshold_ratio
    # If components that are not R peaks (like T waves) are detected, higher␣
 ↪the threshold_ratio

    if len(timeECG) != len(waveData): #Raises an error if the two arrays have␣
 ↪different lengths
        raise Exception("The two arrays have different lengths.")

    interval = max(waveData) - min(waveData)
    threshold = threshold_ratio*interval + min(waveData)
    maxima = []
    maxima_indices = []
    mxs_indices = []
    banner = False

    for i in range(0, len(waveData)):

        if waveData[i] >= threshold:#If a threshold value is surpassed,
            # the indices and values are saved
            banner = True
            maxima_indices.append(i)
            maxima.append(waveData[i])

        elif banner == True and waveData[i] < threshold: #If the threshold␣
 ↪value is crossed
            # the index of the maximum value in the original array is saved
            index_local_max = maxima.index(max(maxima))
            mxs_indices.append(maxima_indices[index_local_max])
            maxima = []
            maxima_indices = []
            banner = False

    return mxs_indices
```

[4]:

```
# If the input of this function is time, the intervals will be given in those␣
 ↪same units
# Obtaining the indexes at which the R peaks occur.
def R_intervals(time_indices):

    length = len(time_indices)
    intervals = np.zeros(length-1)

    for i in range(0, length-1):
        intervals[i] = time_indices[i+1]-time_indices[i]

    return intervals
```

4 Comencing the analysis

For analyzing several recordings at the same time, we must obtain the names of every file. One option is to extract the file names one by one, but another option is just to give a folder's name and extract the recordings from there.

[5]:

```
InputPath = "ECG_samples/meditation_data/" #Folder where the original files are
recordings_path = []
corresponding_folder = []

#In this case, files must be inside folders inside the folder where this␣
 ↪notebook is
TheList = os.listdir(InputPath)

for Folder in TheList:

    for TheFile in os.listdir(InputPath+Folder):
        corresponding_folder.append(Folder)
        TheFileName, TheFileExtension = os.path.splitext(TheFile) # breaks file␣
 ↪name into pieces based on periods

        InputFilePath = InputPath + Folder +"/"+ TheFileName + TheFileExtension␣
 ↪# Full path to file

        if (TheFileExtension==".wav"): # Only interested in .wav files
            recordings_path.append(InputFilePath)
```

[6]:

```
corresponding_folder.append("S1_rest")
corresponding_folder.append("S1_exercise")
corresponding_folder.append("S2_rest")
corresponding_folder.append("S2_exercise")
corresponding_folder.append("S3_rest")
corresponding_folder.append("S3_exercise")

recordings_path.append("ECG_samples/S1_rest.wav")
recordings_path.append("ECG_samples/S1_exercise.wav")

recordings_path.append("ECG_samples/S2_rest.wav")
recordings_path.append("ECG_samples/S2_exercise.wav")

recordings_path.append("ECG_samples/S3_rest.wav")
recordings_path.append("ECG_samples/S3_exercise.wav")

recordings_path
```

[6]:

```
['ECG_samples/meditation_data/respiraciones_profundas_55_abdomen/BYB_Recording_2
018-06-07_18.40.01.wav',
 'ECG_samples/meditation_data/respiraciones_profundas_55_abdomen/BYB_Recording_2
018-06-07_18.43.56.wav',
 'ECG_samples/meditation_data/respiraciones_profundas_55_abdomen/BYB_Recording_2
018-06-07_18.38.19.wav',
 'ECG_samples/meditation_data/control/BYB_Recording_2018-06-07_18.07.34.wav',
 'ECG_samples/meditation_data/control/BYB_Recording_2018-06-07_18.09.49.wav',
 'ECG_samples/meditation_data/control/BYB_Recording_2018-06-07_18.05.04.wav',
 'ECG_samples/meditation_data/respiraciones_profundas_55_pecho/BYB_Recording_201
8-06-07_18.20.29.wav',
 'ECG_samples/meditation_data/respiraciones_profundas_55_pecho/BYB_Recording_201
8-06-07_18.22.37.wav',
 'ECG_samples/meditation_data/respiraciones_profundas_55_pecho/BYB_Recording_201
8-06-07_18.17.12.wav',
 'ECG_samples/meditation_data/sostener_respiracion_abdomen/BYB_Recording_2018-06
-07_18.31.55.wav',
 'ECG_samples/meditation_data/sostener_respiracion_abdomen/BYB_Recording_2018-06
-07_18.34.18.wav',
 'ECG_samples/meditation_data/sostener_respiracion_abdomen/BYB_Recording_2018-06
-07_18.35.39.wav',
 'ECG_samples/meditation_data/sostener_respiracion_pecho/BYB_Recording_2018-06-0
7_18.26.47.wav',
 'ECG_samples/meditation_data/sostener_respiracion_pecho/BYB_Recording_2018-06-0
7_18.28.02.wav',
 'ECG_samples/meditation_data/sostener_respiracion_pecho/BYB_Recording_2018-06-0
7_18.29.22.wav',
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wav',
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wav',
 'ECG_samples/meditation_data/respiracion_ola/BYB_Recording_2018-06-07_18.53.00.
wav',
 'ECG_samples/S1_rest.wav',
 'ECG_samples/S1_exercise.wav',
 'ECG_samples/S2_rest.wav',
 'ECG_samples/S2_exercise.wav',
 'ECG_samples/S3_rest.wav',
 'ECG_samples/S3_exercise.wav']
```

Now we introduce the object used in previous notebooks. This will make it easier handling several recordings at once.

[7]:

```python
# Object
class Sujeto:
  def __init__(self, timeECG, waveData):
    self.timeECG = timeECG
    self.waveData = waveData

    self.mxs_indices = detecta_maximos_locales(timeECG, waveData)
    self.RR = R_intervals(timeECG[self.mxs_indices])
    self.timeRpeaks = timeECG[self.mxs_indices]
```

[8]:

```python
recordings = []
```

```
for i in range(0, len(recordings_path)):
    timeECG, waveData = ecg(recordings_path[i])
    recordings.append(Sujeto(timeECG, waveData))
    print("Finished recording ", i+1)
```

```
Finished recording  1
Finished recording  2
Finished recording  3
Finished recording  4
Finished recording  5
Finished recording  6
Finished recording  7
Finished recording  8
Finished recording  9
Finished recording  10
Finished recording  11
Finished recording  12
Finished recording  13
Finished recording  14
Finished recording  15
Finished recording  16
Finished recording  17
Finished recording  18
Finished recording  19
Finished recording  20
Finished recording  21
Finished recording  22
Finished recording  23
Finished recording  24
```

5 Phase space reconstruction

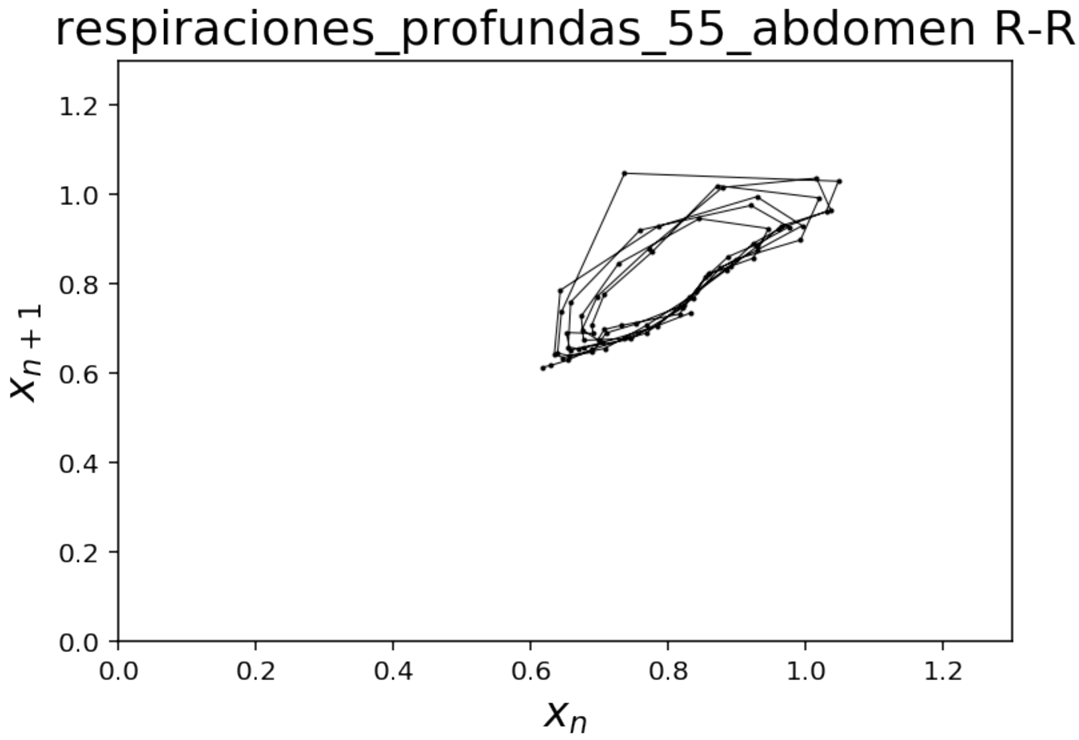
In the previos technique we only compared the R intervals with the next interval. What would happen if we compare not the R interval, but the whole recording with a certain time delay we choose. Instead of comparing one data point with its next in time, we choose an arbitrary time delay? In other words, we are going to generalize what we applied in the previous technique with the whole ECG data series and with an arbitrary time delay.

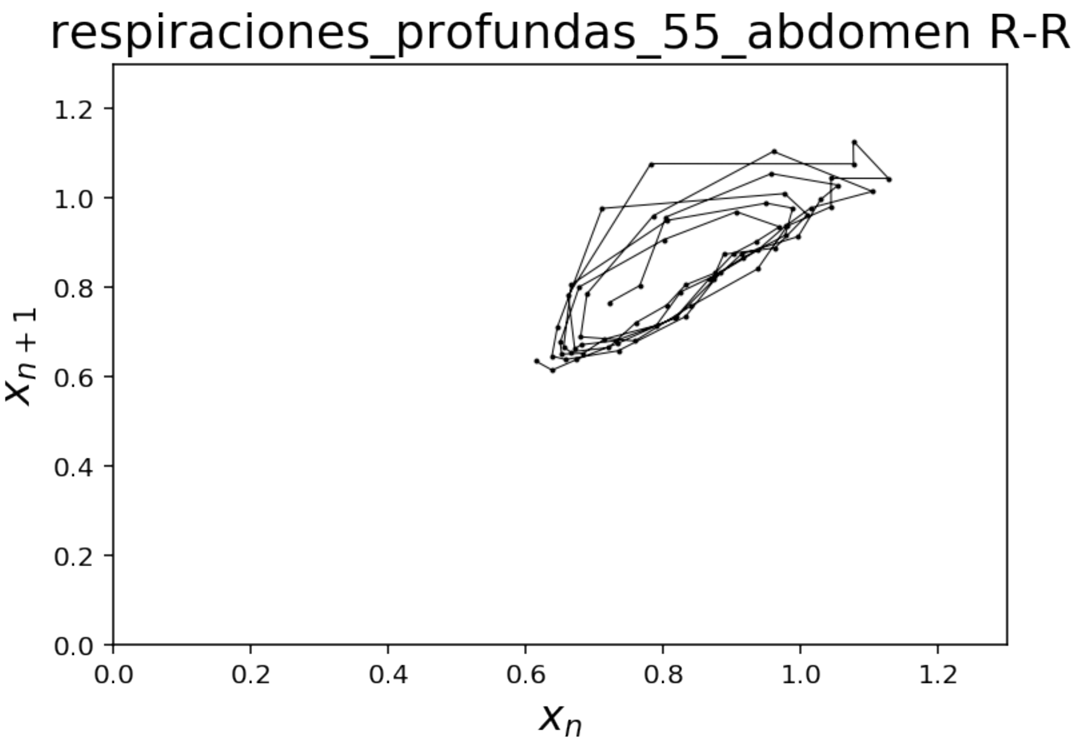
[9]:

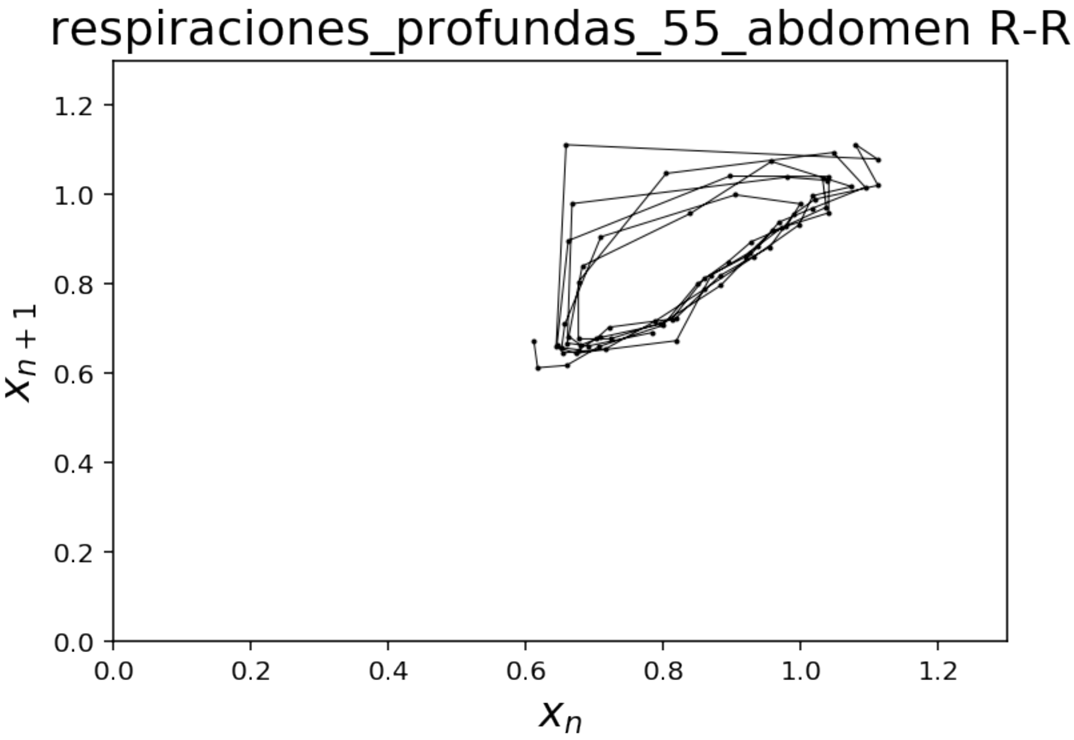
```
#Generating a function that will reconstruct the phase space for a certain time␣
 ↪delay
# data_series is the voltage of our signal
# period is the time delay
# identifier is a string that will help us identify that particular graph

def graph_phase_space(waveData, period = 210, identifier = "xx"):
    time = period*0.1 #time is in miliseconds
    n = np.size(waveData) #size of the voltage vector
    plt.figure(2)
    plt. plot(waveData[0: n-period], waveData[period: n],
              marker = "o", markersize = 1, linewidth = 0.5, color = "black")
    plt.title(identifier+" R-R")
    plt.xlabel(r"$x_n$")
    y = r'$x_{n+1}$'
    plt.ylabel(y)
    plt.xlim(0, 1.3)
    plt.ylim(0, 1.3)
    plt.show()
    return None
```

[10]:

