

## Language in Time - 1 - Data and Recurrence Rudiments

To begin, let's get some data into R. We will start the manual with what is recognized as a sort of tradition in recurrence quantification of text. In the early 2000's, a demonstration of recurrence applied to text was conducted using Dr. Seuss' Green Eggs and Ham. Its small number of unique words (50) and characteristic weaving of rhyme and repetition make it a useful first demonstration. We uphold this tradition here.

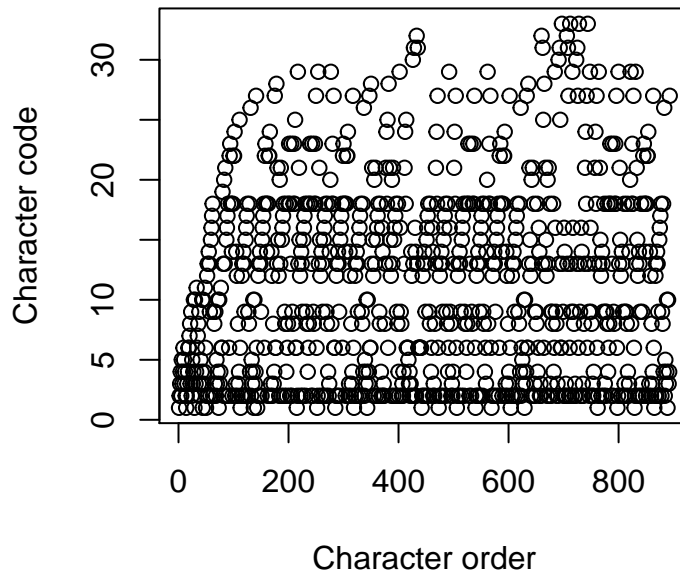
```
setwd('~/.Dropbox/new.projects/recurrence.recipes')
options(warn = -1)
library(crqa)
library(tm)
library(zoo)
rawText = readChar('data/Sam I Am.txt',
  file.info('data/Sam I Am.txt')$size)
```

Once we have these data, let us convert them at the character level. The following code takes all the unique characters in our text and converts these to numeric (nominal) identifiers. The reason for this is that recurrence algorithms (such as in `crqa`) can be adapted for use with text if we have numeric variable types.

```
chars = unlist(strsplit(rawText, ""))
uniqChars = unique(chars)
charSeries = as.vector(sapply(chars,function(x) {
  which(x == uniqChars)
}))
```

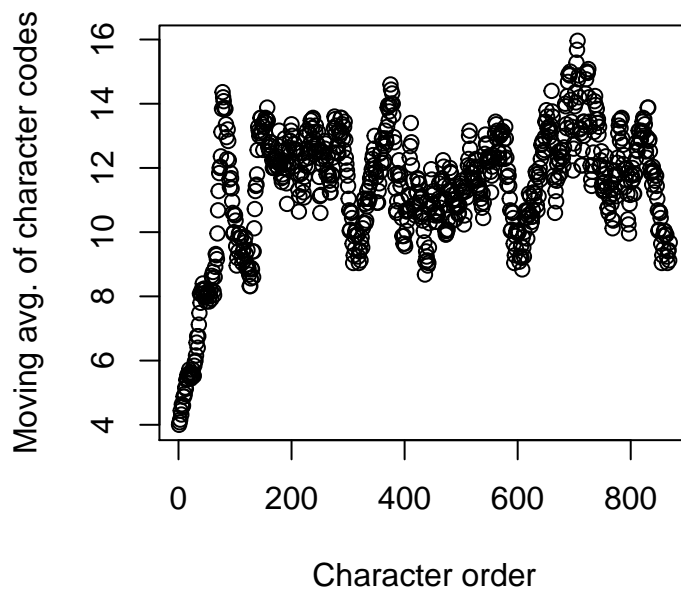
The following plots our sequence of characters, encoded with unique identifiers. We can then see the text as being, in a sense, a sequence of numeric identifiers changing over time. This is a “discrete” dynamic system that is not changing in real time, of course, but it has “time-ordered” properties that we will assume for our analysis.

```
plot(charSeries,type='p',ylab='Character code',xlab='Character order')
```