```
for i in range(len(recordings)):
    graph_phase_space(recordings[i].RR, 1, corresponding_folder[i])
```




respiraciones_profundas_55_abdomen R-R
x_{n+1}
x_n
0.0
0.2
0.4
0.6
0.8
1.0
1.2
0.0
0.2
0.4
0.6
0.8
1.0
1.2


respiraciones_profundas_55_abdomen R-R
x_{n+1}
x_n
0.0
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0.8
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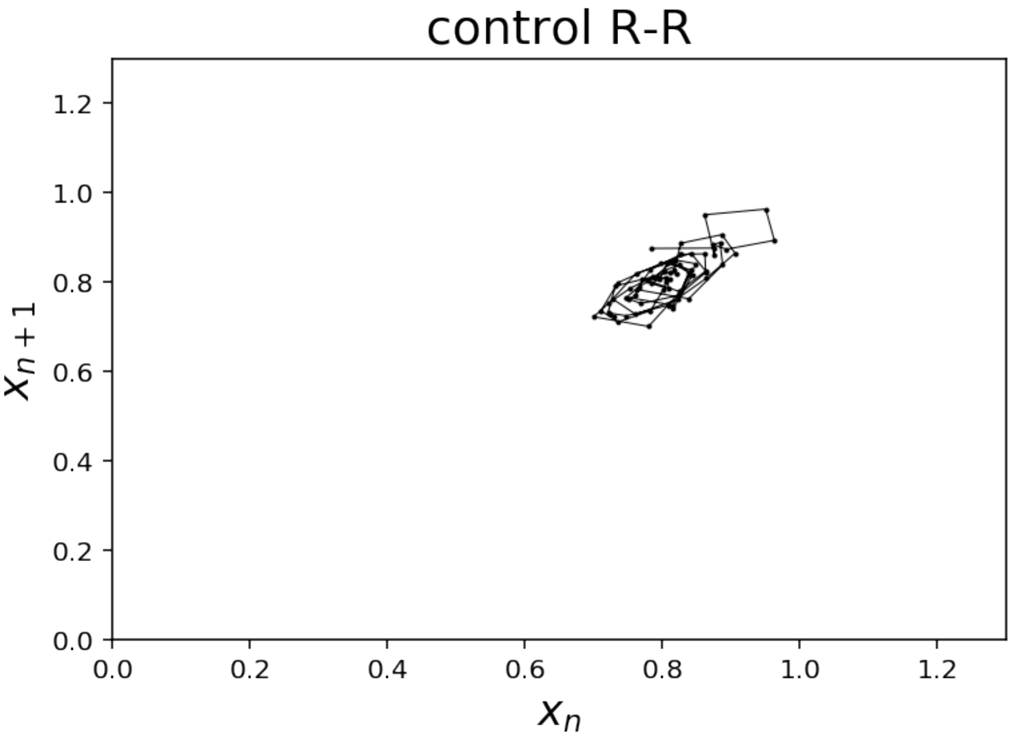
1.2


control R-R
x_{n+1}
x_n
0.0
0.2
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0.6
0.8
1.0
1.2
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0.2
0.4
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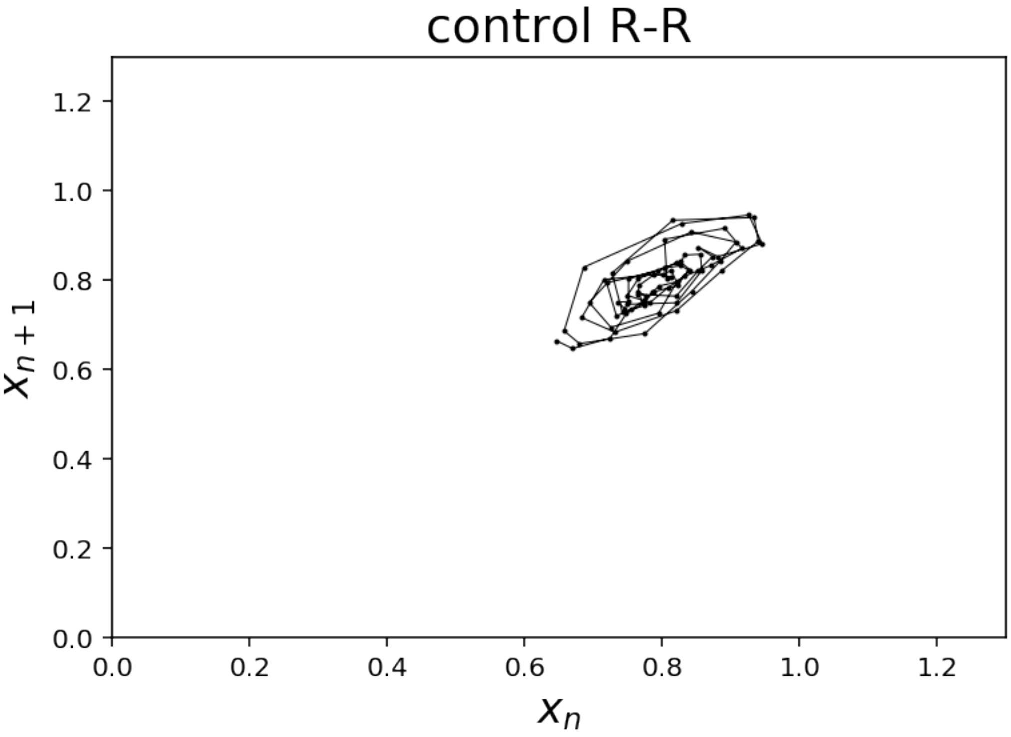
1.2


control R-R
x_{n+1}
x_n
0.0
0.2
0.4
0.6
0.8
1.0
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0.2
0.4
0.6
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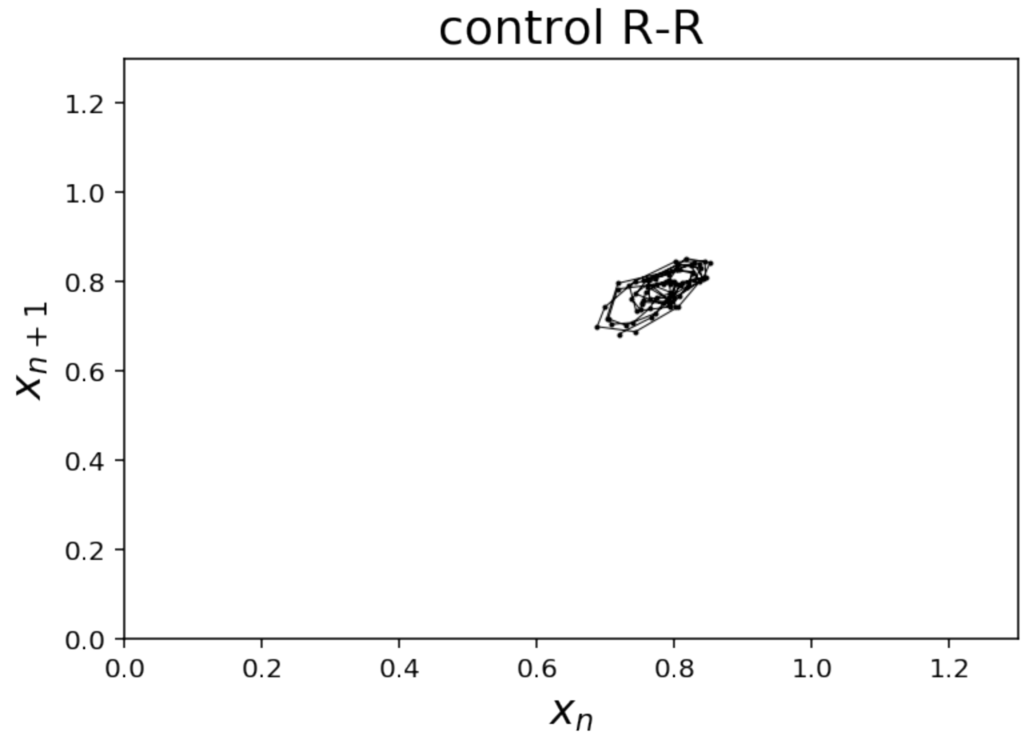
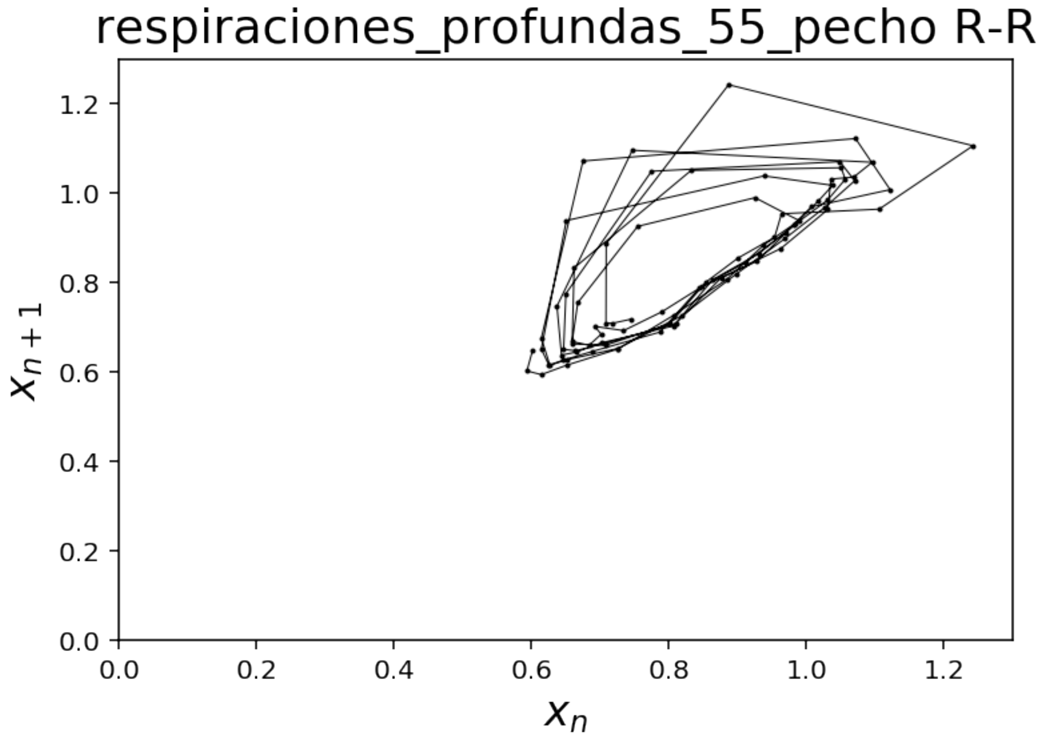
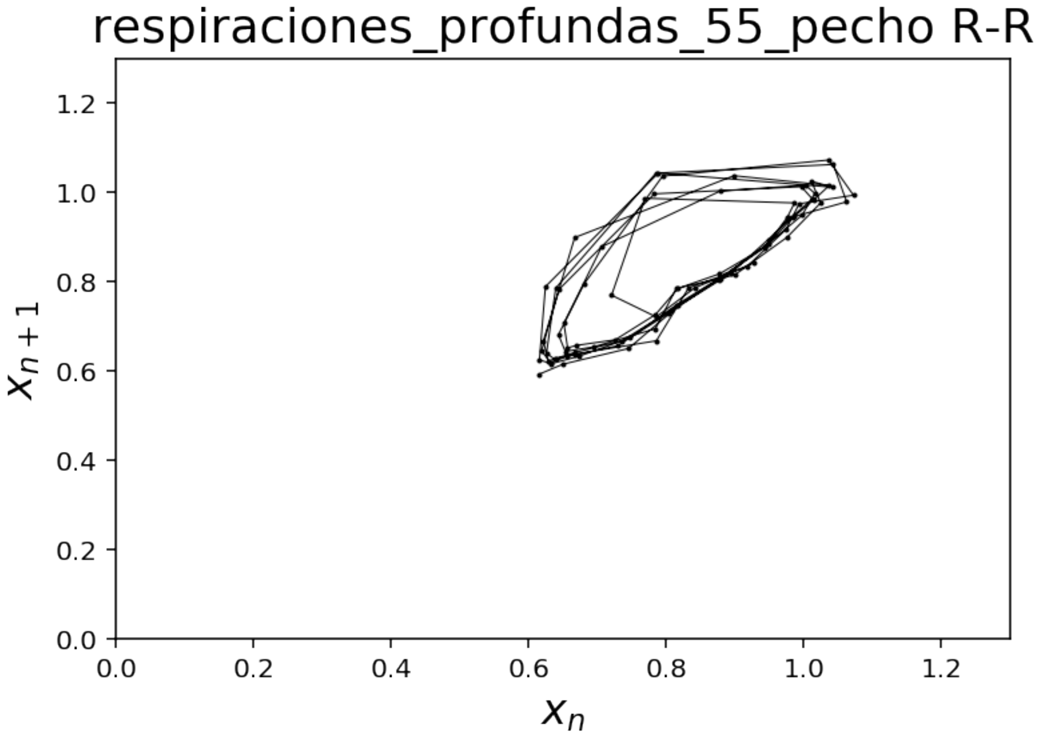

control R-R
1.2
1.0
0.8
0.6
0.4
0.2
0.0
x_{n+1}
0.0
0.2
0.4
0.6
0.8
1.0
1.2
x_n


respiraciones_profundas_55_pecho R-R
1.2
1.0
0.8
0.6
0.4
0.2
0.0
x_{n+1}
0.0
0.2
0.4
0.6
0.8
1.0
1.2
x_n


respiraciones_profundas_55_pecho R-R
x_{n+1}
x_n
0.0
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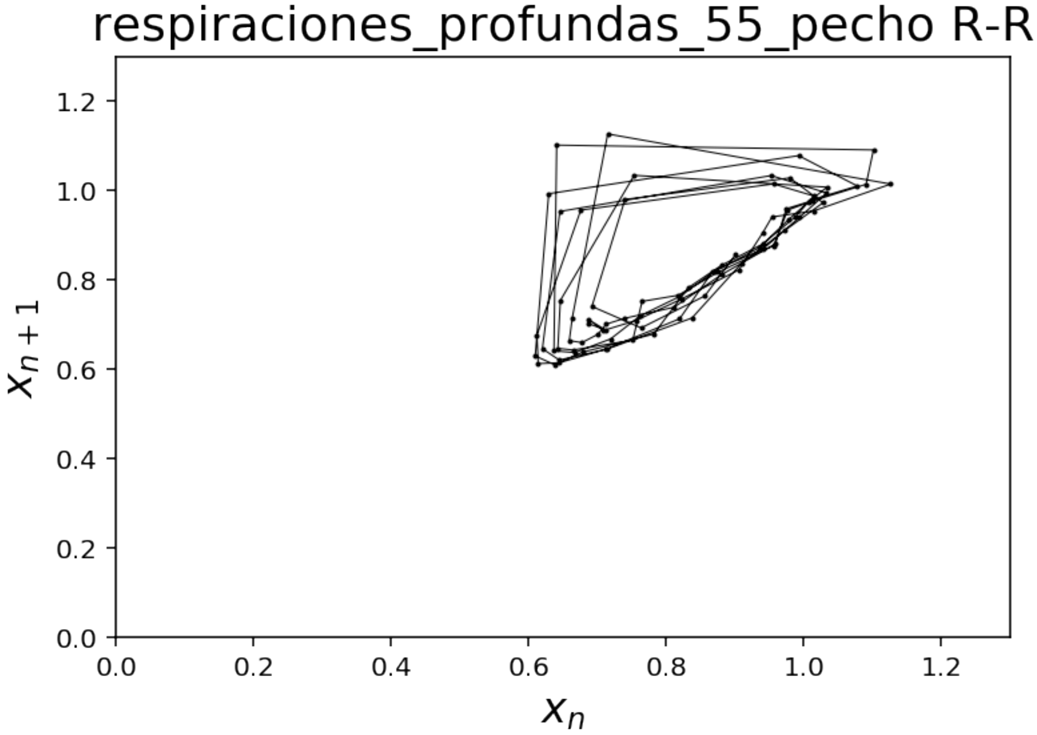
1.2


respiraciones_profundas_55_pecho R-R
x_{n+1}
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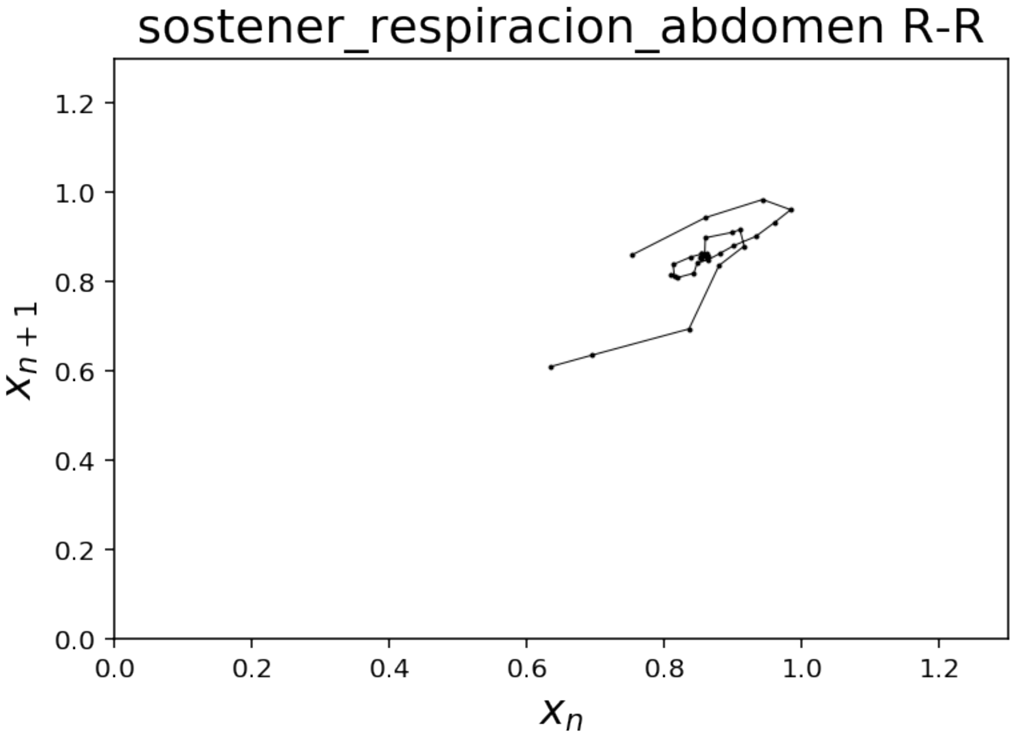
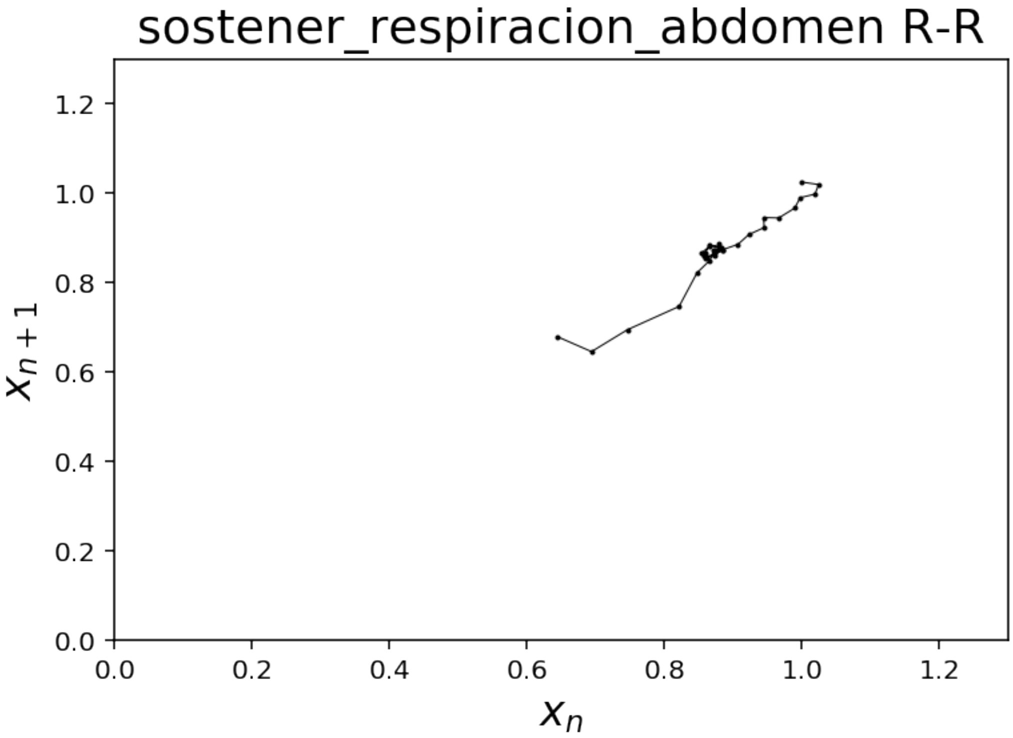
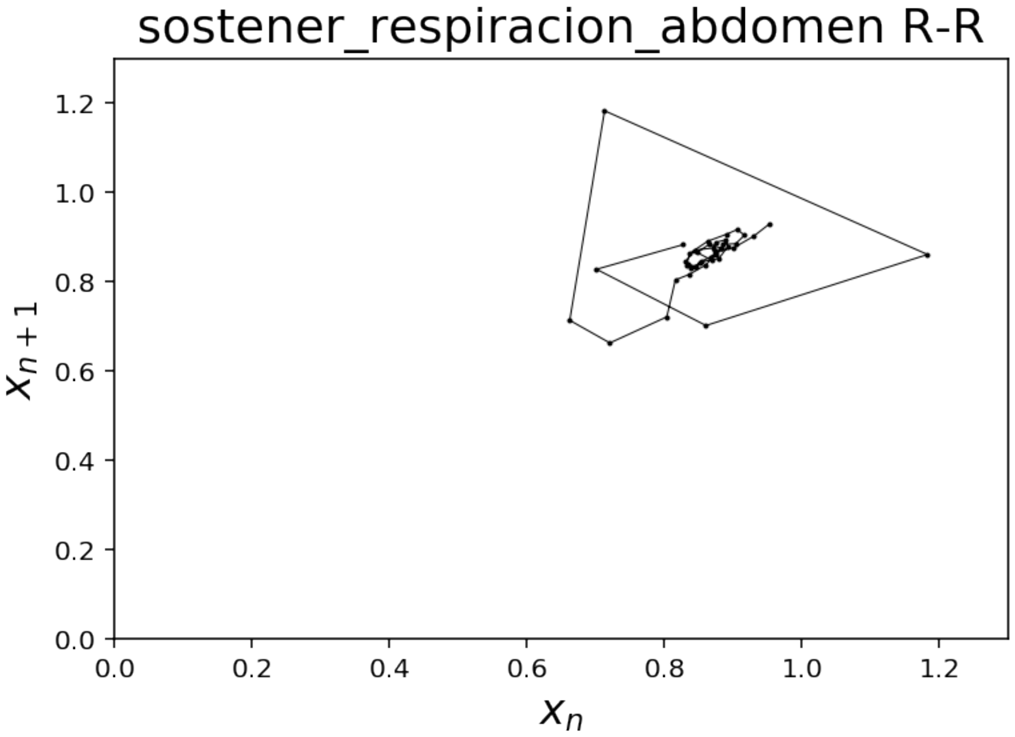

sostener_respiracion_abdomen R-R


sostener_respiracion_abdomen R-R


sostener_respiracion_abdomen R-R
x_{n+1}
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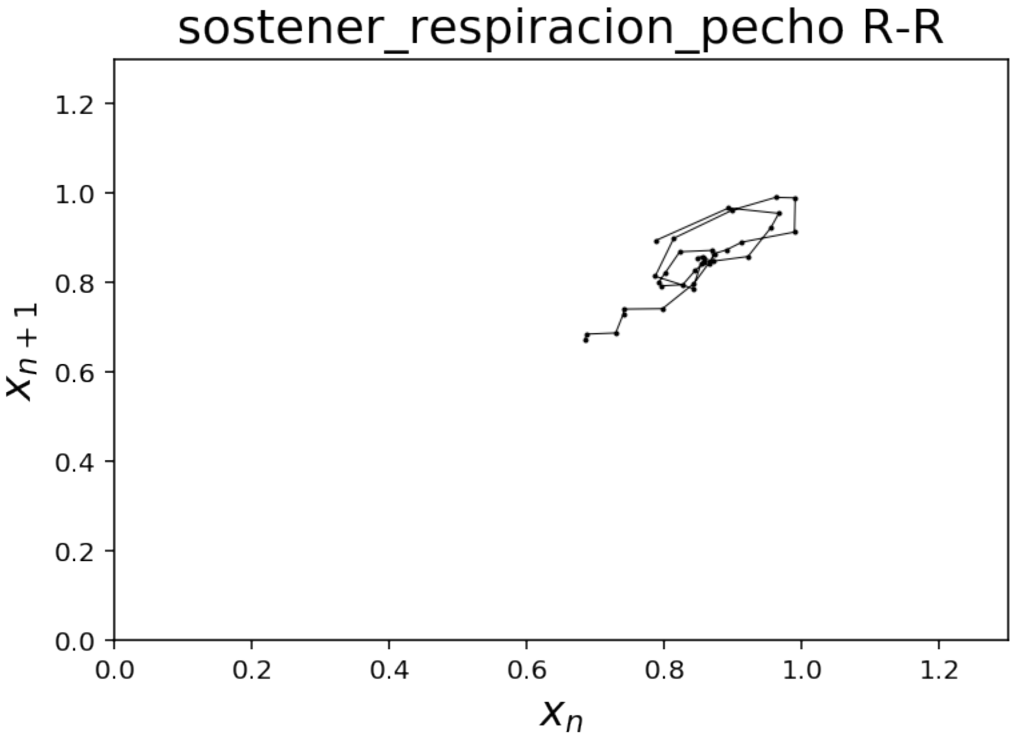
sostener_respiracion_pecho R-R
x_{n+1}
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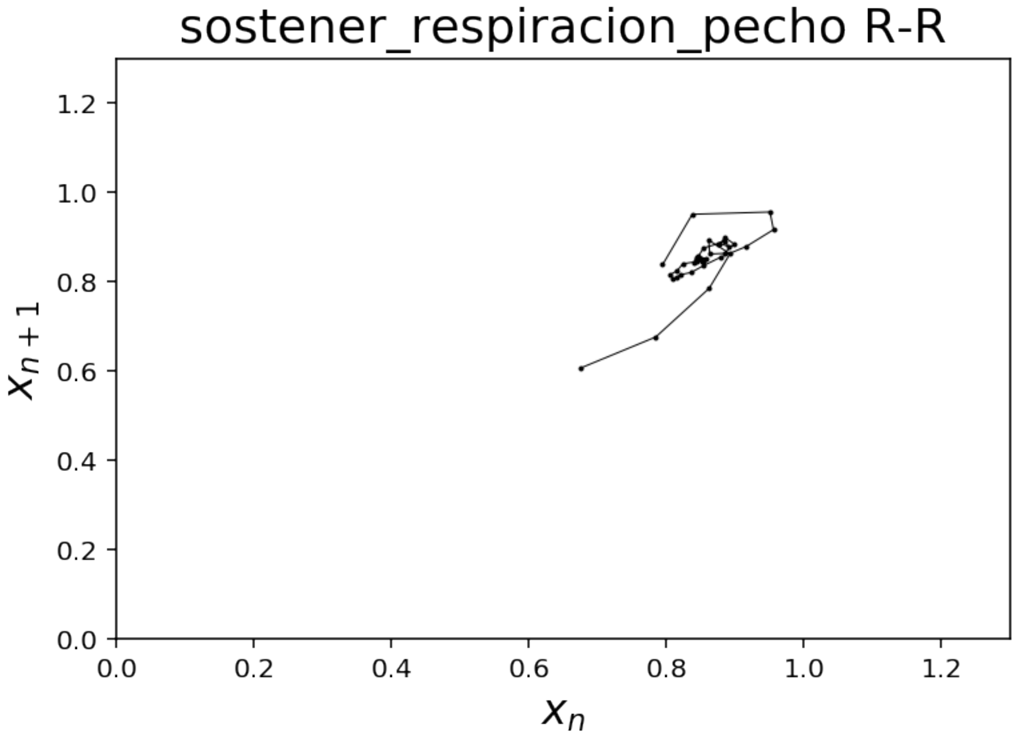
sostener_respiracion_pecho R-R
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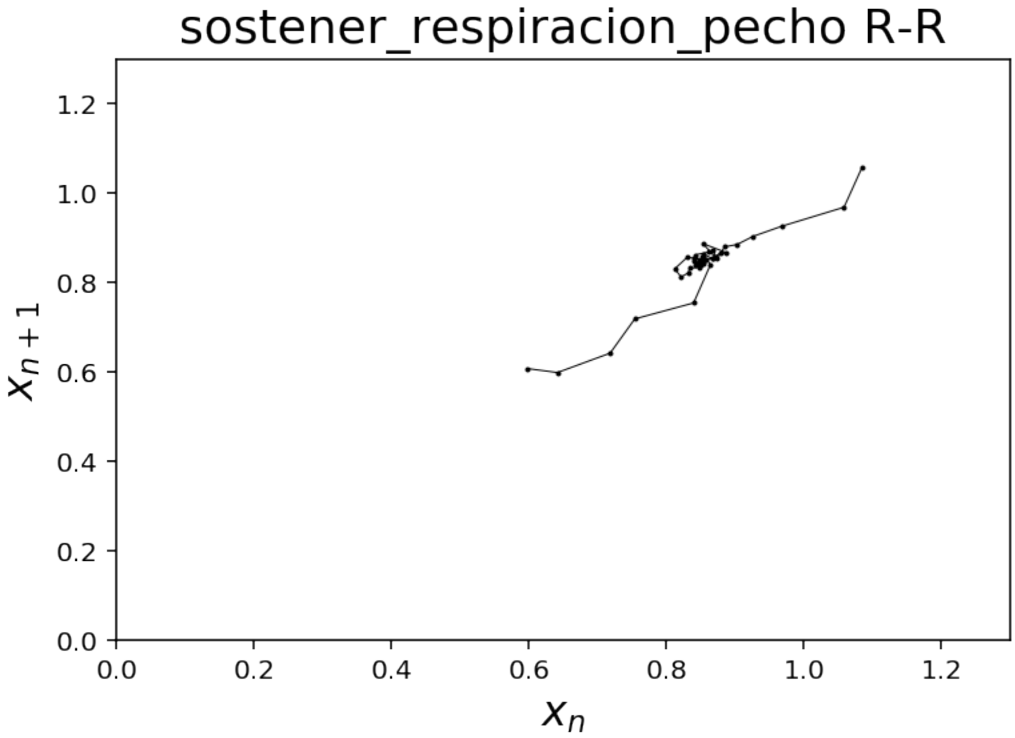
sostener_respiracion_pecho R-R
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x_n
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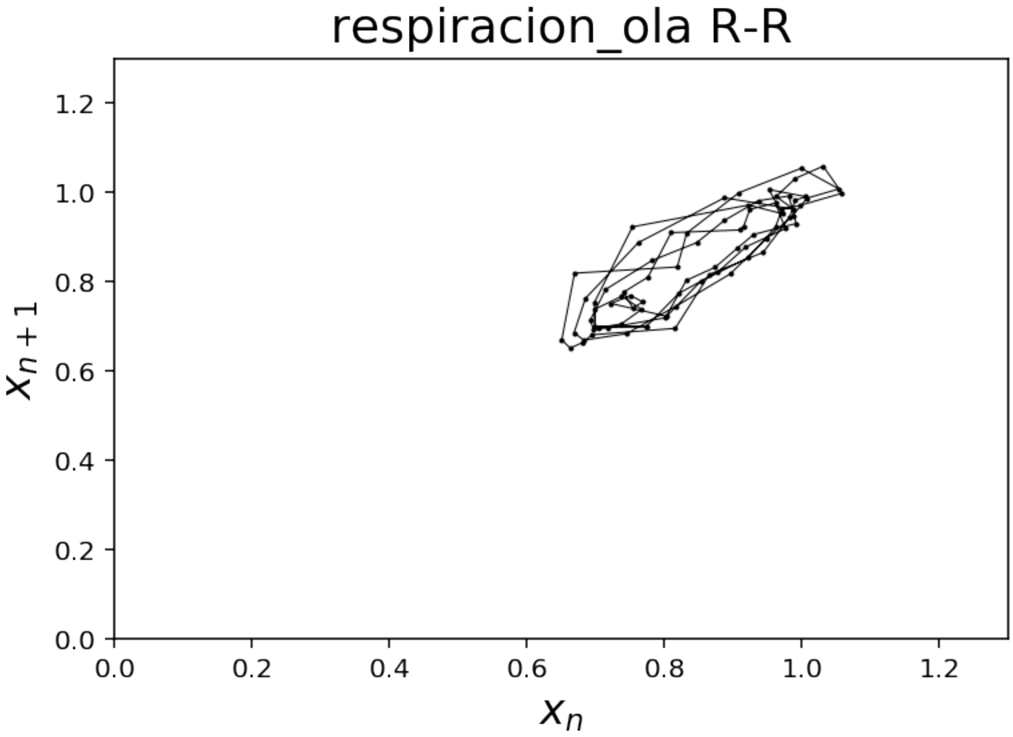
0.6
0.8
1.0
1.2


respiracion_ola R-R
x_{n+1}
x_n
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0.2
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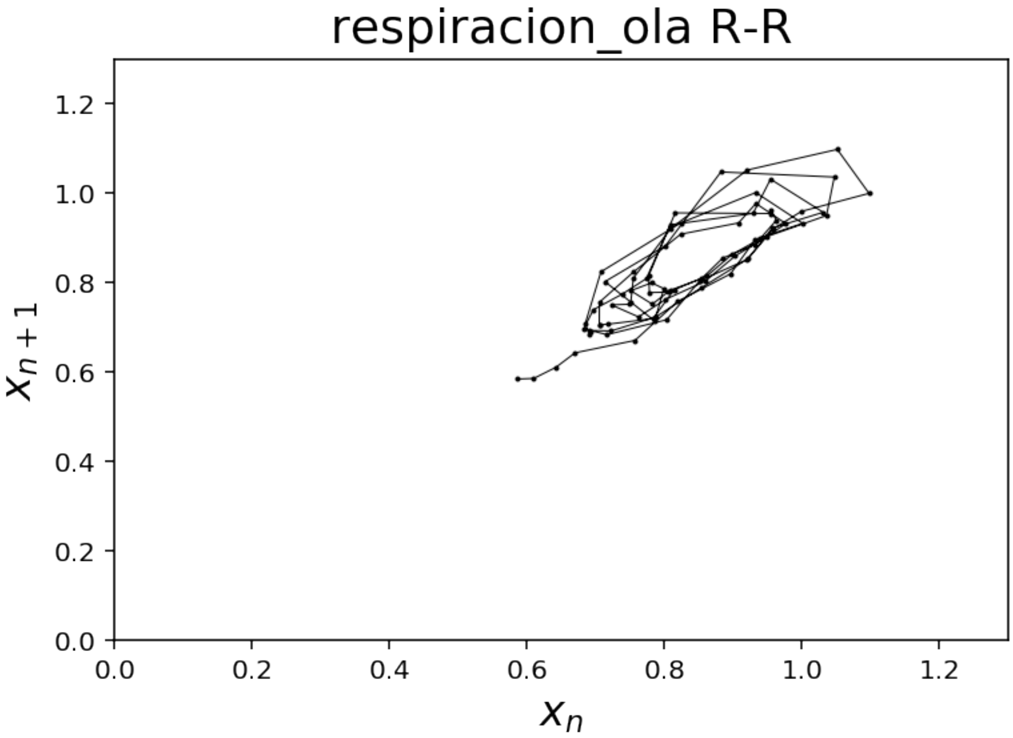
0.2
0.4
0.6
0.8
1.0
1.2


respiracion_ola R-R
x_{n+1}
x_n
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1.2
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0.2
0.4
0.6
0.8
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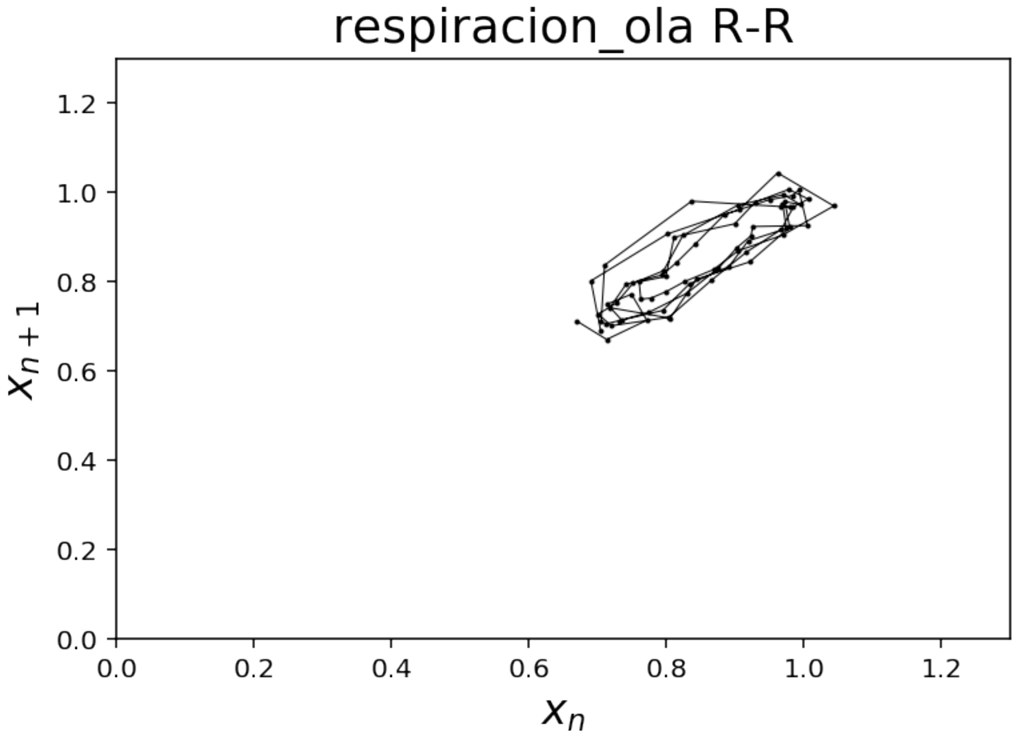
1.2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x_{n+1}
x_n
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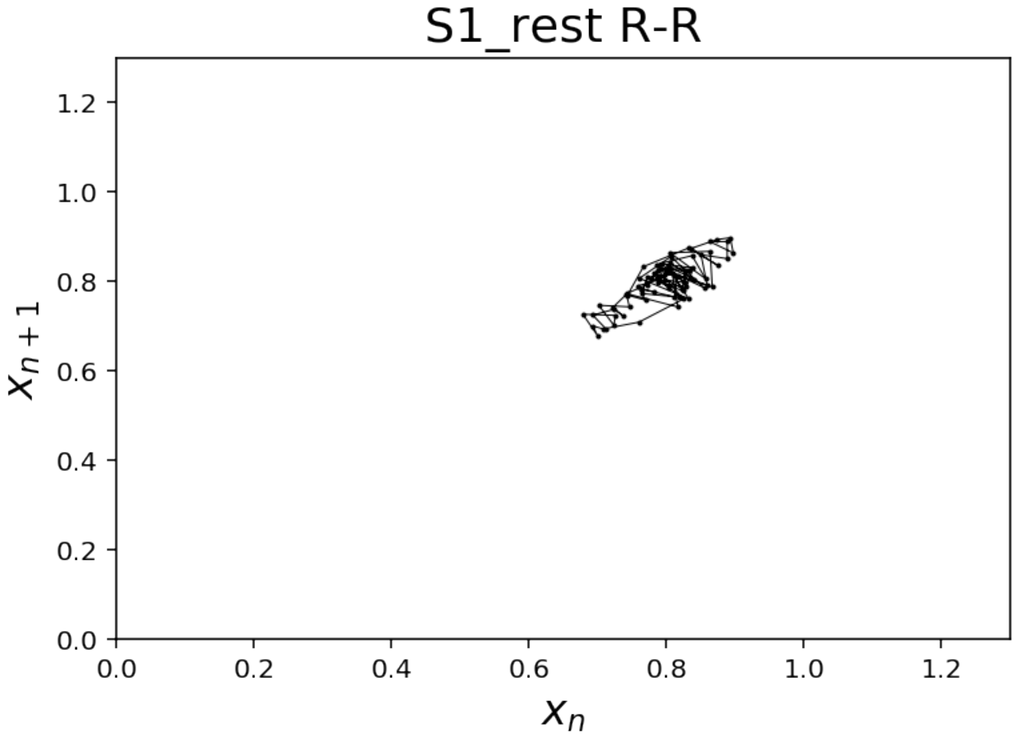
0.2
0.4
0.6
0.8
1.0
1.2


S1_rest R-R
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x_n
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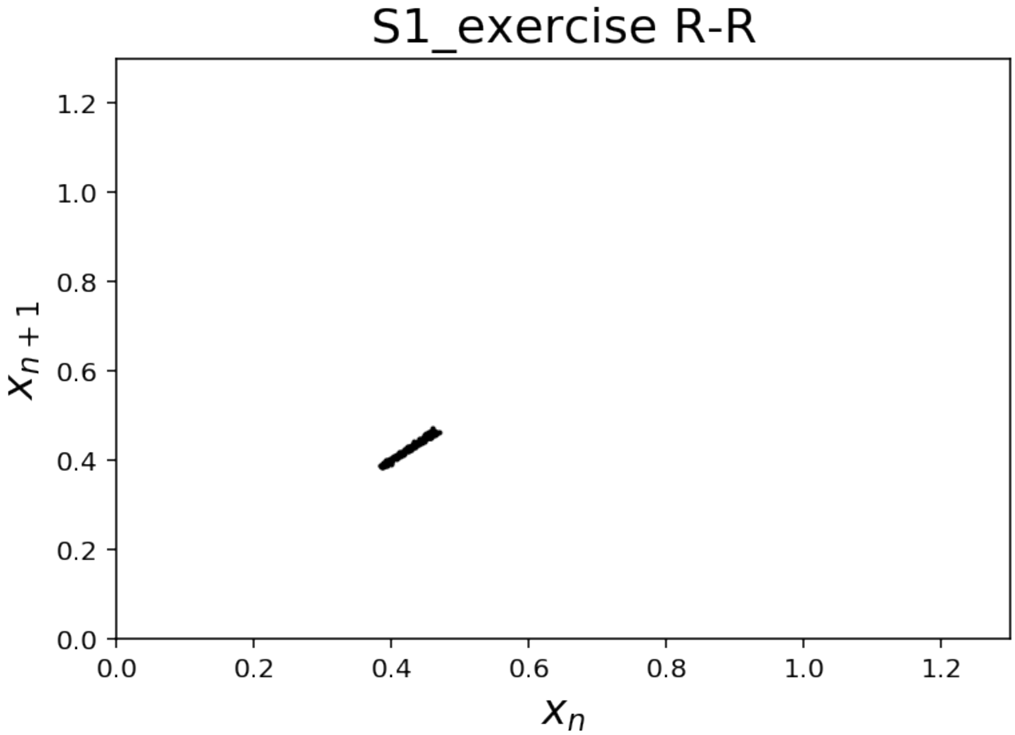
0.2
0.4
0.6
0.8
1.0
1.2


S1_exercise R-R
x_{n+1}
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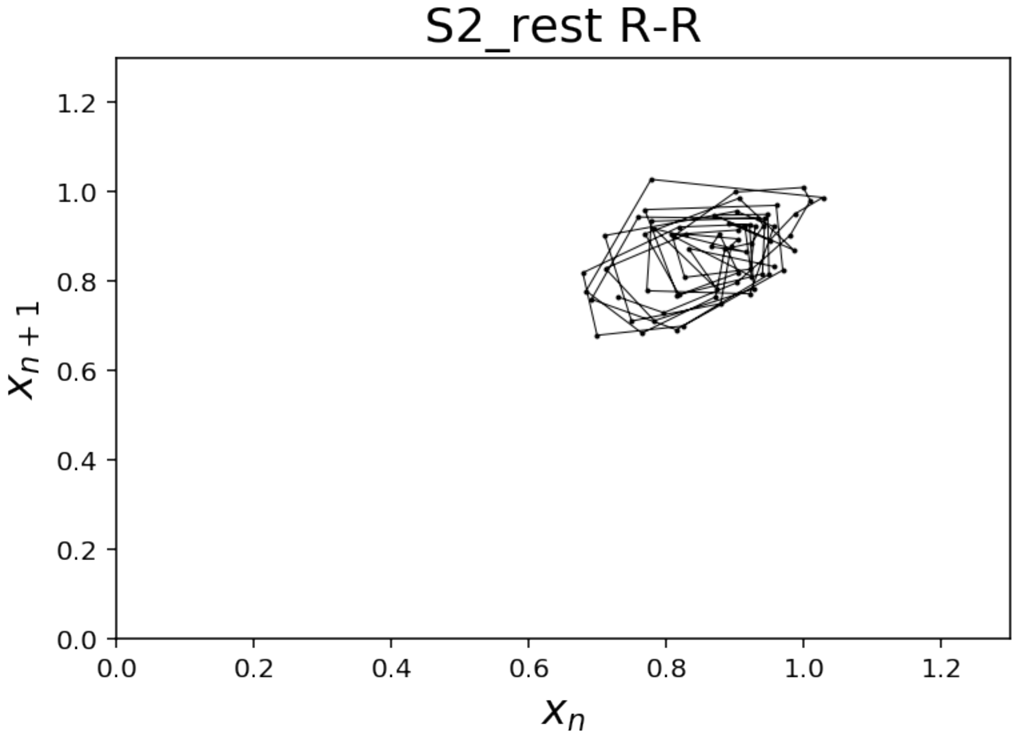
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
1.2
x_n


S2_rest R-R
x_{n+1}
1.2
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0.8
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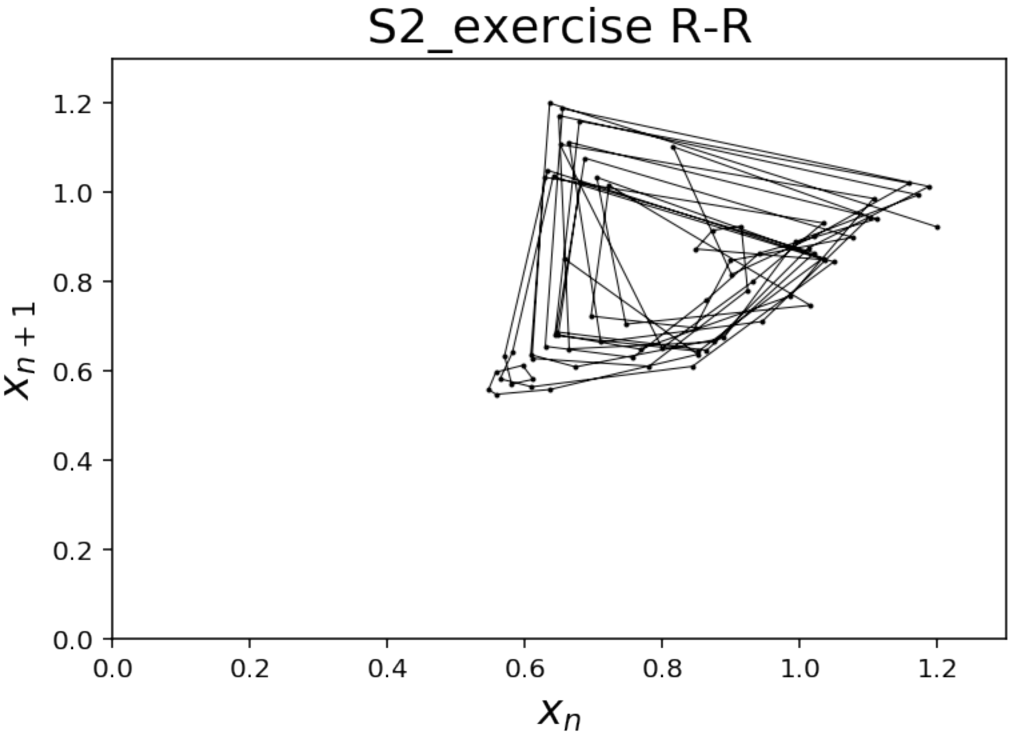
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
1.2
x_n


S2_exercise R-R
x_{n+1}
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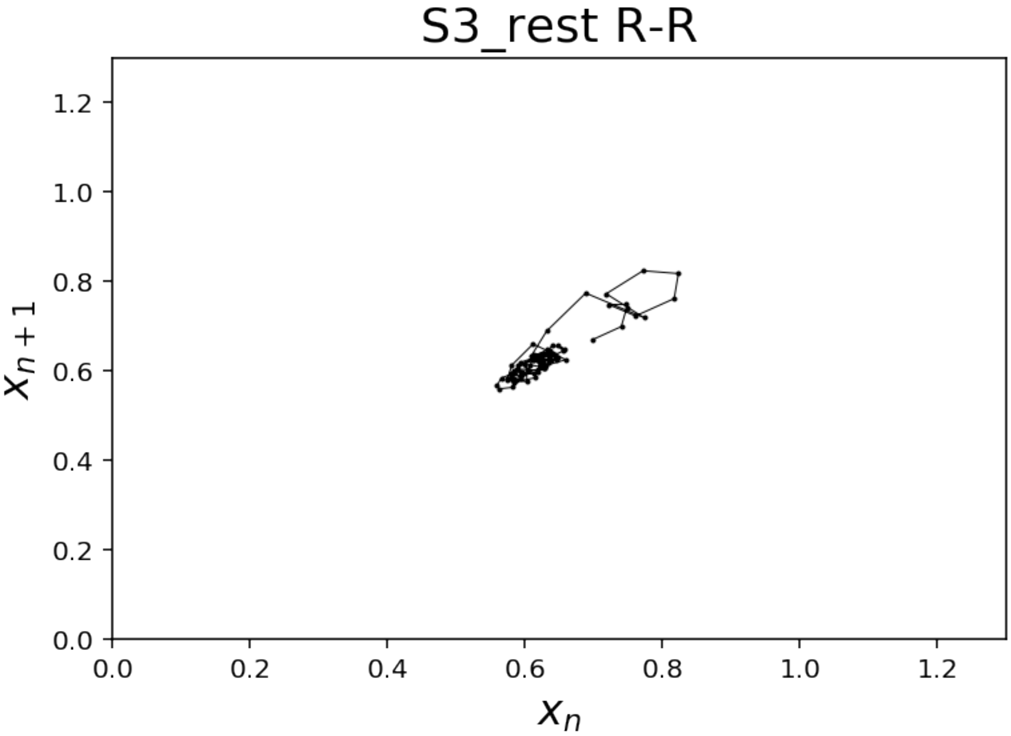
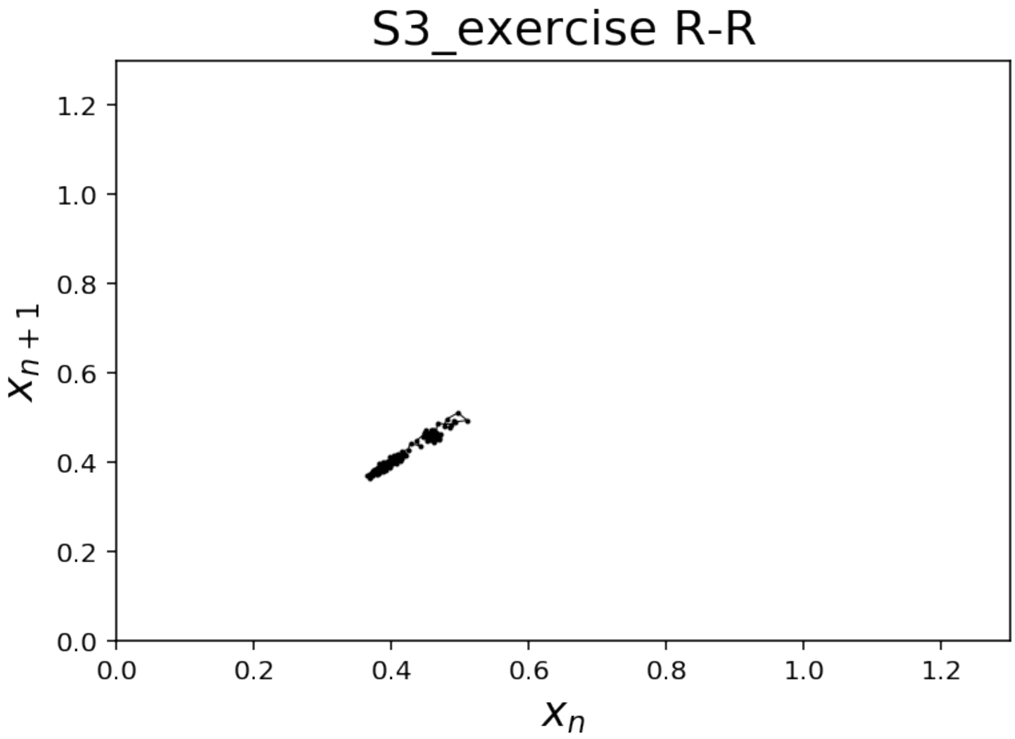
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
1.2
x_n


S3_rest R-R
x_{n+1}
1.2
1.0
0.8
0.6
0.4
0.2
0.0
0.0
0.2
0.4
0.6
0.8
1.0
1.2
x_n

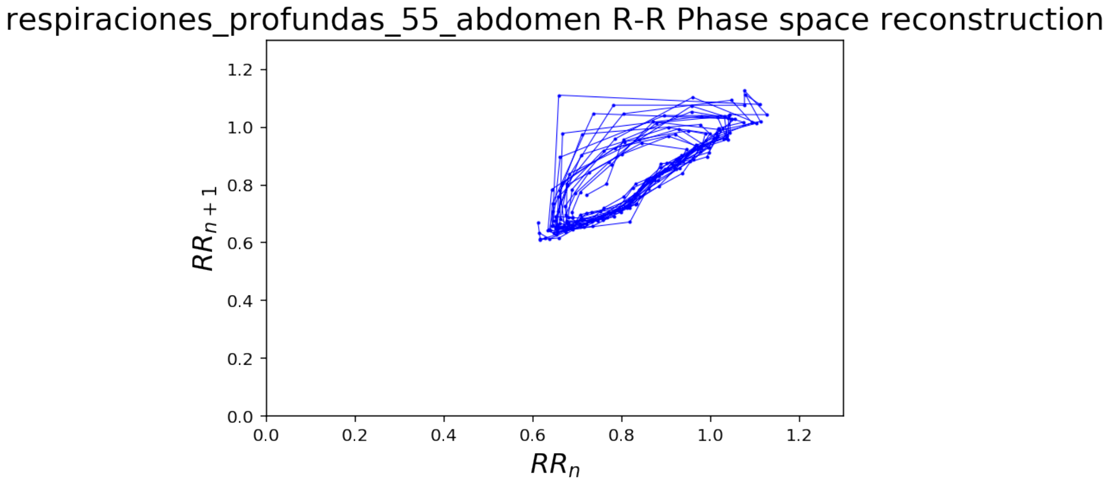


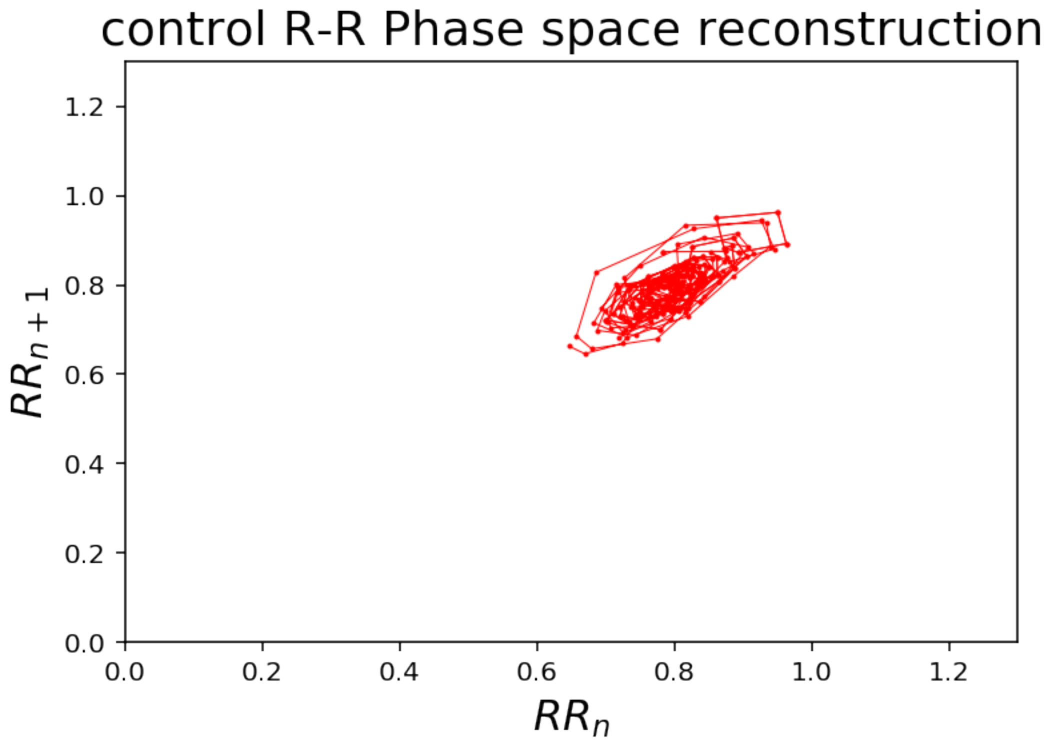
Notice how the trajectory in phase space becomes smaller when the subject is holdings his breath.

With this time series, we will use Takens theorem to see what we can recontruct. The time delay we will use is 1 R-R interval.

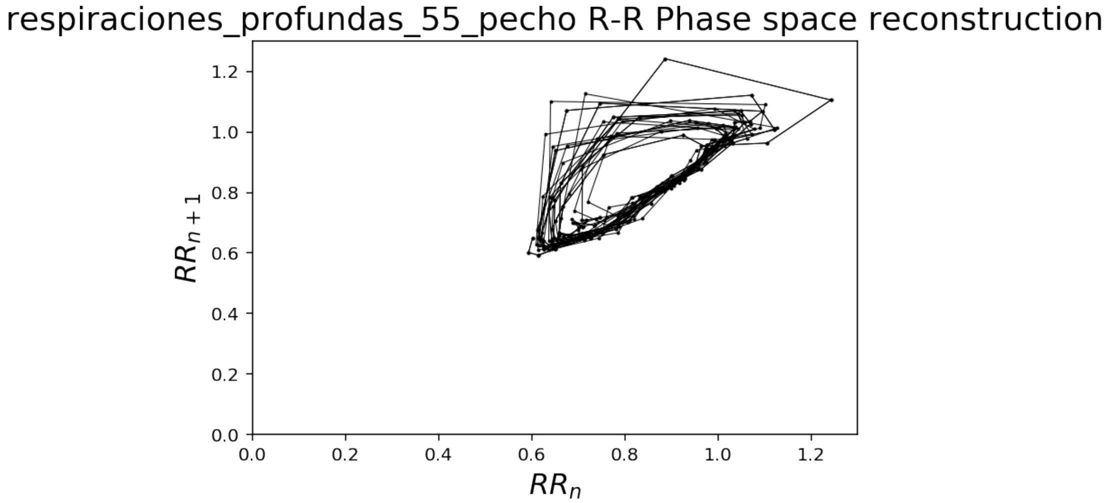
Recording superposition when the person holds his/her breath. The same colors as in the Poincaré plot are used to make it easier observe a pattern.

[12]:
```
colors = ['blue', 'red', 'black', 'purple', "orange", "green", "grey",␣
 ↪"darkred", "violet", "royalblue",
          "chocolate", "orangered", "darkcyan"]
color_index = 0
time_delay = 1

for i in range(len(recordings)):
    n = np.size(recordings[i].RR) #size of the voltage vector

    if i!= 0 and corresponding_folder[i] != corresponding_folder[i-1]:
        color_index = color_index+1
        plt.title(str(corresponding_folder[i-1]) + " R-R Phase space␣
 ↪reconstruction")
        plt.xlim(0, 1.3)
        plt.ylim(0, 1.3)
        plt.xlabel(r"$RR_n$")
        plt.ylabel(r"$RR_{n+1}$")
        plt.savefig('RR_intervals/phase_space_'+str(corresponding_folder[i])+'.
     ↪jpg')#Saves images in folder

        plt.show()

        plt. plot(recordings[i].RR[0: n-time_delay], recordings[i].
     ↪RR[time_delay: n],
              marker = "o", markersize = 1, linewidth = 0.5, c=␣
     ↪colors[color_index])

    plt. plot(recordings[i].RR[0: n-time_delay], recordings[i].RR[time_delay:␣
     ↪n],
              marker = "o", markersize = 1, linewidth = 0.5, c=␣
     ↪colors[color_index])

plt.title(str(corresponding_folder[i-1]) + " R-R")
plt.xlim(0, 1.3)
plt.ylim(0, 1.3)
plt.xlabel(r"$RR_n$")
plt.ylabel(r"$RR_{n+1}$")
plt.savefig('RR_intervals/phase_space_'+str(corresponding_folder[i])+'.
     ↪jpg')#Saves images in folder
plt.show()
```

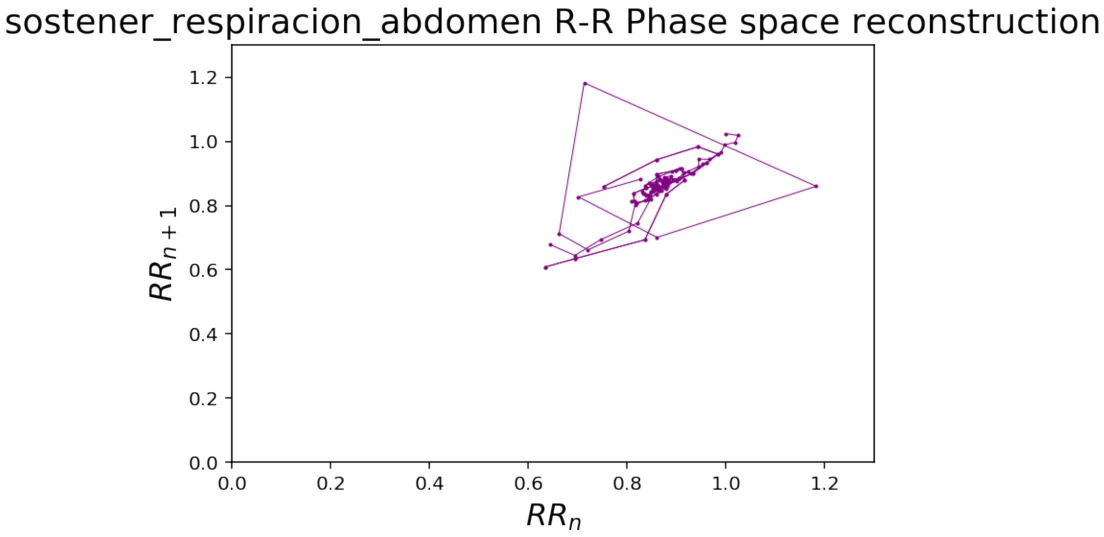


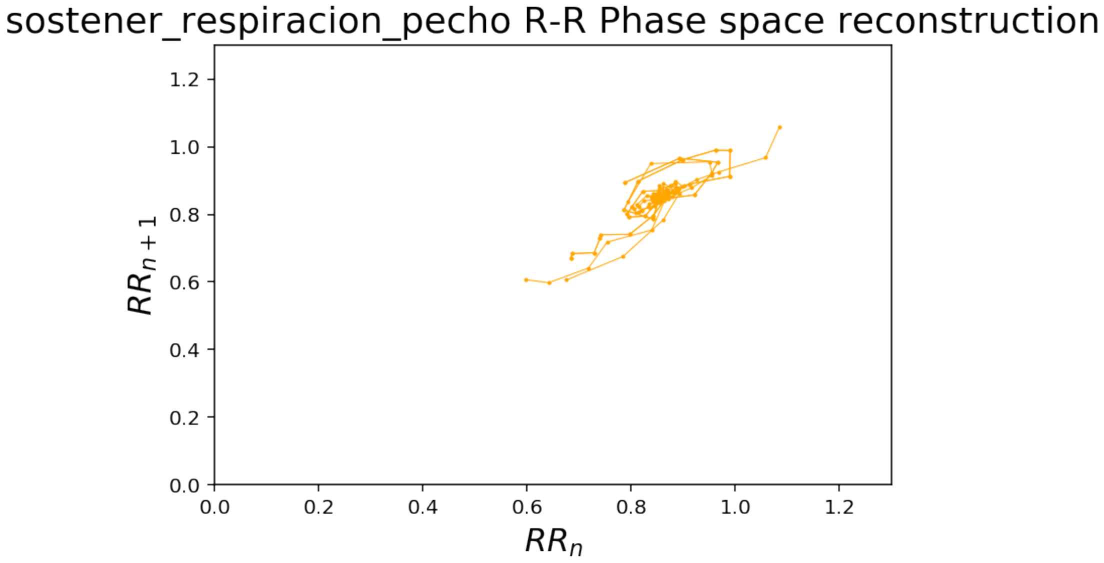


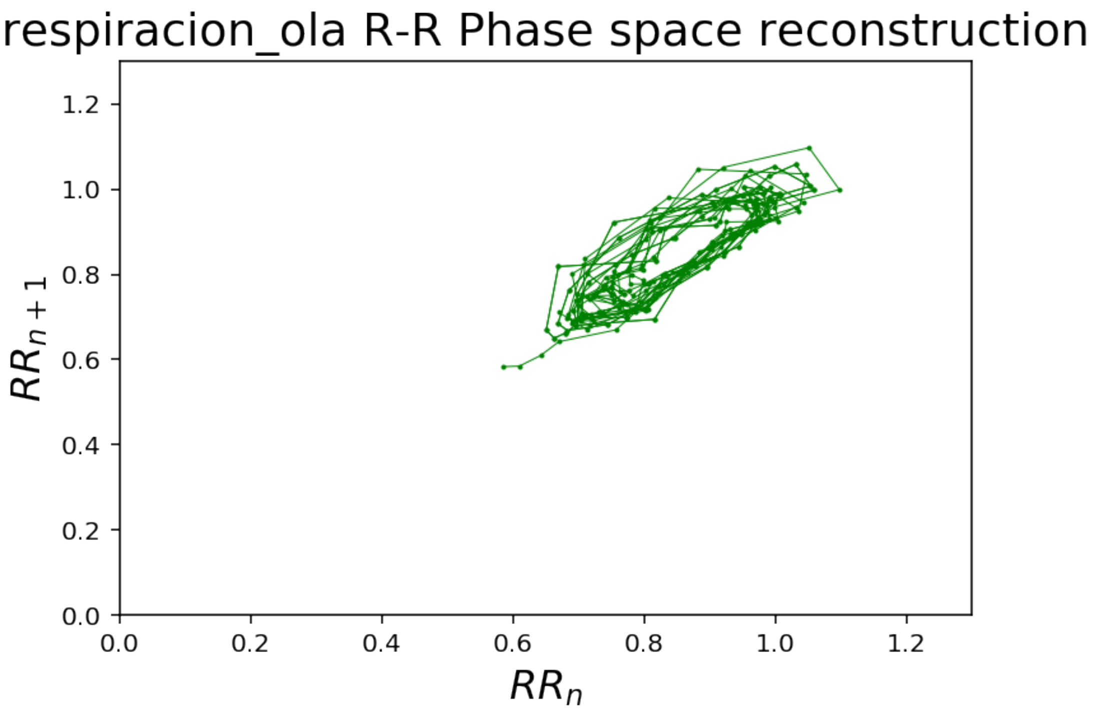
control R-R Phase space reconstruction

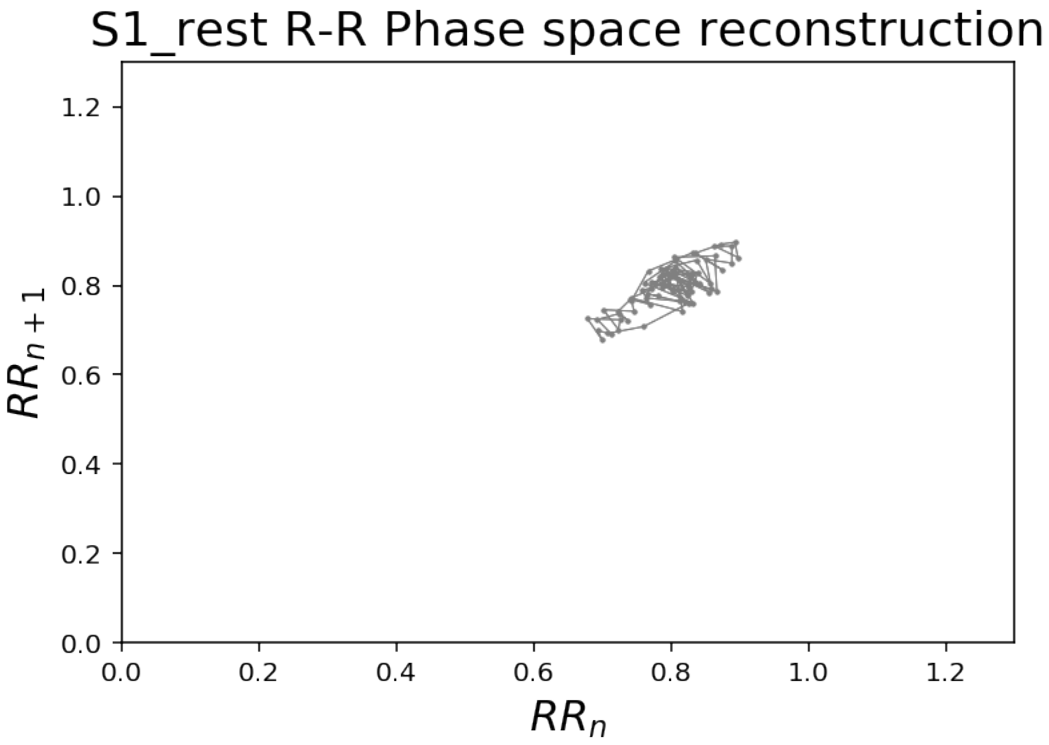


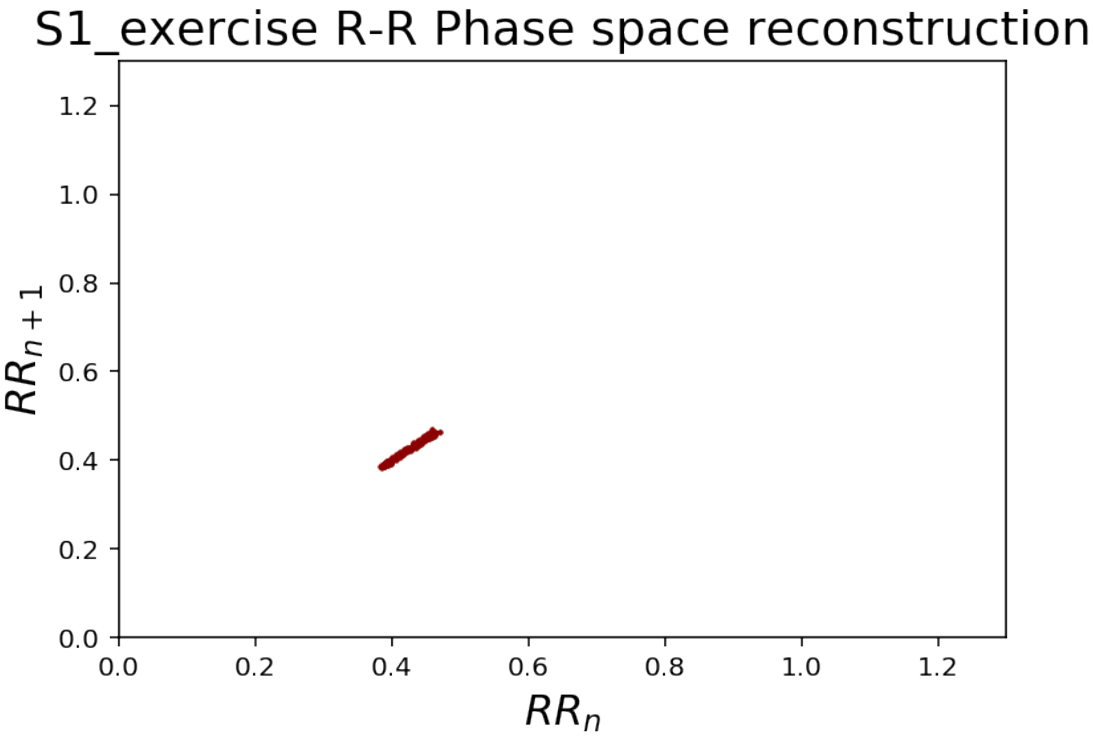
respiraciones_profundas_55_pecho R-R Phase space reconstruction

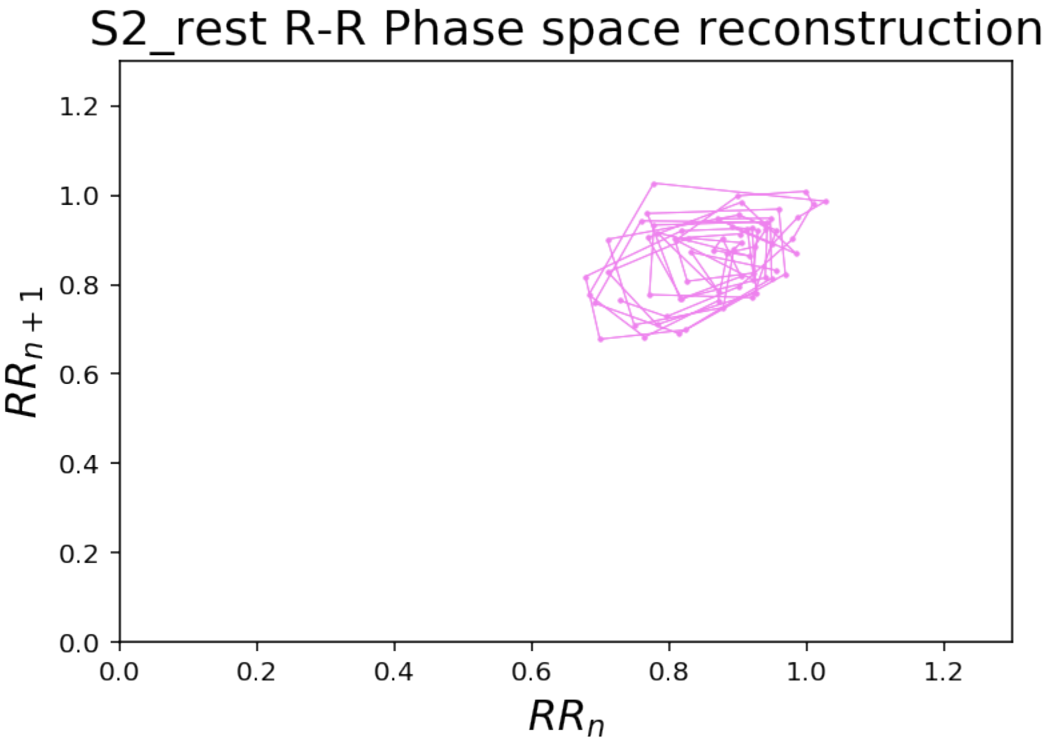

sostener_respiracion_abdomen R-R Phase space reconstruction

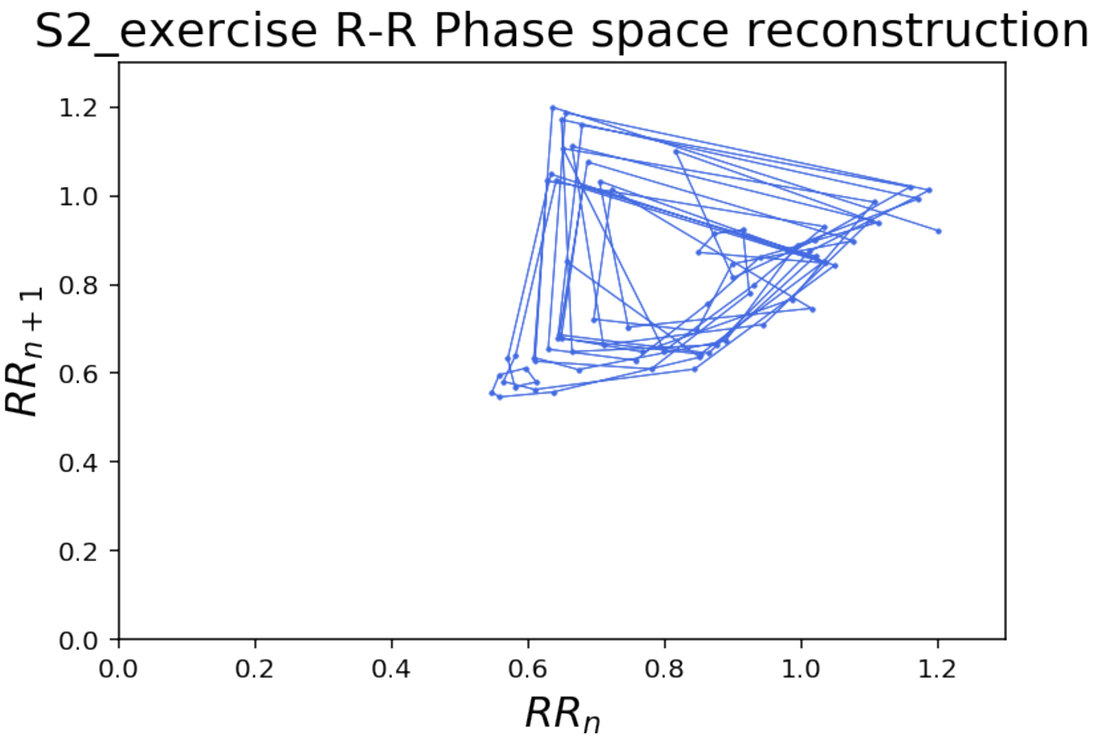

sostener_respiracion_pecho R-R Phase space reconstruction

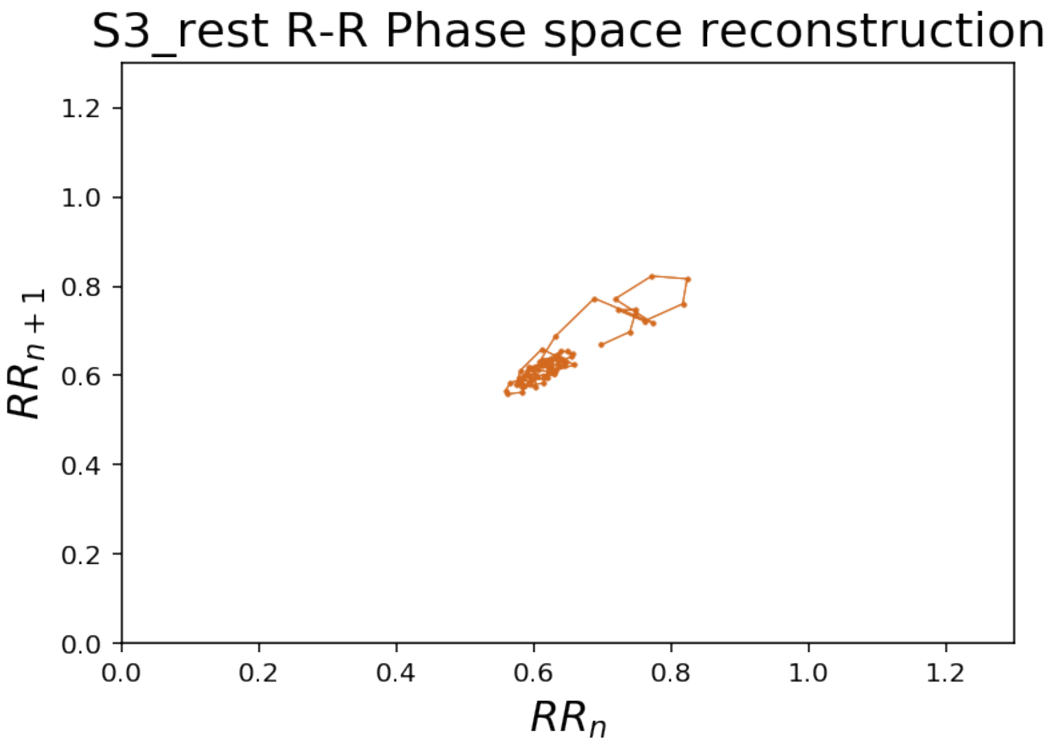

respiracion_ola R-R Phase space reconstruction
1.2
1.0
0.8
0.6
0.4
0.2
0.0
RR_{n+1}
0.0
0.2
0.4
0.6
0.8
1.0
1.2
RR_n

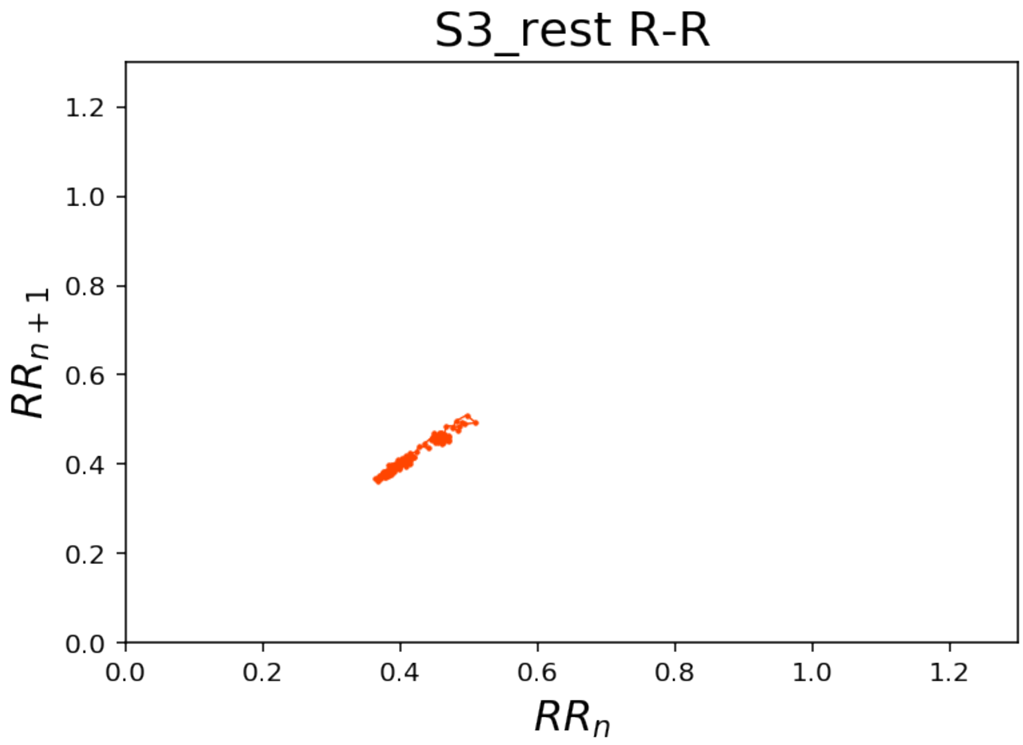

S1_rest R-R Phase space reconstruction
1.2
1.0
0.8
0.6
0.4
0.2
0.0
RR_{n+1}
0.0
0.2
0.4
0.6
0.8
1.0
1.2
RR_n


S1_exercise R-R Phase space reconstruction
RR_{n+1}
RR_n
0.0
0.2
0.4
0.6
0.8
1.0
1.2
0.0
0.2
0.4
0.6
0.8
1.0
1.2


S2_rest R-R Phase space reconstruction
RR_{n+1}
RR_n
0.0
0.2
0.4
0.6
0.8
1.0
1.2
0.0
0.2
0.4
0.6
0.8
1.0
1.2

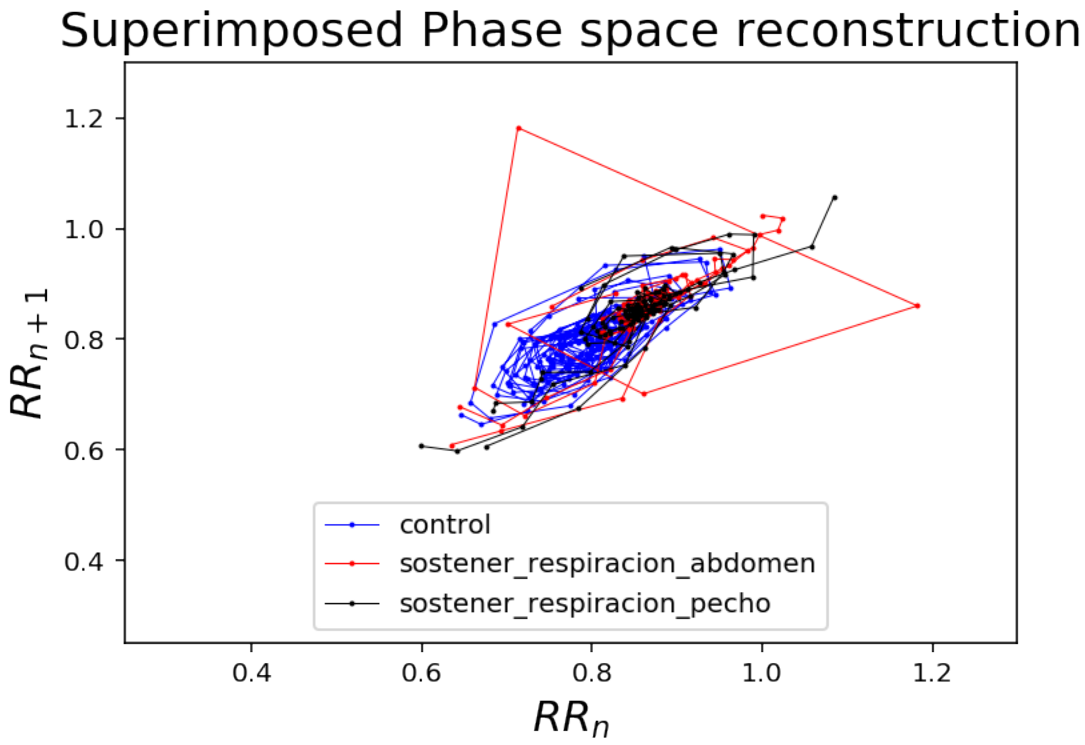

S2_exercise R-R Phase space reconstruction
RR_{n+1}
RR_n
0.0
0.2
0.4
0.6
0.8
1.0
1.2


S3_rest R-R Phase space reconstruction
RR_{n+1}
RR_n
0.0
0.2
0.4
0.6
0.8
1.0
1.2



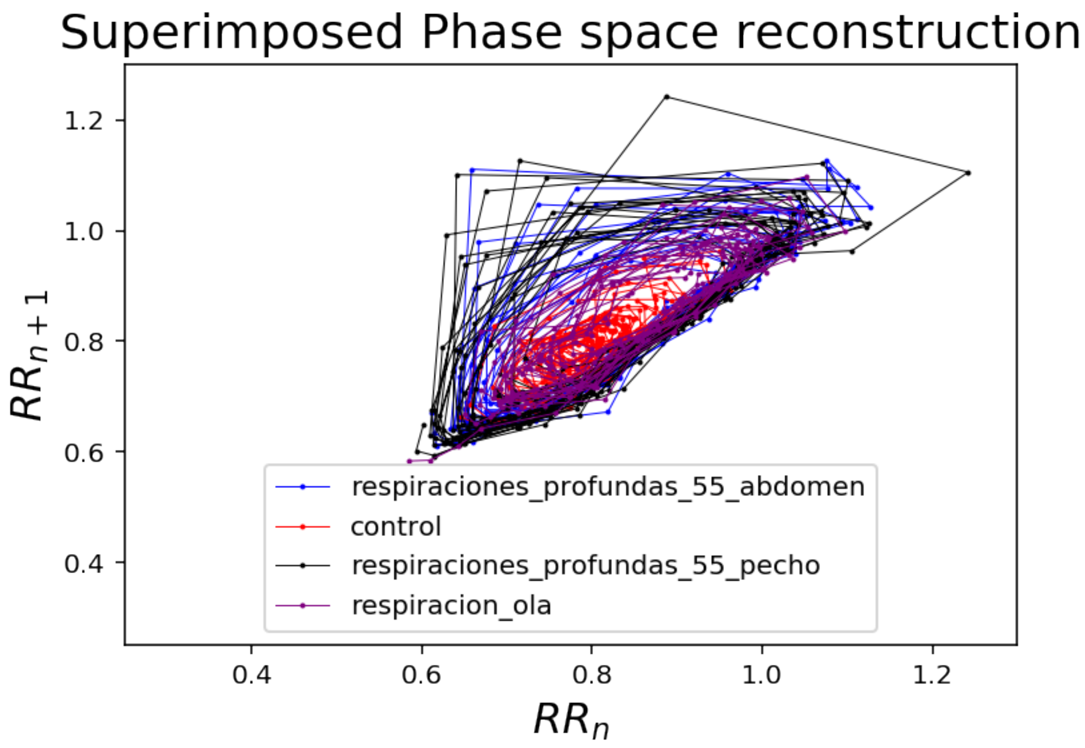
```
[13]: # Comparison between control, holding breath in chest and holding breath in␣
       ↪abdomen
      colors = ['blue', 'red', 'black', 'purple', "orange", "green"]
      color_index = 0
      banner = False
      time_delay = 1

      for i in range(len(recordings)):
          if corresponding_folder[i]=="control" or "sostener" in␣
       ↪corresponding_folder[i]: #First event
              n = np.size(recordings[i].RR) #size of the voltage vector

              if banner == False: #First event
                  plt. plot(recordings[i].RR[0: n-time_delay], recordings[i].
       ↪RR[time_delay: n],
                            marker = "o", markersize = 1, linewidth = 0.5, c=␣
       ↪colors[color_index],
                            label = corresponding_folder[i])
              else: #Other events, does not plot label
```

```
            plt. plot(recordings[i].RR[0: n-time_delay], recordings[i].
↪RR[time_delay: n],
                      marker = "o", markersize = 1, linewidth = 0.5, c=␣
↪colors[color_index])
        banner = True

    if len(recordings)-1 != i:
        if banner == True and corresponding_folder[i] !=␣
↪corresponding_folder[i+1]:
            color_index = color_index+1
            banner = False


plt.title("Superimposed Phase space reconstruction")
plt.xlim(0.25, 1.3)
plt.ylim(0.25, 1.3)
plt.xlabel(r"$RR_n$")
plt.ylabel(r"$RR_{n+1}$")
plt.legend(loc='lower center')
plt.savefig('RR_intervals/phase_space_superimposed_sostener.jpg') #Saves images␣
↪in folder
plt.show()
```



[14]:

```
# Comparar: control, respiraciones profundas 55 pecho, respiraciones profundas␣
↪55 abdomen, respiraciones en ola.

colors = ['blue', 'red', 'black', 'purple', "orange", "green"]
color_index = 0
banner = False
time_delay = 1

for i in range(len(recordings)):
    if corresponding_folder[i]=="control" or "55" in corresponding_folder[i] or␣
↪"ola" in corresponding_folder[i]: #First event
        n = np.size(recordings[i].RR) #size of the voltage vector

        if banner == False: #First event
            plt. plot(recordings[i].RR[0: n-time_delay], recordings[i].
↪RR[time_delay: n],
                      marker = "o", markersize = 1, linewidth = 0.5, c=␣
↪colors[color_index],
                      label = corresponding_folder[i])
        else: #Other events, does not plot label
            plt. plot(recordings[i].RR[0: n-time_delay], recordings[i].
↪RR[time_delay: n],
                      marker = "o", markersize = 1, linewidth = 0.5, c=␣
↪colors[color_index])
        banner = True

    if len(recordings)-1 != i:
        if banner == True and corresponding_folder[i] !=␣
↪corresponding_folder[i+1]:
            color_index = color_index+1
            banner = False

plt.title("Superimposed Phase space reconstruction")
plt.xlabel(r"$RR_n$")
y = r'$RR_{n+1}$'
plt.ylabel(y)
plt.xlim(0.25, 1.3)
plt.ylim(0.25, 1.3)
plt.legend(loc='lower center')
plt.savefig('RR_intervals/phase_space_superimposed_respirar.jpg') #Saves images␣
↪in folder
plt.show()
```



[ ]:

[ ]:

5.0.1 Exercise: Are the results obtained in a Poincaré plot and in a recurrence plot contradictory? While we are observing a loss in the first plot's variability with exercise, we are seeing the opposite in a recurrence plot. Why?

[ ]:

6 Recurrence plots

This is a technique which compares every single data point to every other. Because of this reason, it is a very expensive algorithm computationaly. To reduce this computational time, we must create a surrogate data set. Be sure to create a surrogate data set that includes at least two QRS complexes.

In the following cell, change the start and end values to obtain two QRS complexes.

[15]:

```
# Heat map Recurrence plot
def recurrence_plot(surrogate, data_point_delay = 25):
    n = len(surrogate)
    euclid = np.zeros((n,n), dtype = 'float')
    normal_euclid = np.zeros((n,n), dtype = 'float')

    #Cycle for obtaining the euclid distance between any two points
    for i in range(0, n-data_point_delay):
        for j in range(data_point_delay, n):
            euclid[i][j] = np.sqrt(np.abs(surrogate[i]**2 - surrogate[j]**2))␣
 ↪#euclidian norm

    normal_aux = np.max(euclid)

    # Cycle for normalizing the distance
    for i in range(0, n-data_point_delay):
        for j in range(data_point_delay, n):
            normal_euclid[i][j] = np.abs(euclid[i][j]/normal_aux-1)
            #Normalizing the values, and the farthest points have the lowest␣
 ↪value (0),
            #while the nearest points have a value near 1

    return normal_euclid

def graph_recurrence(surrogate_data, index_surrogate, normal_euclid, label):

    #Initializing the graphic space
    fig = plt.figure(figsize=(6,8))
    gs = mpl.gridspec.GridSpec(2, 2, height_ratios=[1, 1], width_ratios=[2, 1])
    ax1 = fig.add_subplot(gs[1, 0])
    ax2 = fig.add_subplot(gs[0, 0], sharex=ax1)
    plt.tick_params(which='both', top=False, right=False)
    ax2.set_autoscalex_on(False)

    # Tachogram
    ax1.set_title("Tachogram")
    ax1.set_ylabel('R-R interval')
    ax1.set_xlabel('Time index')
    ax1.set_xlim(0, len(surrogate_data))
    ax1.set_ylim(0.3, 1.3)
    ax1.plot(index_surrogate, surrogate_data, marker="o", c="k")␣
 ↪#index_surrogate or time_surrogate (ms)

    # Recurrence plot
    ax2.set_title("Recurrence plot")
    ax2.set_ylabel('Time index')
    ax2.set_xlabel('Time index')
    plot = ax2.imshow(normal_euclid, origin='lower', aspect="auto", cmap="jet")
    axins = inset_axes(ax2,
                   width="5%", # width = 10% of parent_bbox width
                   height="100%", # height : 50%
                   loc=6,
                   bbox_to_anchor=(1.05, 0., 1, 1),
                   bbox_transform=ax2.transAxes,
                   borderpad=0,)

    cbar = plt.colorbar(plot, cax=axins)

    fig.tight_layout()
    fig.savefig('recurrence_images/'+str(label)+'.jpg')#, bbox_inches='tight', dpi=150) #Saves images in folder

    plt.show()
    return None
```

An important detail to mention is that every recurrence plot is being normalized by its own metric. The biggest distance is being taken to normalize each individual recurrence plot. That means that colors in different plots are not necessarily equivalent. For example, what is red in one plot could be a lighter shade of orange in another.

[16]:

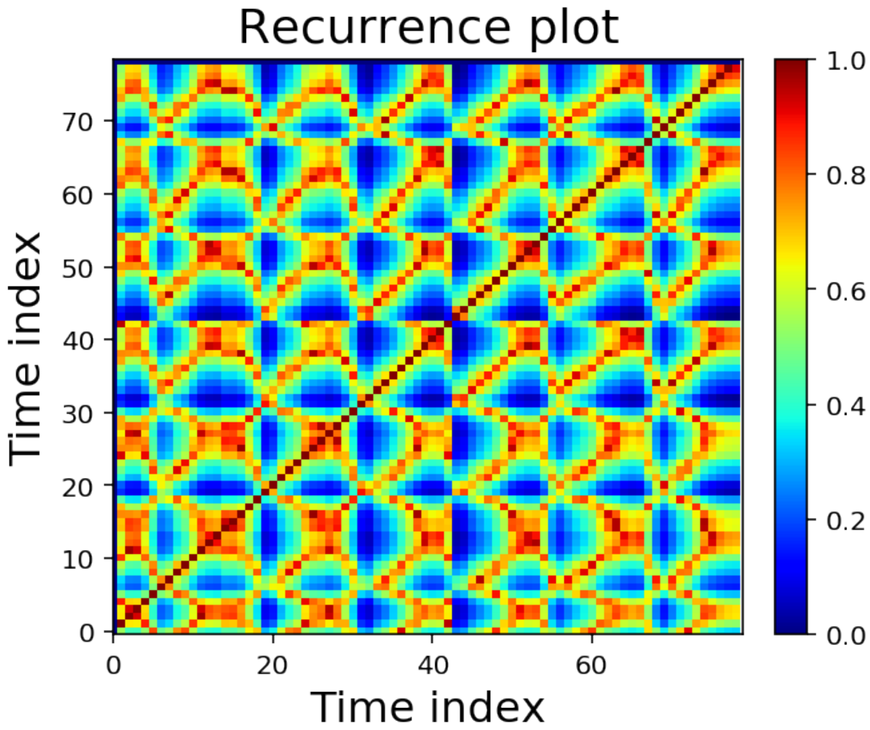
```
normal_euclid = []

for i in range(len(recordings)):
    normal_euclid.append(recurrence_plot(recordings[i].RR, 1))
    print("Finished recording "+str(i+1))
```

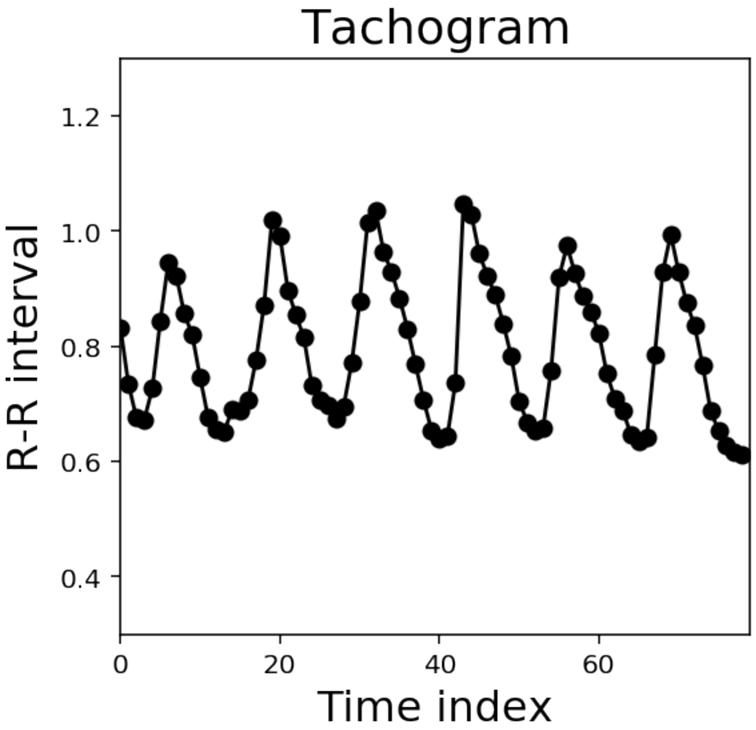
```
Finished recording 1
Finished recording 2
Finished recording 3
Finished recording 4
Finished recording 5
Finished recording 6
Finished recording 7
Finished recording 8
Finished recording 9
Finished recording 10
Finished recording 11
Finished recording 12
Finished recording 13
Finished recording 14
Finished recording 15
Finished recording 16
Finished recording 17
Finished recording 18
Finished recording 19
Finished recording 20
Finished recording 21
Finished recording 22
Finished recording 23
Finished recording 24
```

[18]:

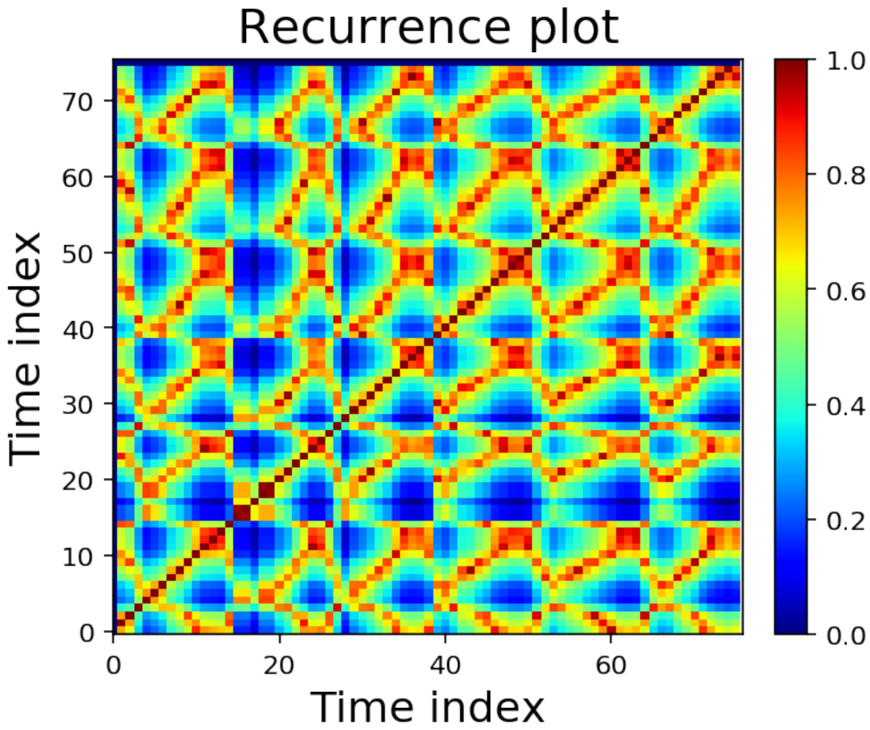
```
for i in range(len(recordings)):
    print("Recording " + corresponding_folder[i])
    graph_recurrence(recordings[i].RR,
                     [i for i in range(0, len(recordings[i].RR))], #Array of␣
 ↪indexes
                     normal_euclid[i],
                     "rec"+str(i)+"_"+str(corresponding_folder[i]))
```

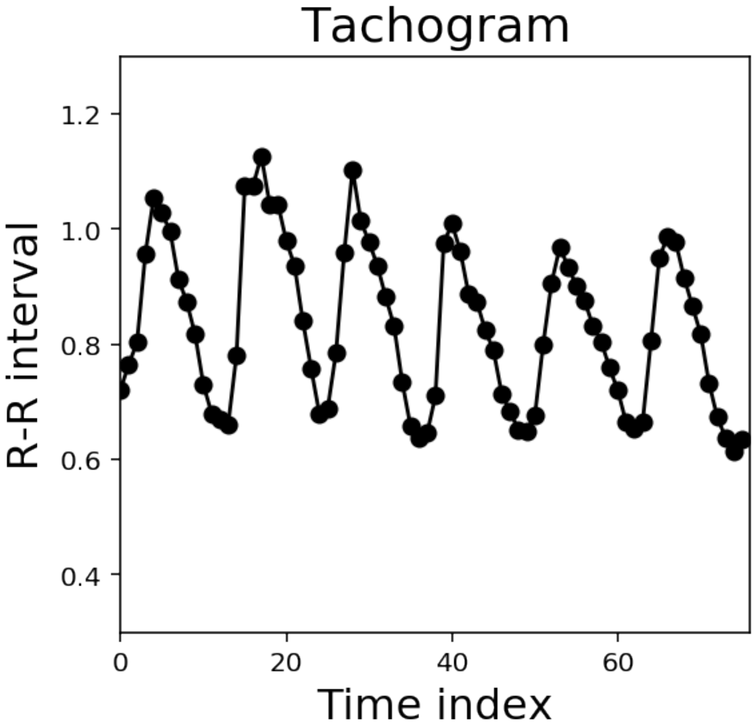
```
Recording respiraciones_profundas_55_abdomen
```



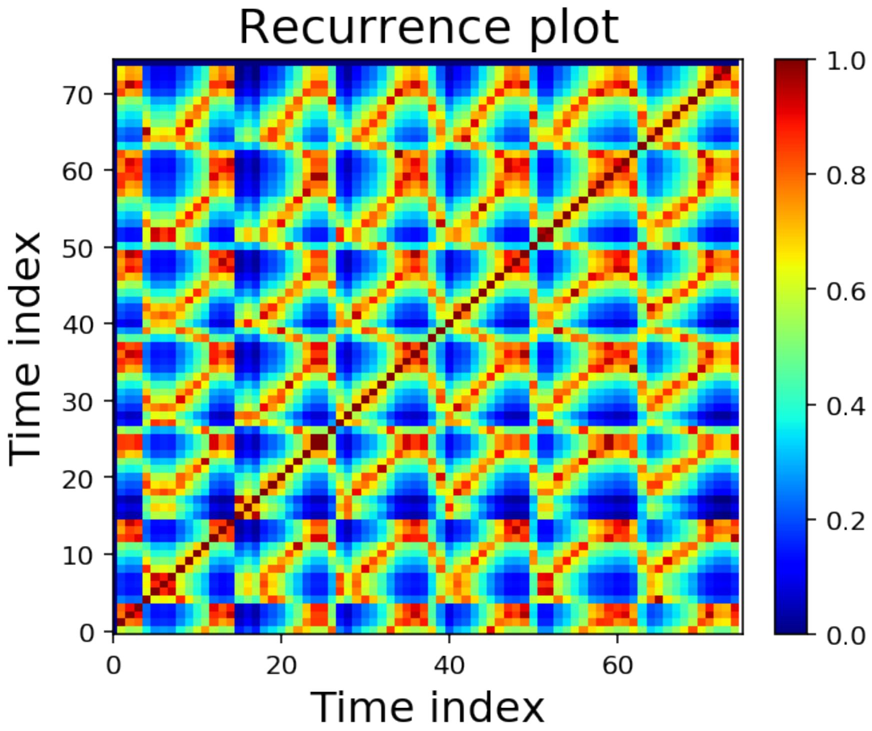


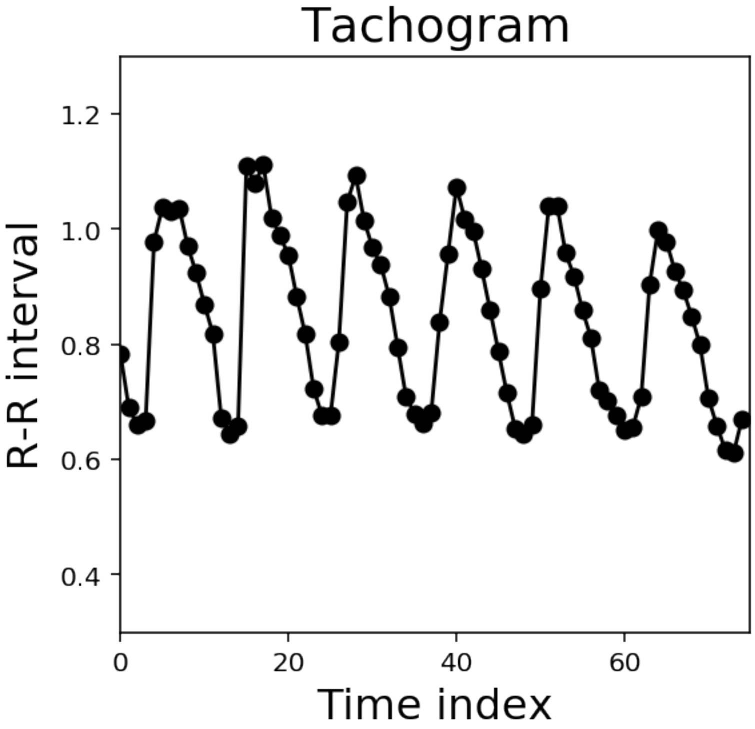
`Recording respiraciones_profundas_55_abdomen`



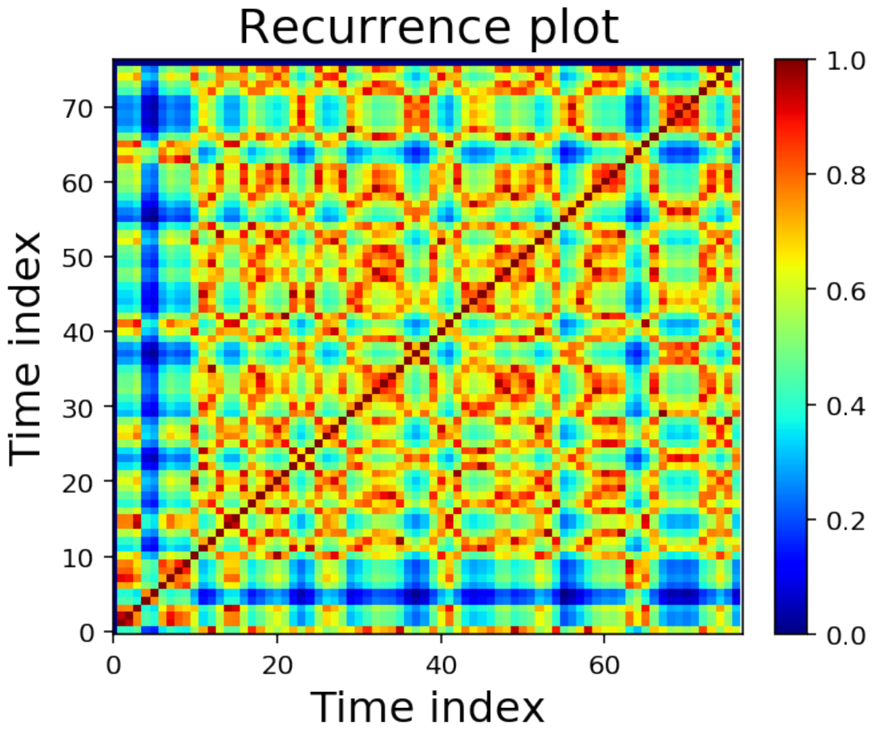


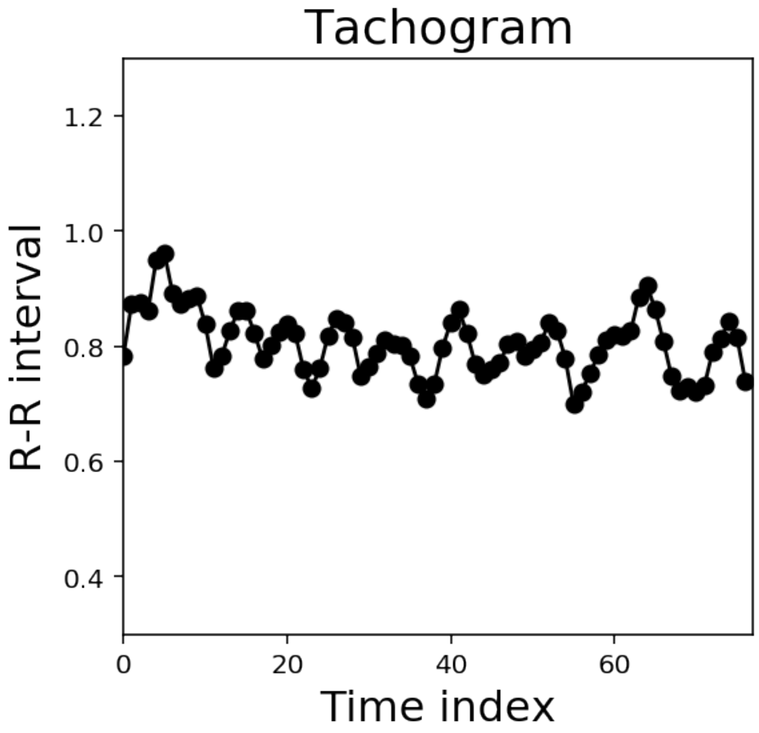
`Recording respiraciones_profundas_55_abdomen`



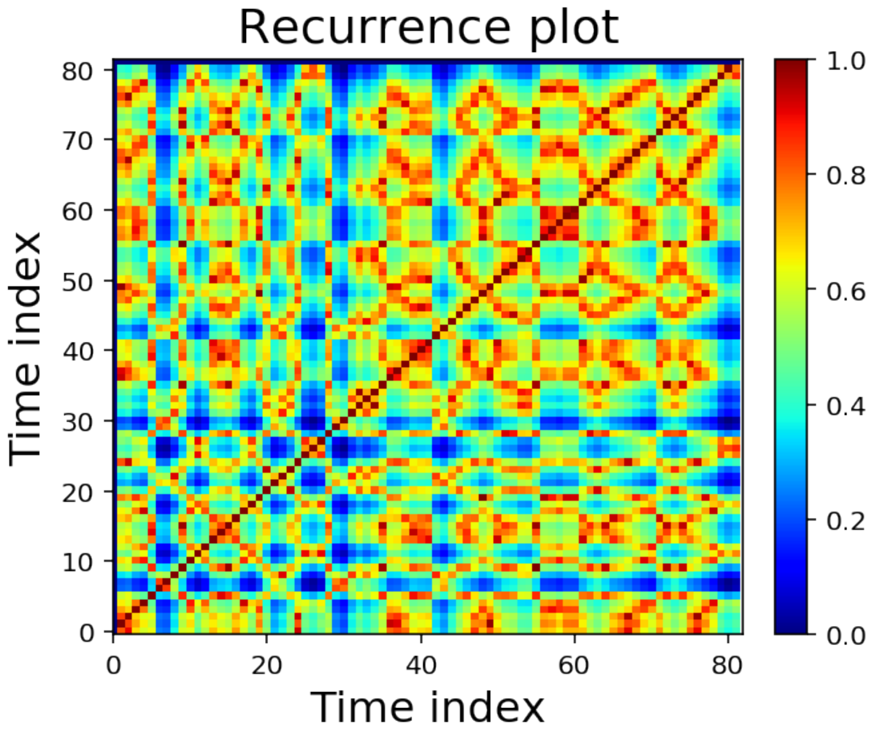


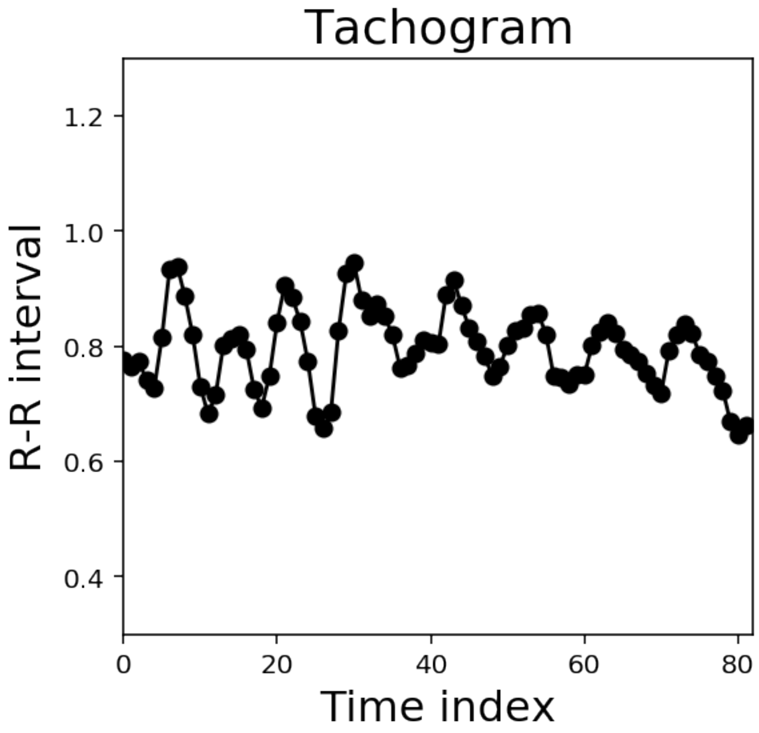
`Recording control`



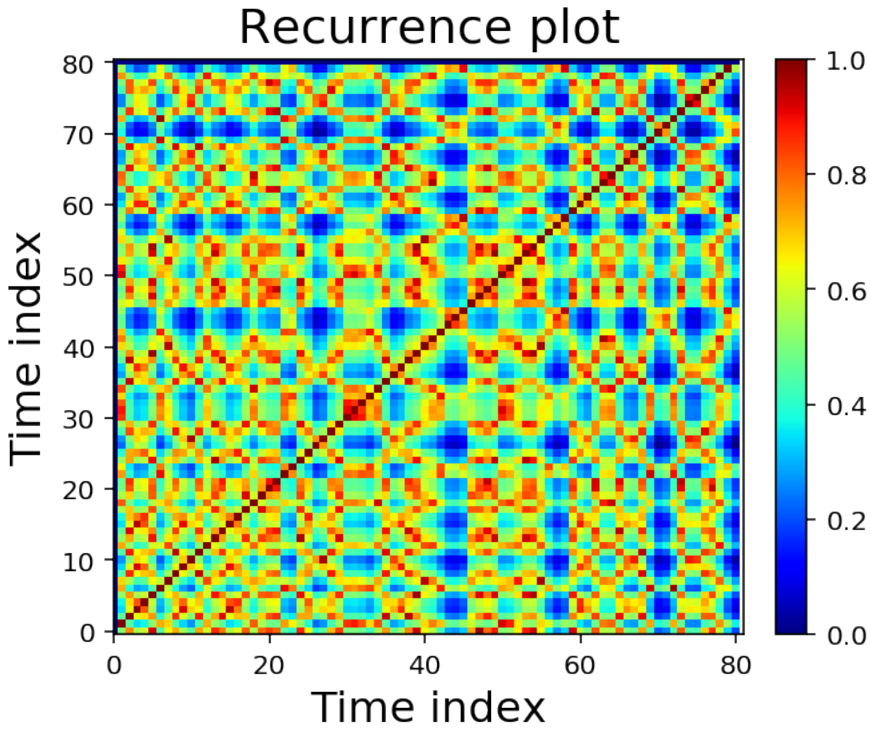


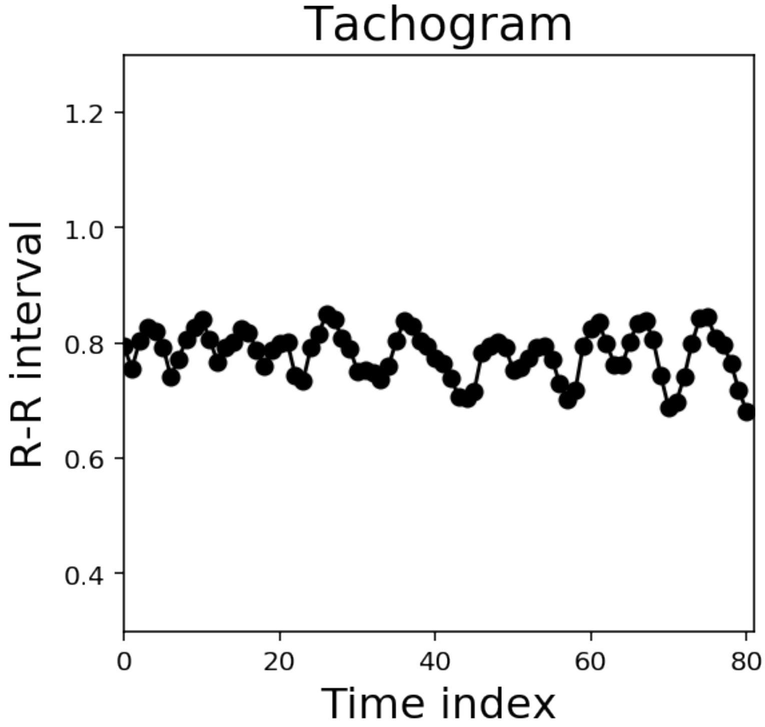
`Recording control`



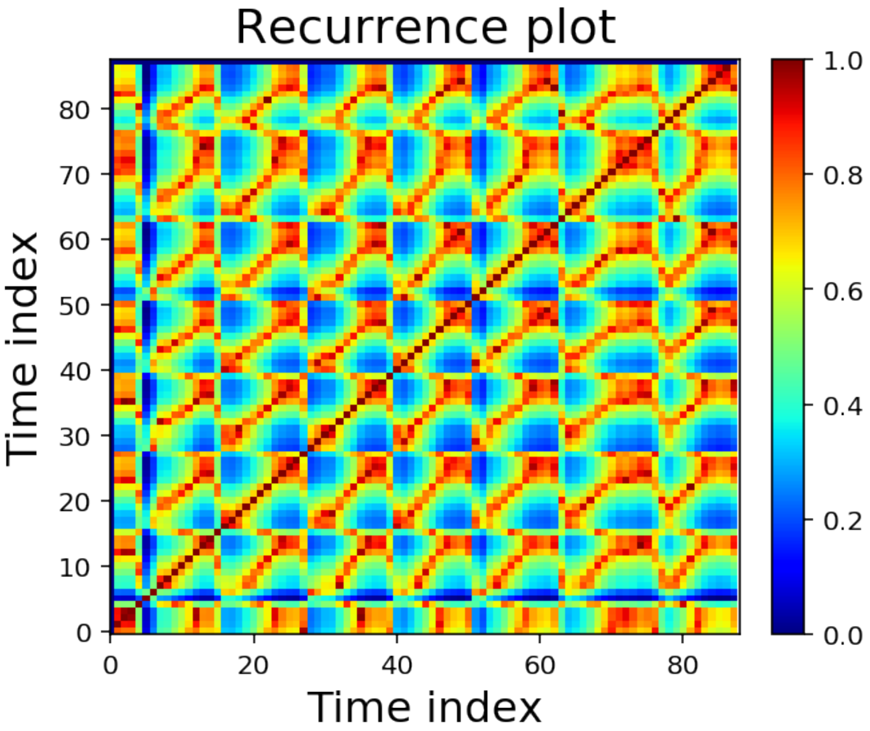


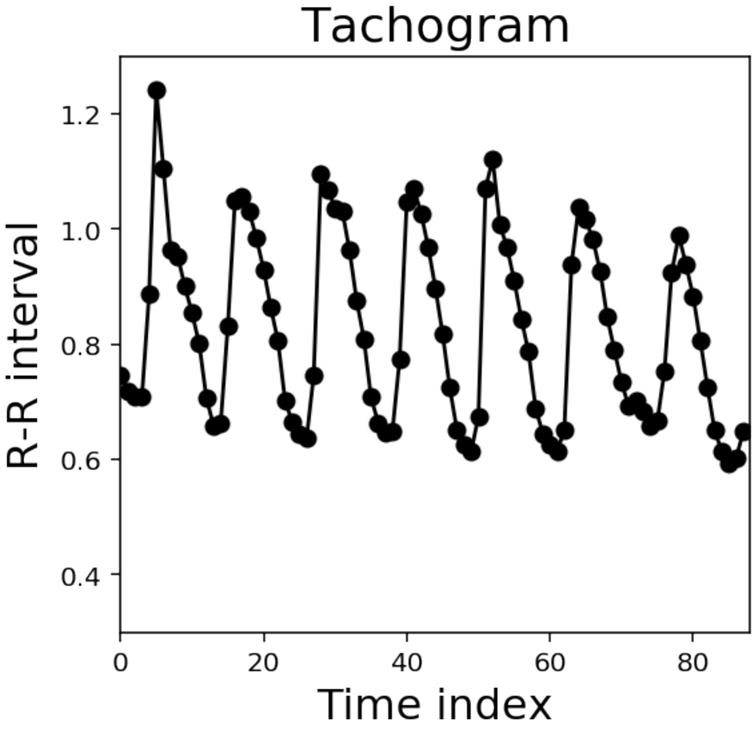
`Recording control`



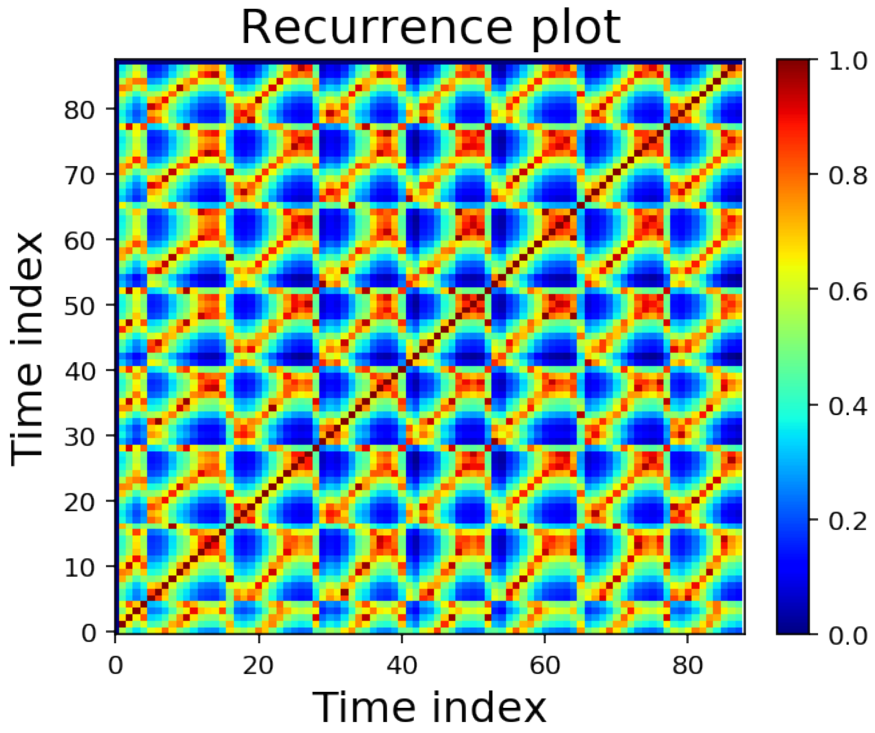


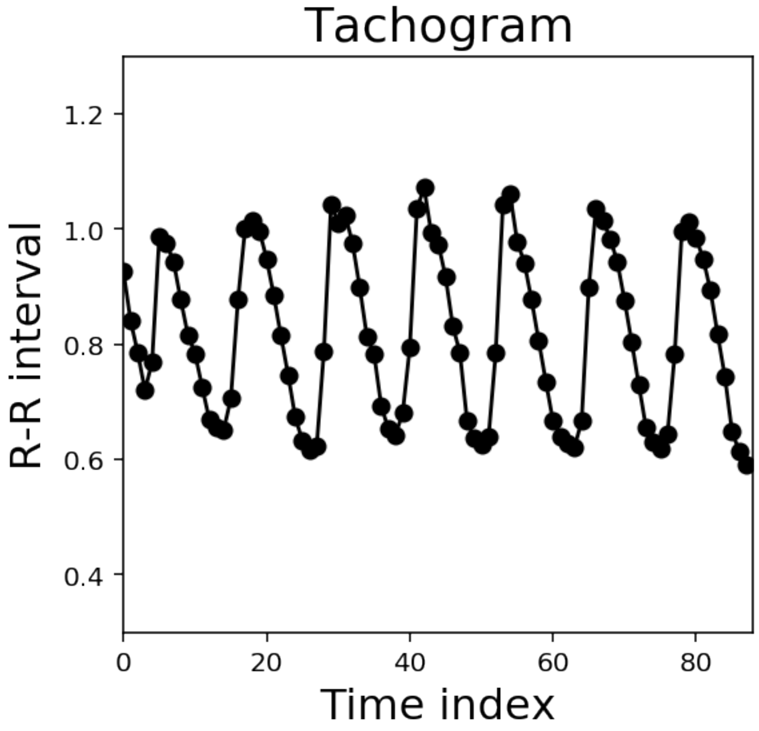
```
Recording respiraciones_profundas_55_pecho
```



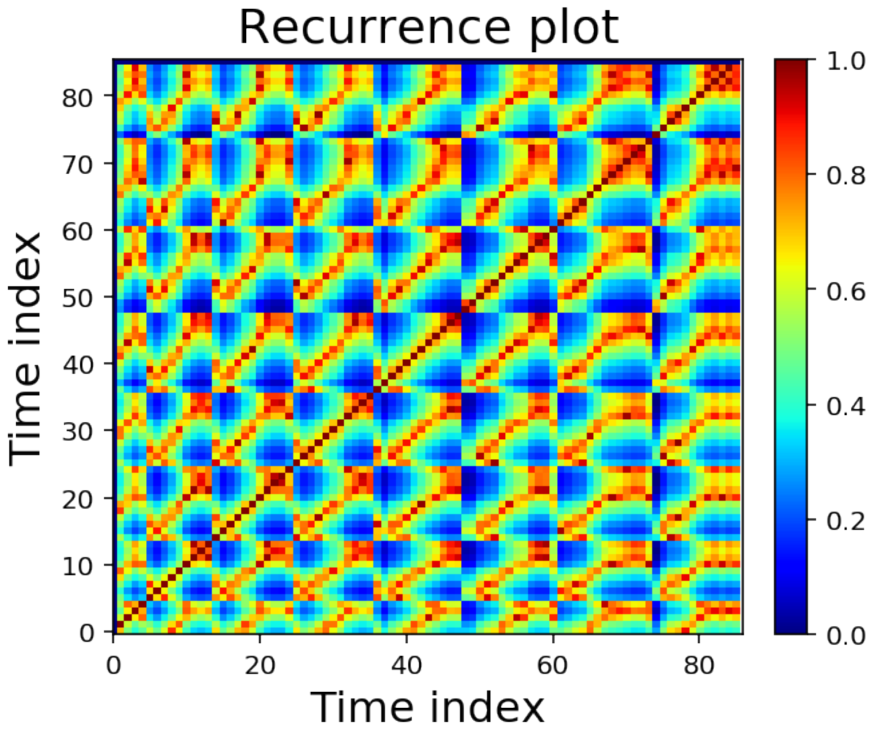


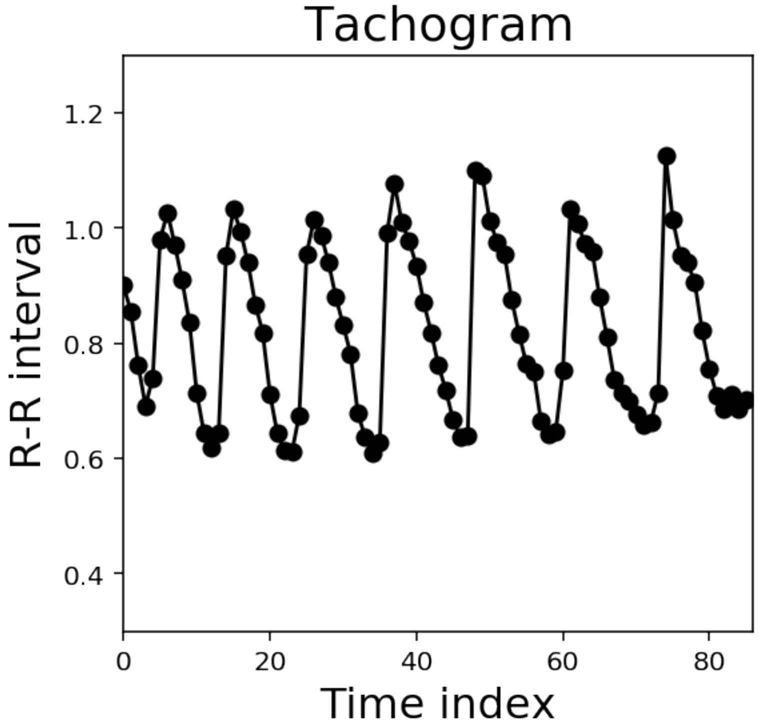
`Recording respiraciones_profundas_55_pecho`



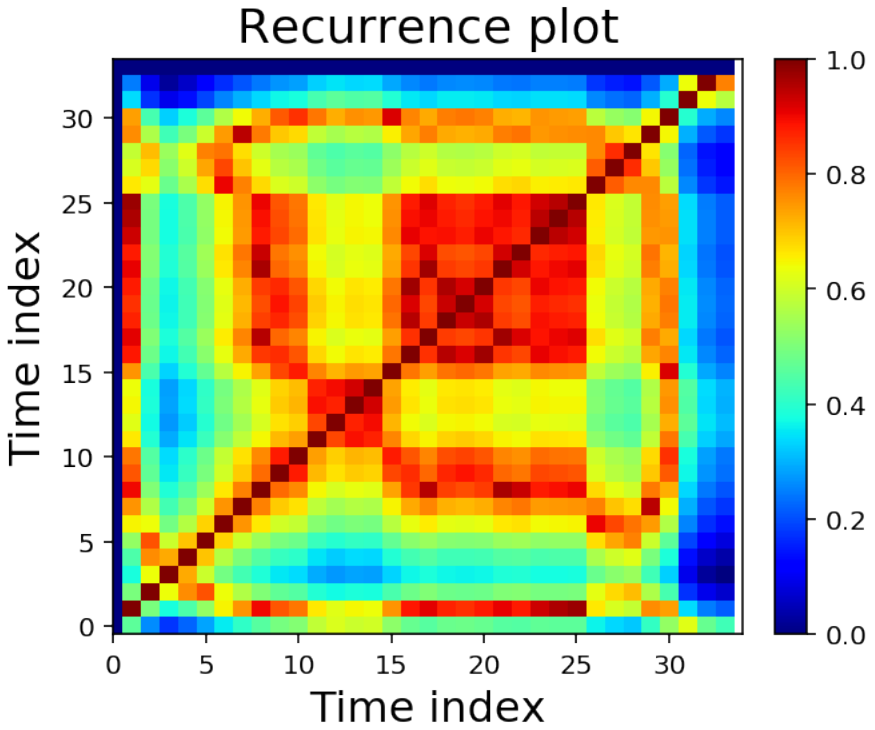


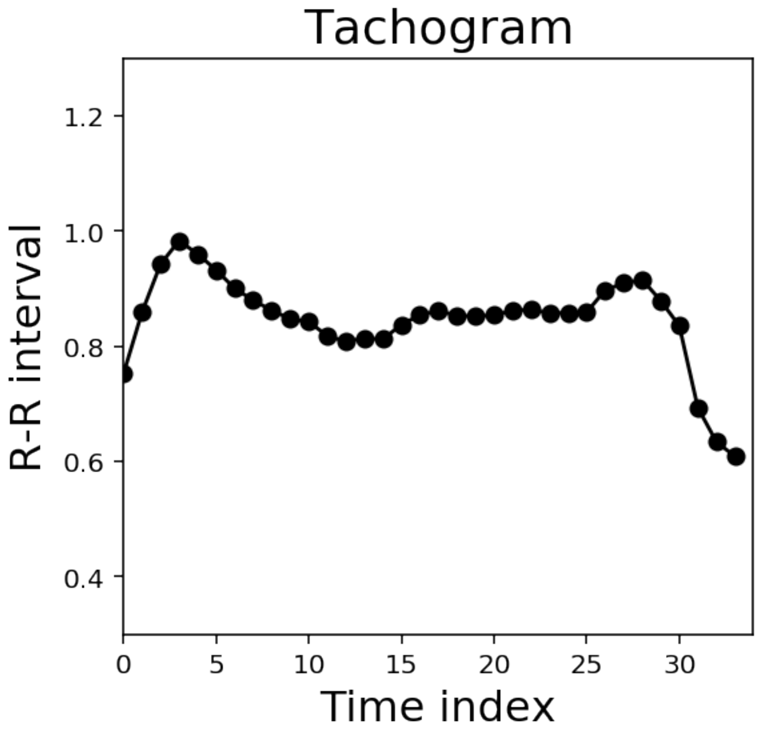
Recording respiraciones_profundas_55_pecho



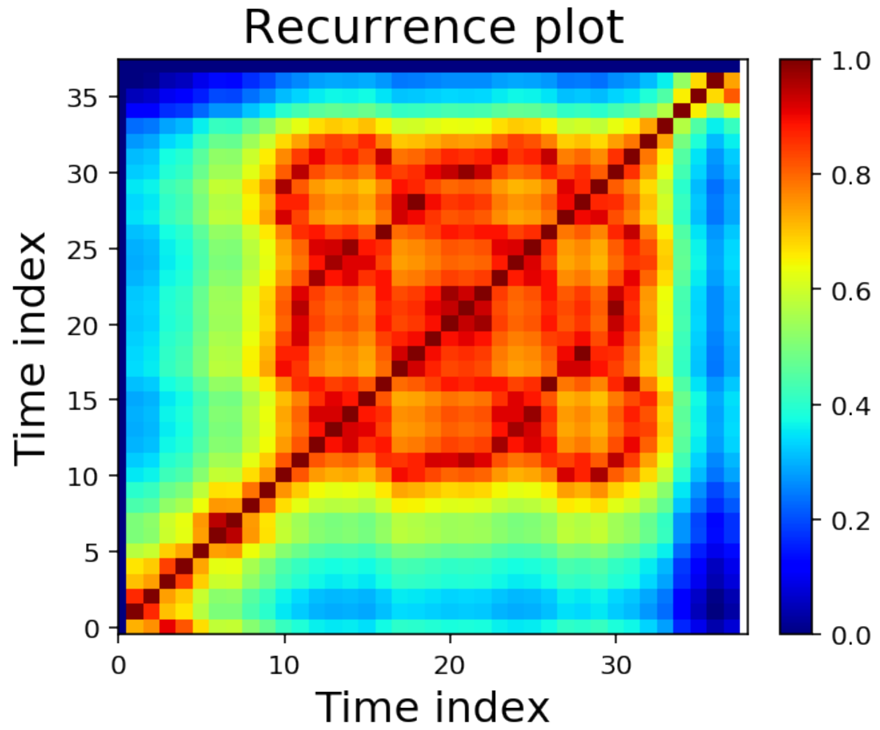


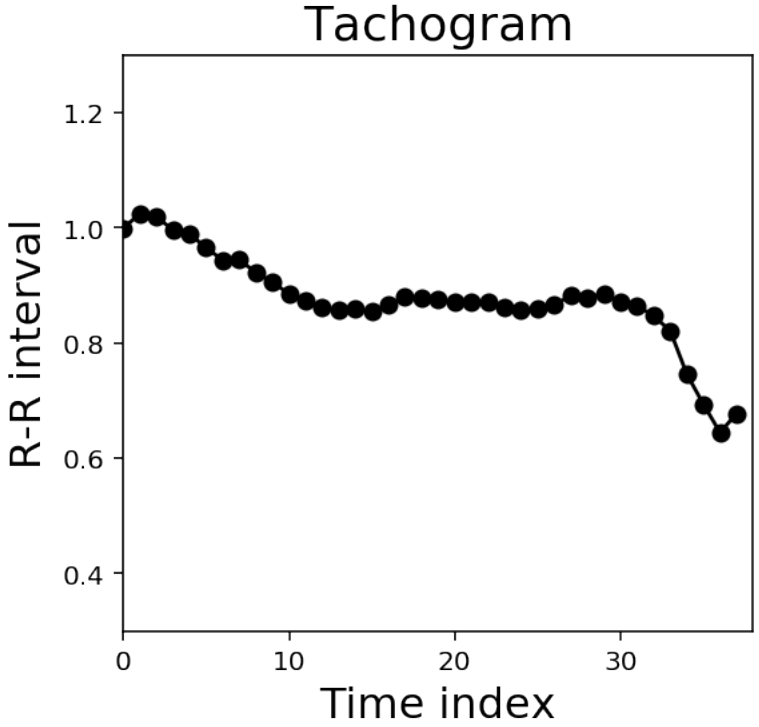
`Recording sostener_respiracion_abdomen`



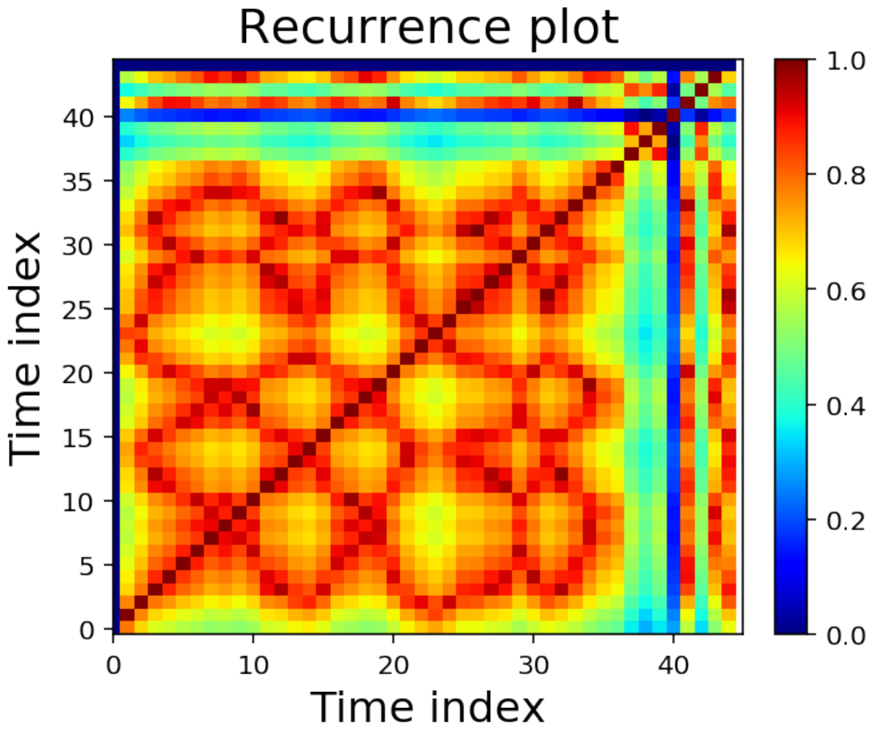


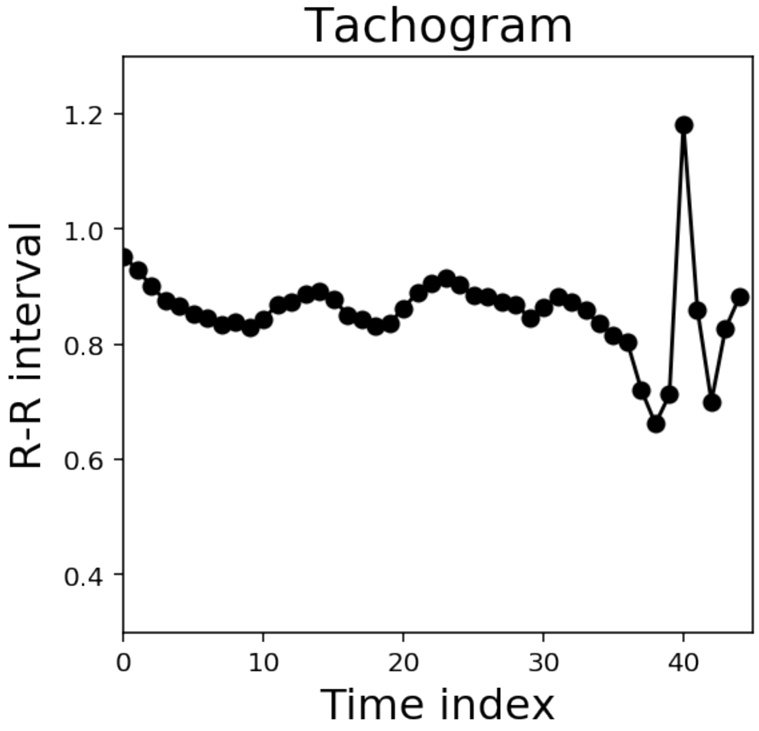
`Recording sostener_respiracion_abdomen`



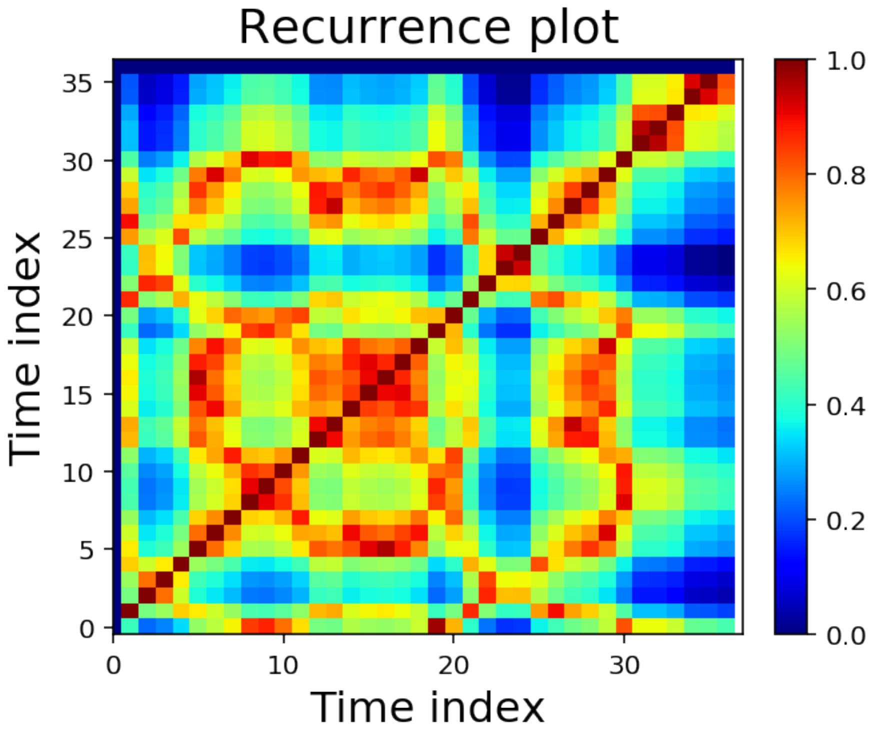


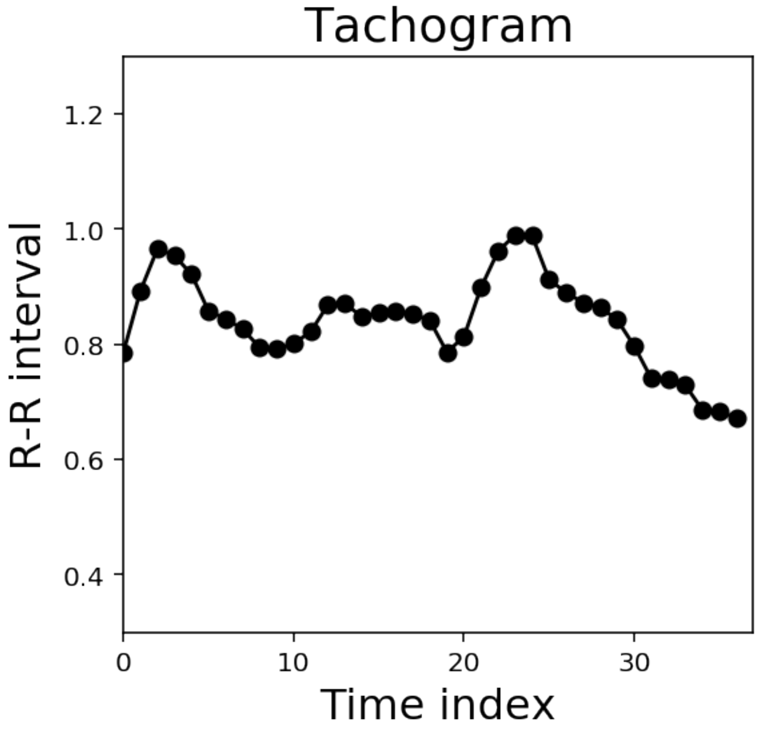
`Recording sostener_respiracion_abdomen`



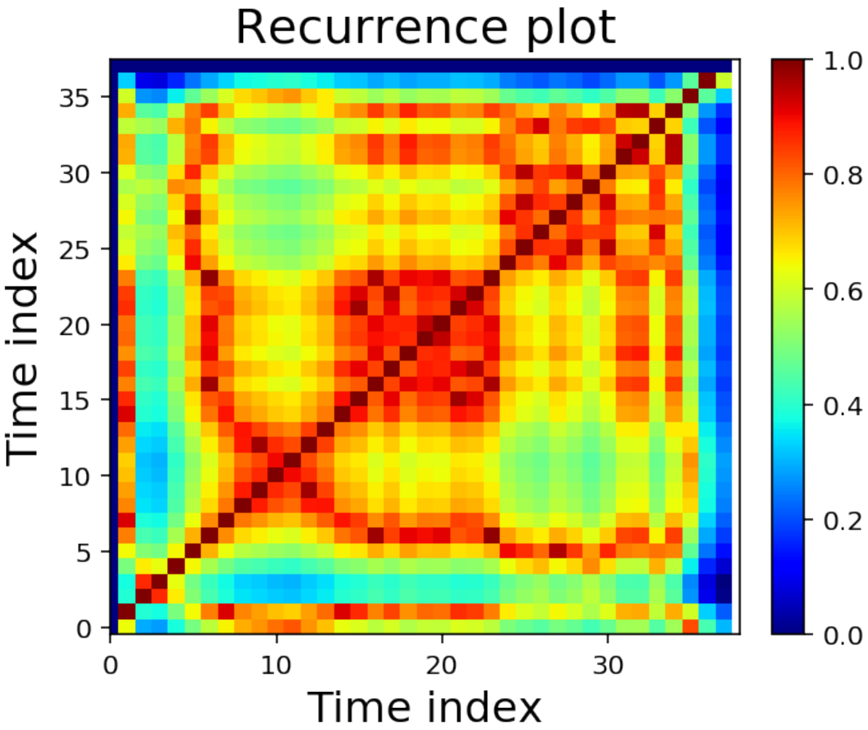


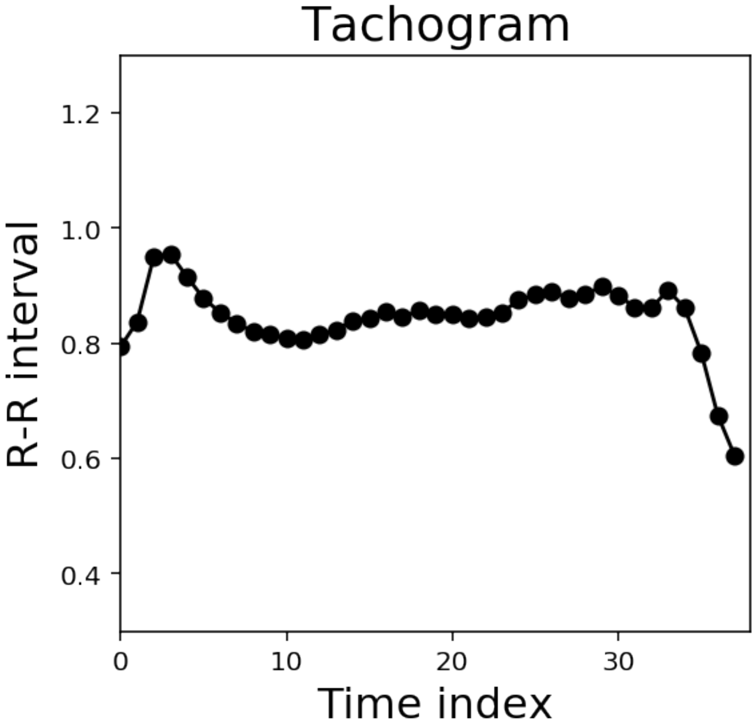
`Recording sostener_respiracion_pecho`



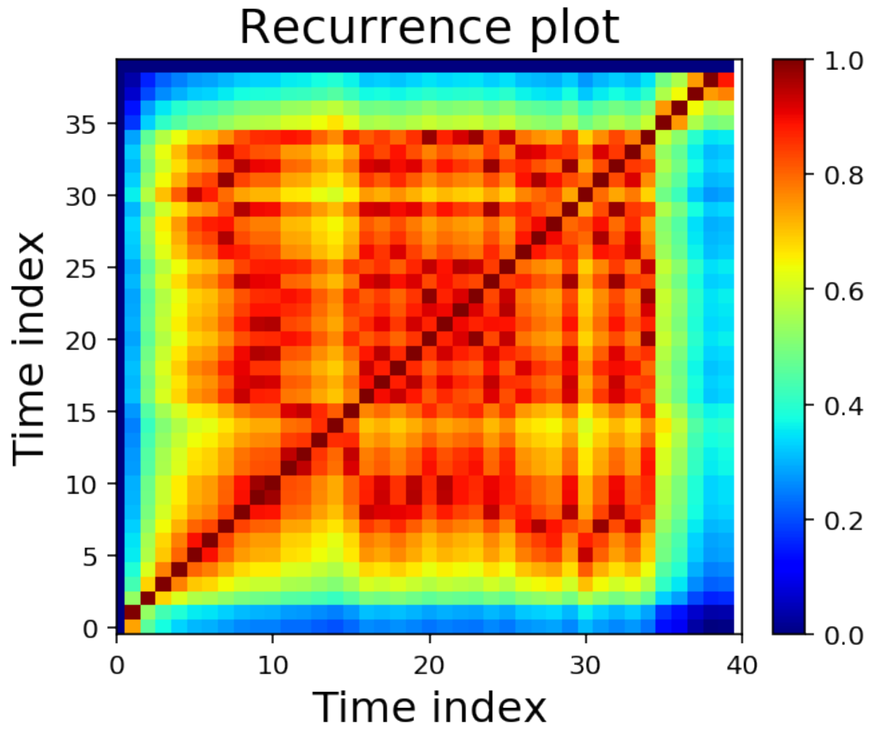


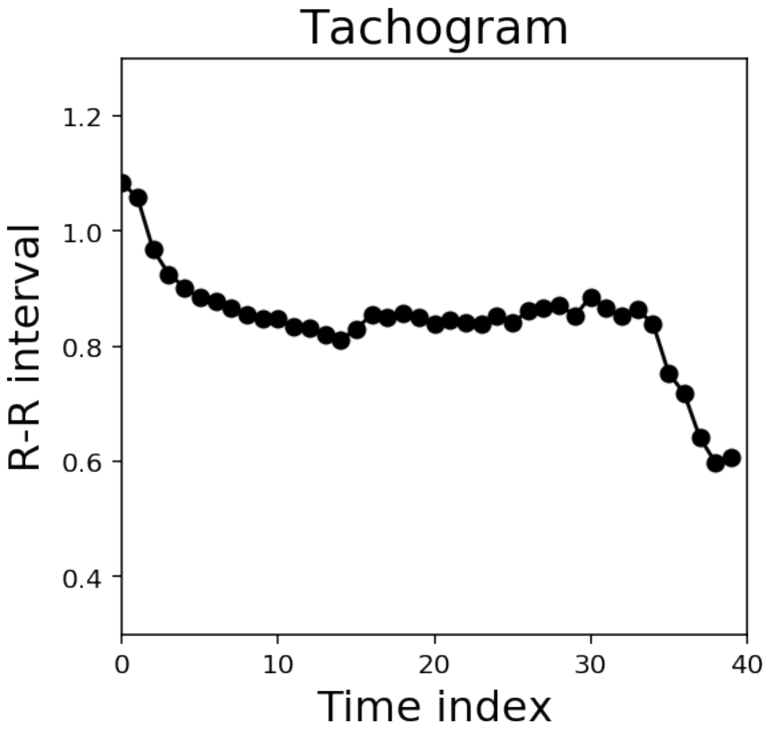
Recording sostener_respiracion_pecho



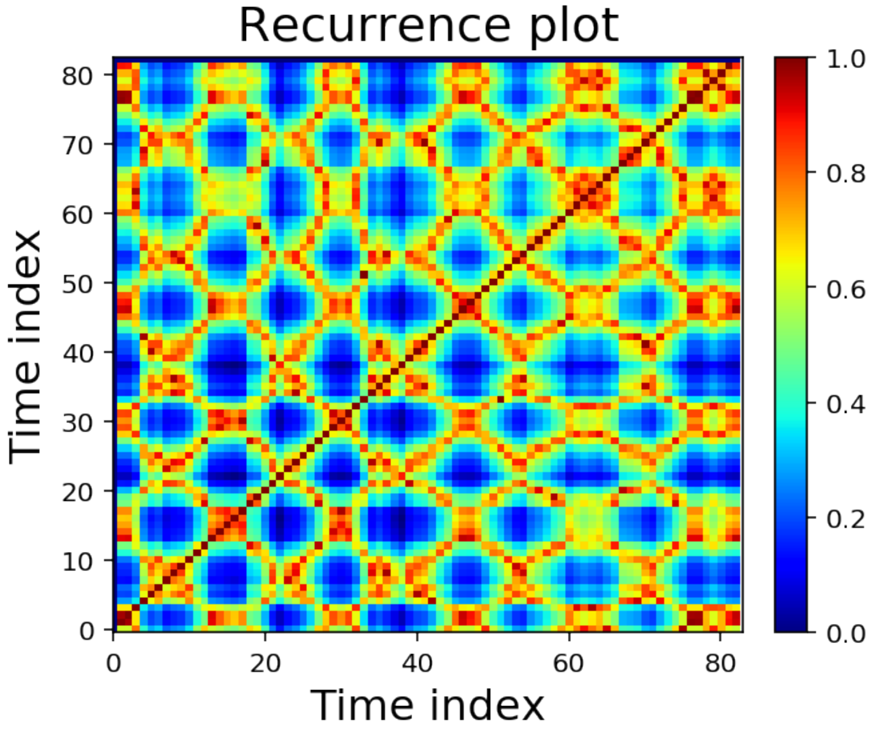


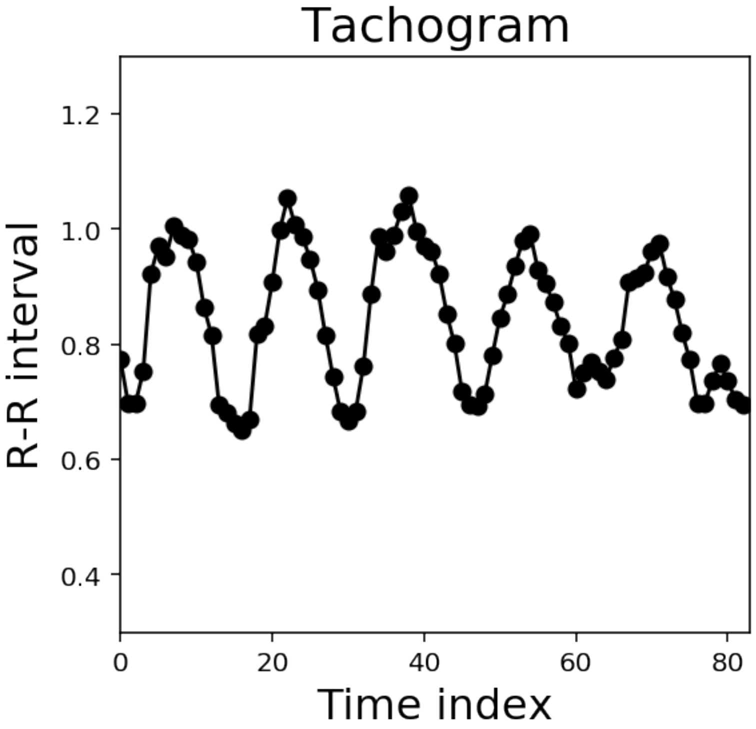
Recording sostener_respiracion_pecho





`Recording respiracion_ola`





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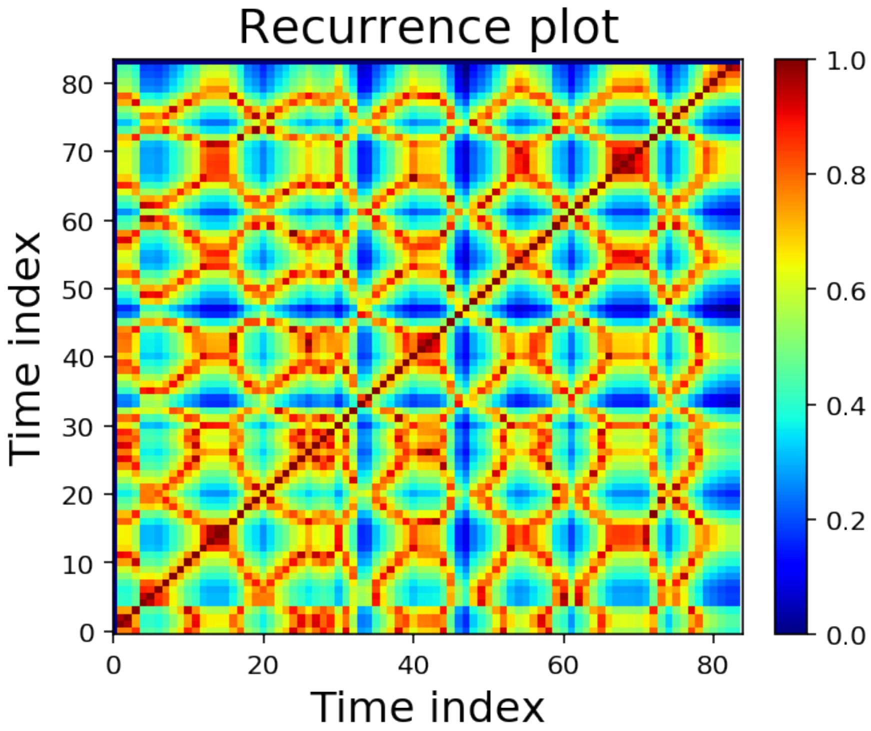

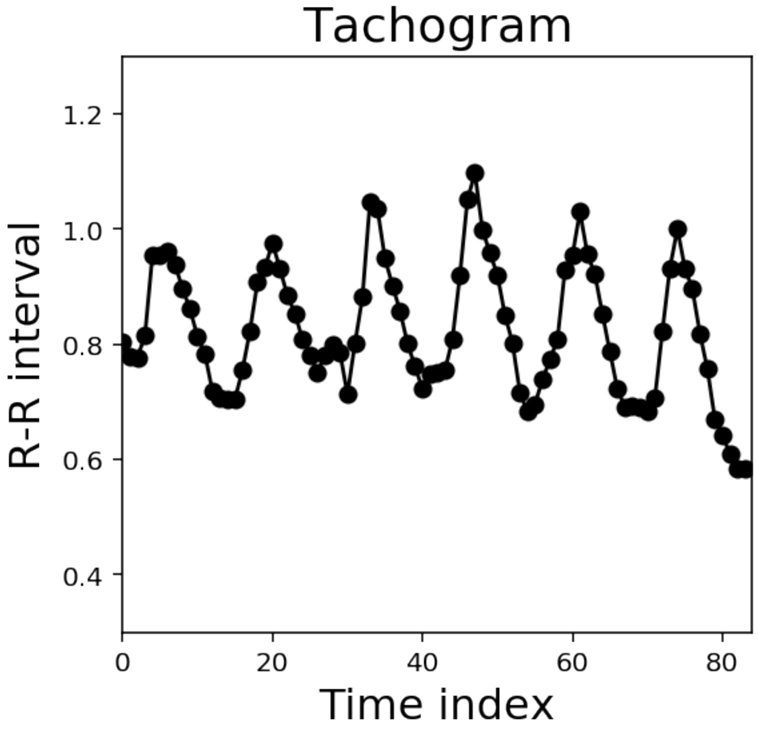

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Recording respiracion_ola
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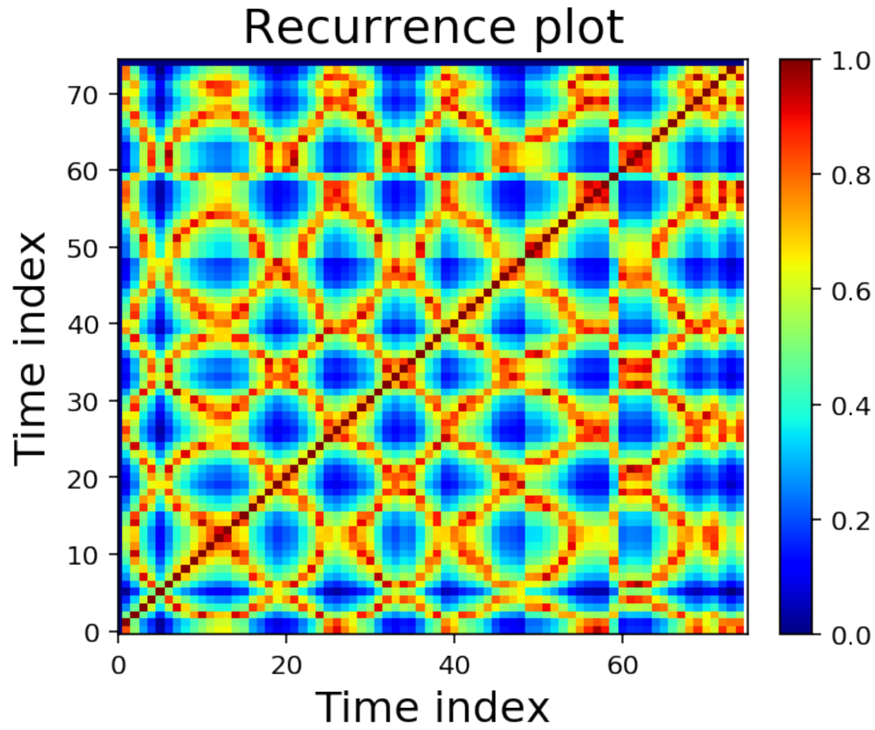

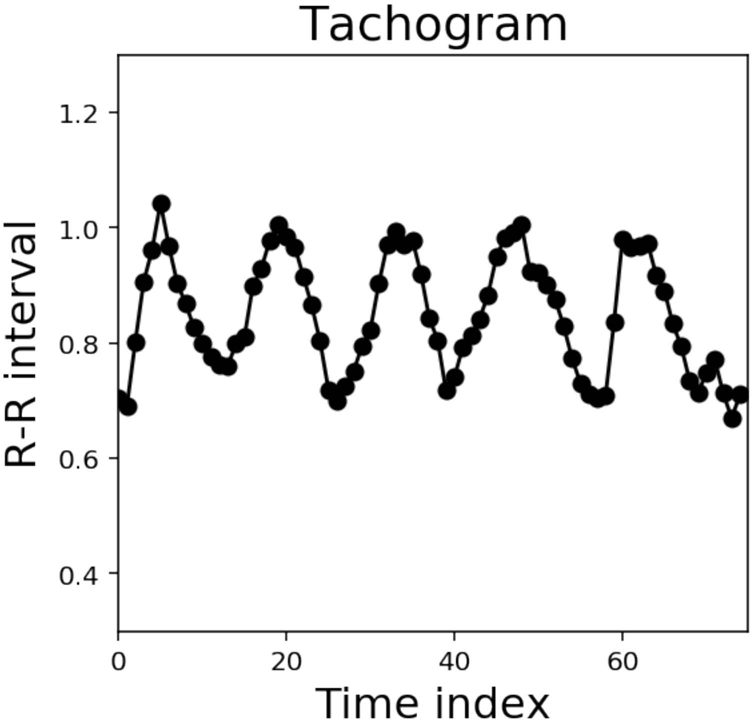

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Recording S1_rest
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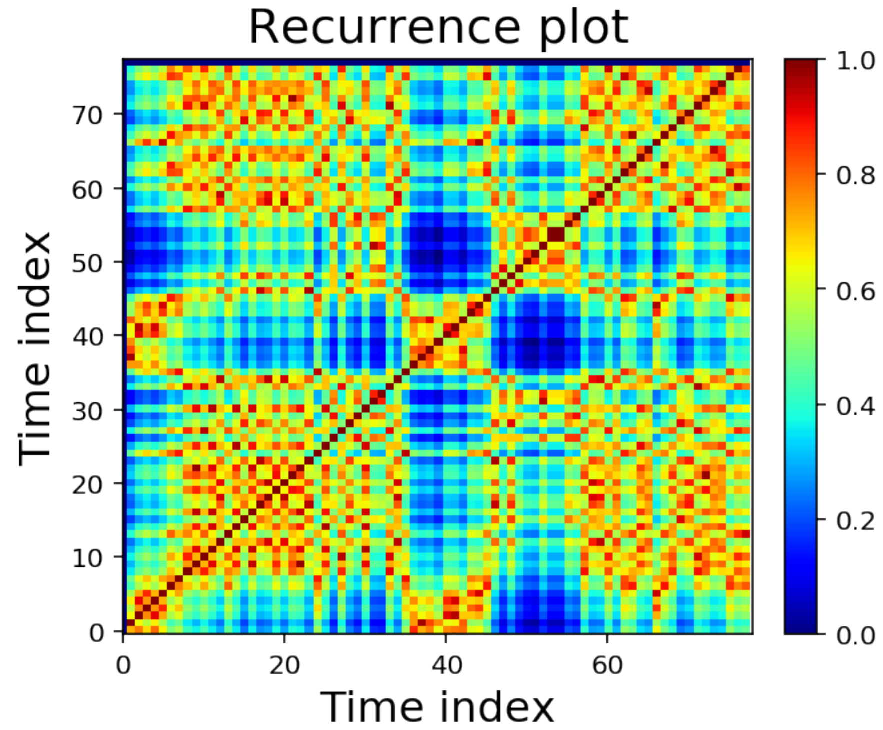
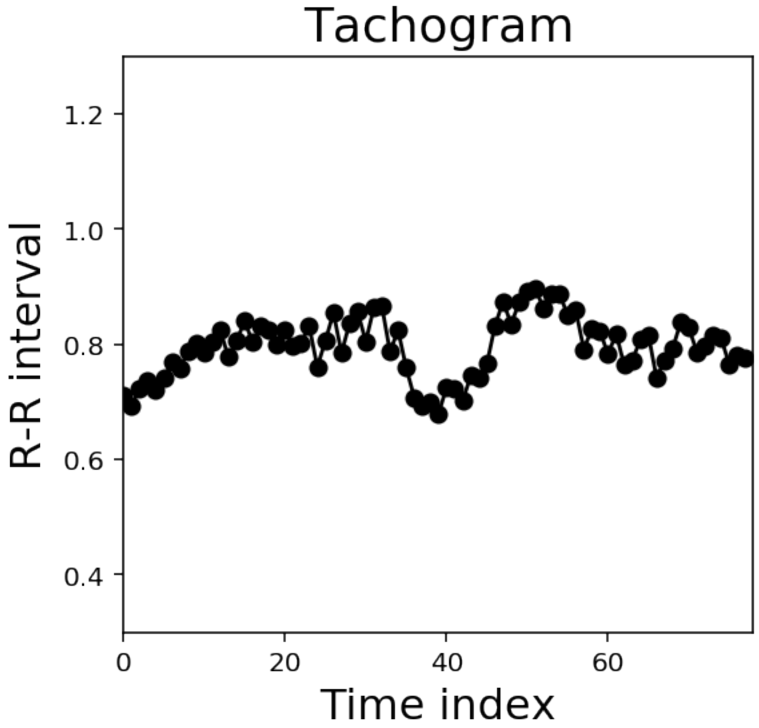
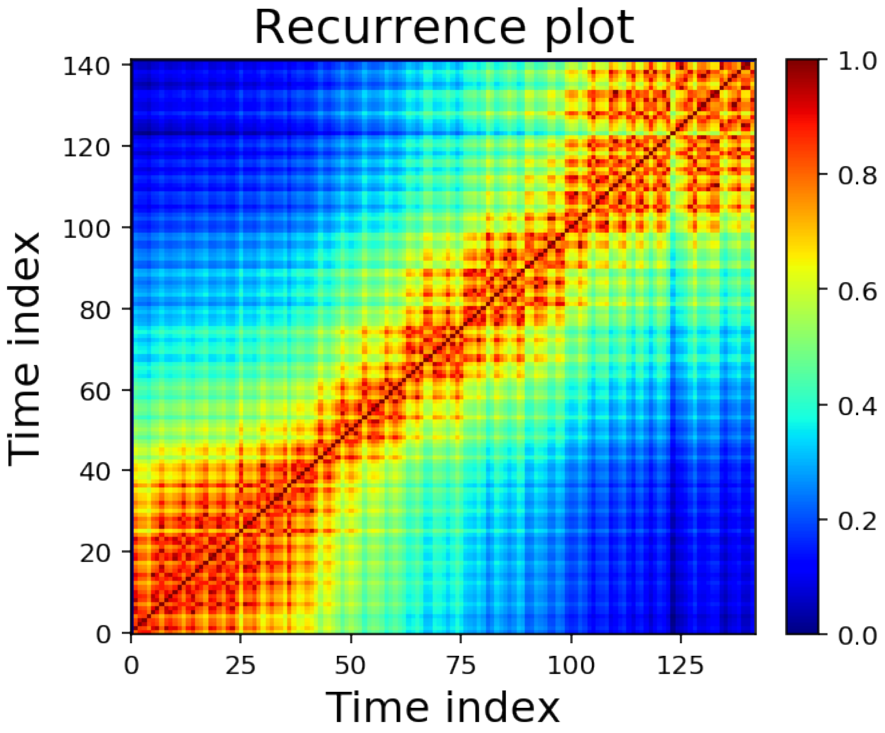
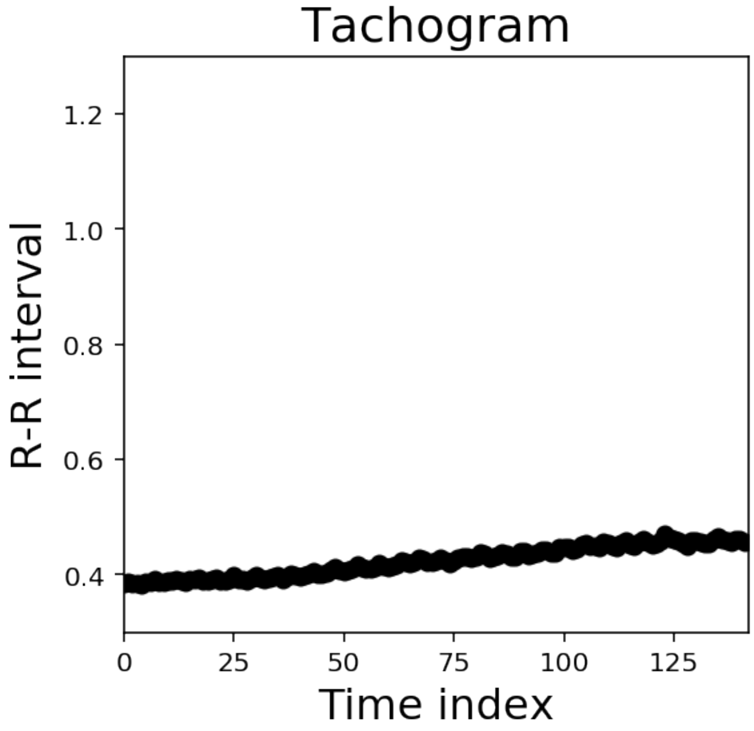


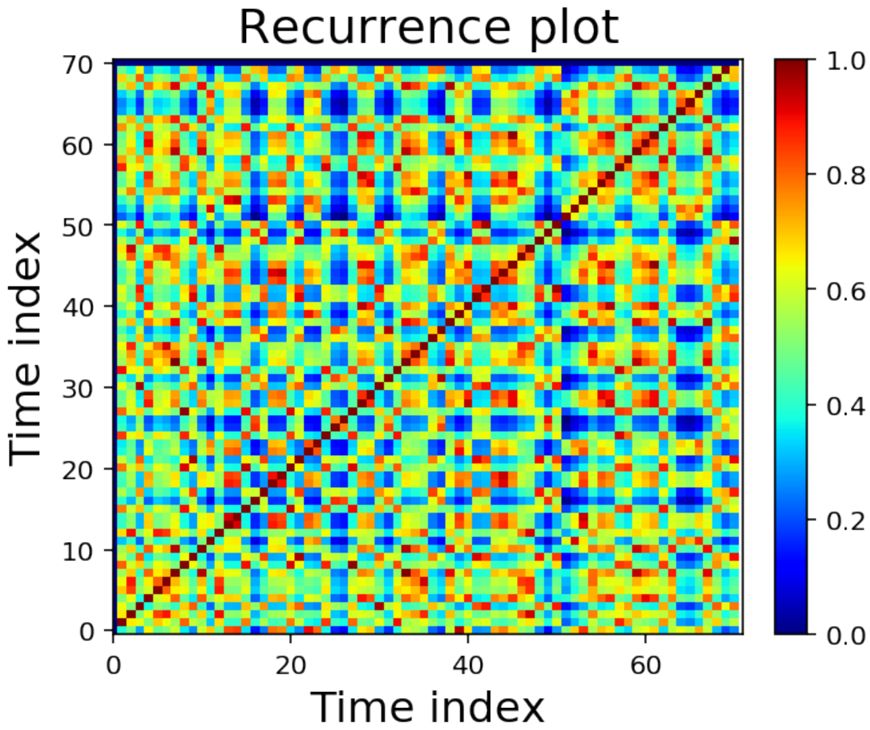


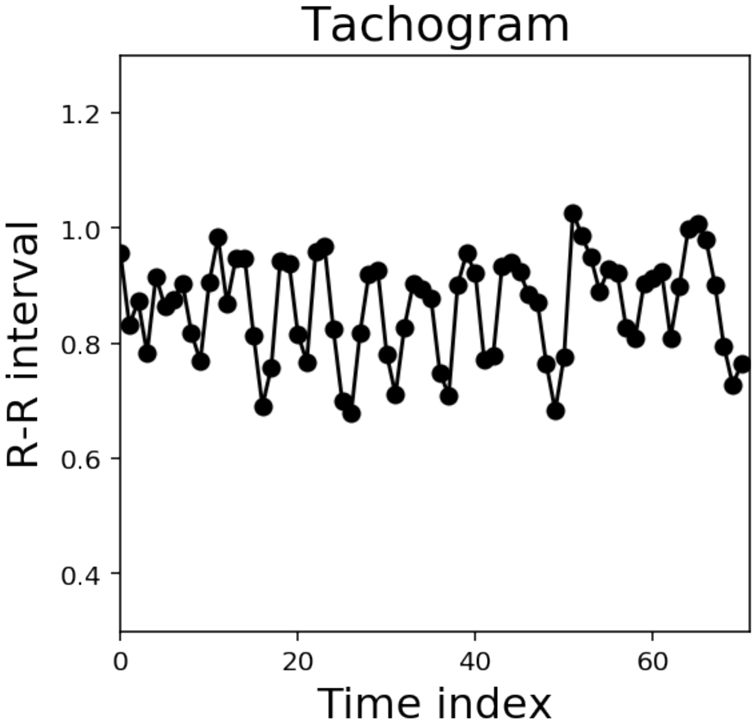
Recording S1_exercise



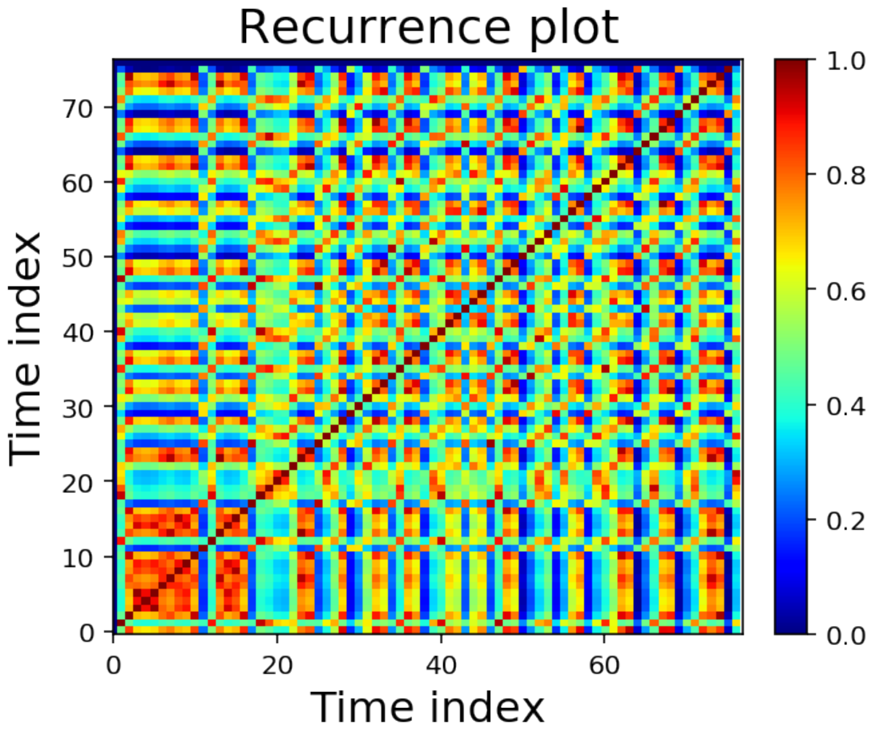


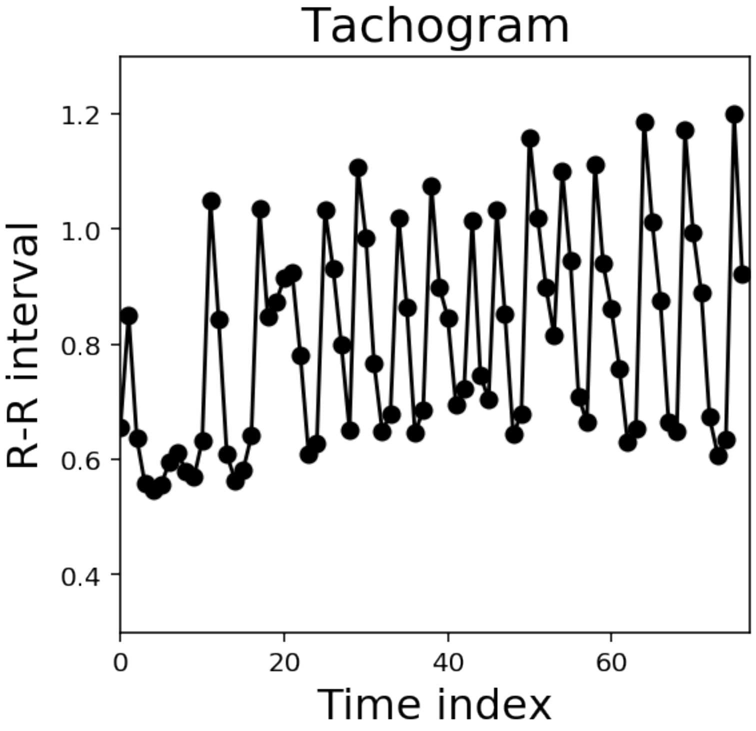
Recording S2_rest



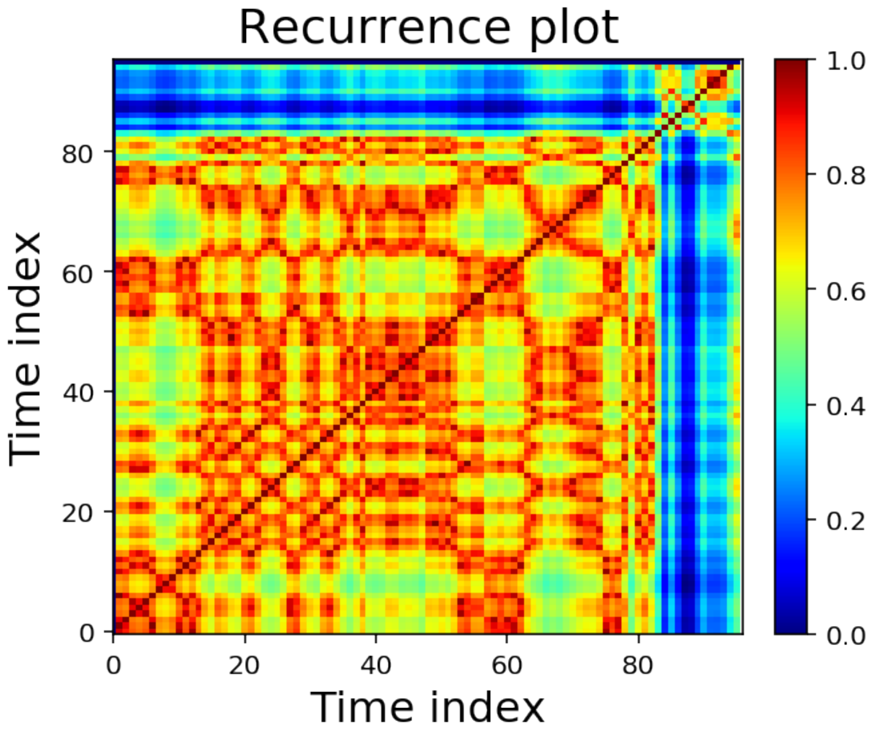


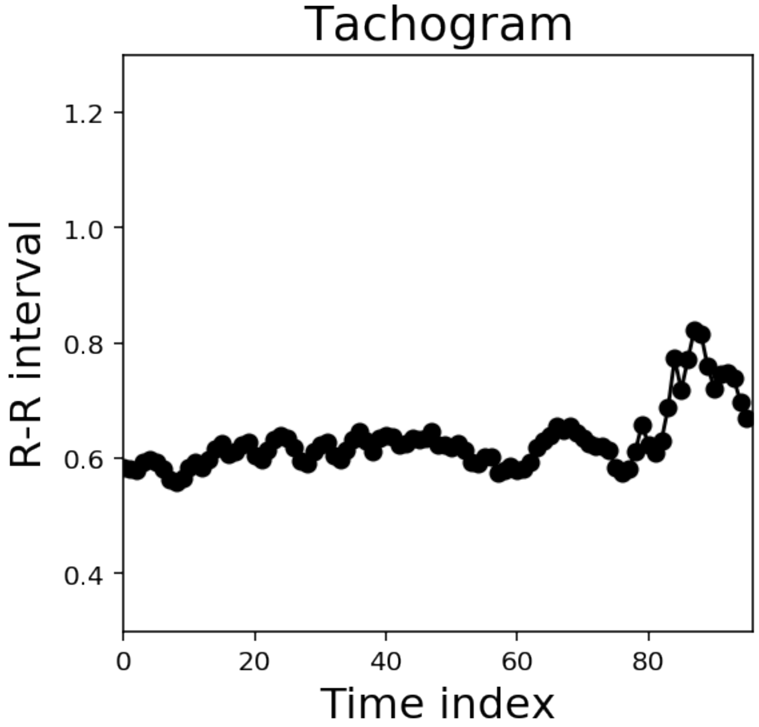
Recording S2_exercise



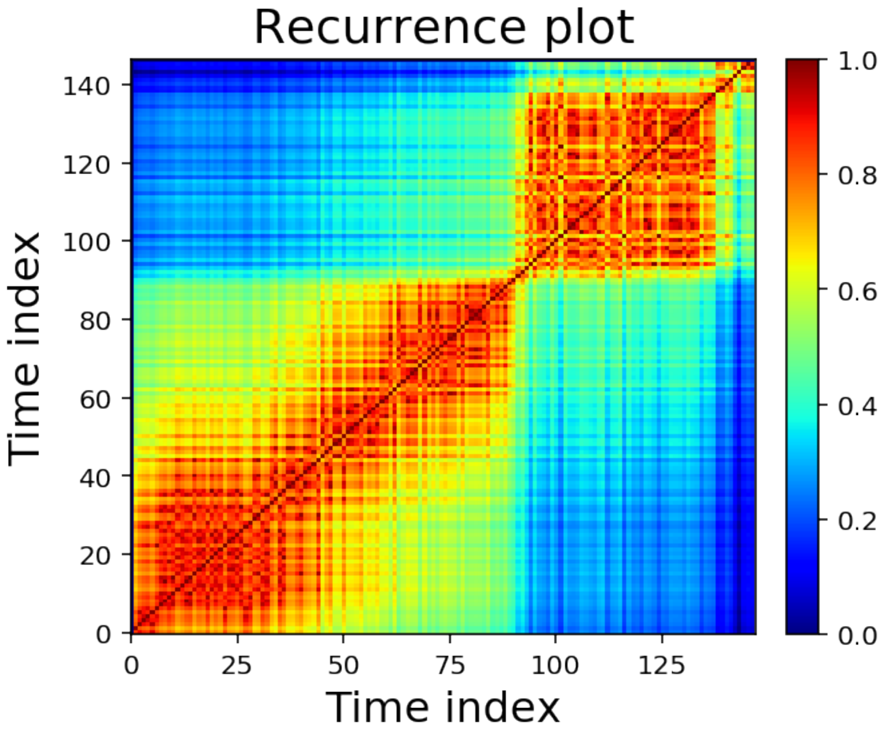


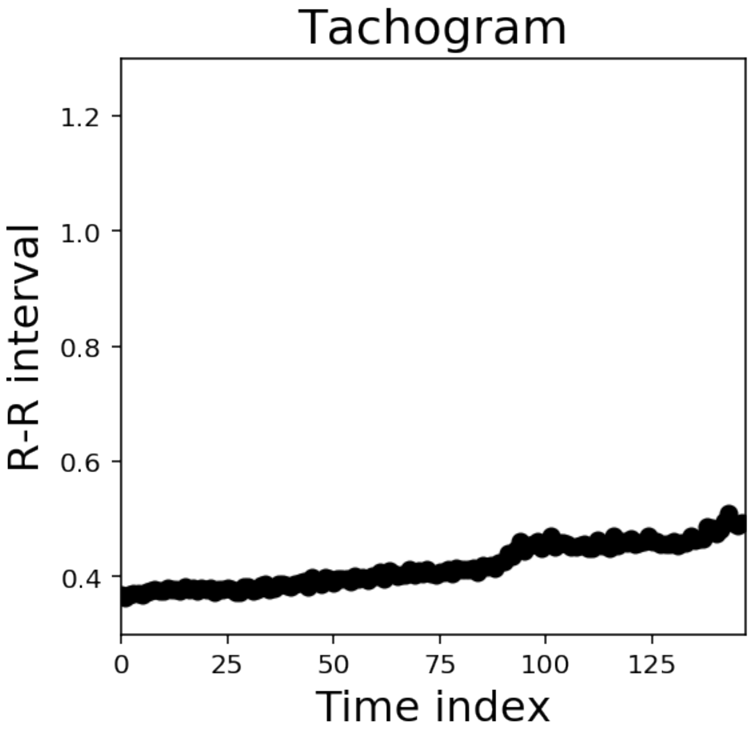
Recording S3_rest





Recording S3_exercise


Recurrence plot
Time index
140
120
100
80
60
40
20
0
0
25
50
75
100
125
Time index
1.0
0.8
0.6
0.4
0.2
0.0


Tachogram
R-R interval
1.2
1.0
0.8
0.6
0.4
0
25
50
75
100
125
Time index

7 Final remarks

As you have seen in this notebook, the R-R interval time series does provide valuable information for the analysis, even though there is lost information.