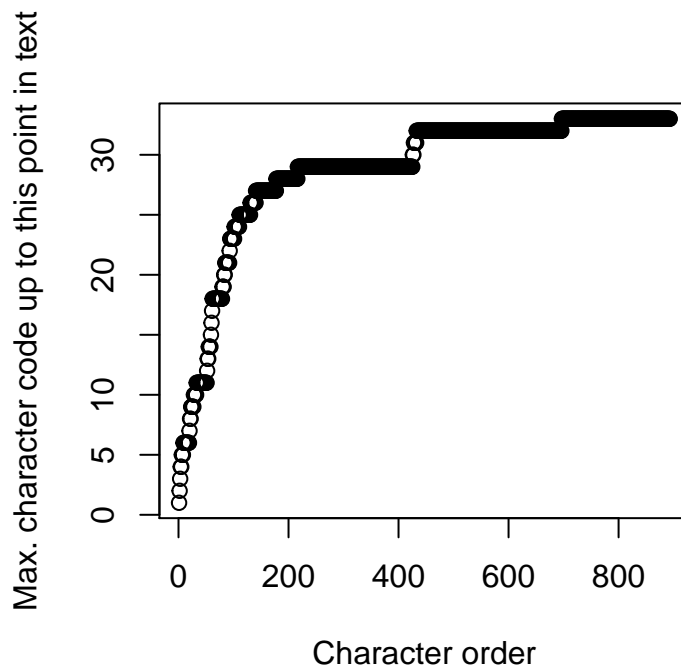
This plot isn't especially meaningful, but it does give us an opportunity to draw our first connection to NLP and corpus linguistics. A well-known regularity referred to as Heaps' Law relates the number of unique words in a document to the length of that document. The characteristic rise and gradual asymptote of the plot you see above reflects this law. Our code above uniquely numbers words in order. Since words are finite, the occurrence of a new identifier becomes less likely as the document is processed. The relationship between document length and the rise of numeric identifiers is  $T(n) = an^b$ , with  $a$  and  $b$  parameters determined by observation. Take a look at how the moving average of this function. You can see the average identifier top off pretty quickly, especially for so repetitive and short a text as Green Eggs and Ham!

```
plot(rollmeanr(charSeries,25),type='p',ylab='Moving avg. of character codes',xlab='Character order')
```



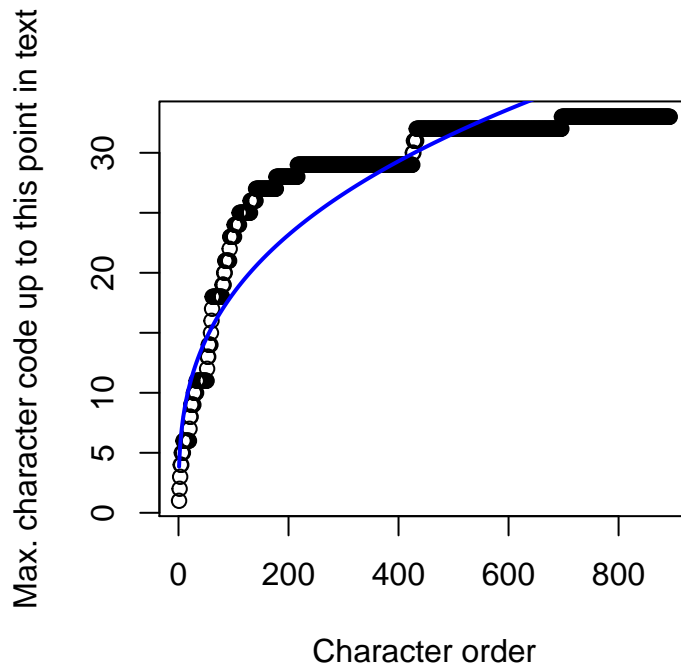
A typical way to display this is to show the maximum identifier value as a function of the length of our consideration. Like this:

```
maxByN = apply(data.frame(1:length(charSeries)),1,function(x) {
  return(max(charSeries[1:x]));
})
plot(maxByN,type='p',ylab='Max. character code up to this point in text',xlab='Character order')
```



We can create a fit to this result pretty easily in R in the following way. Taking the log of each side of the equation above, we get  $\log(T(n)) = \log(a) + b * \log(n)$ , which is equivalent to a linear function fitting  $\log(T(n))$  to  $\log(n)$ , with  $\log(a)$  and  $b$  determined by the fit.

```
x = 1:length(maxByN)
linFit = fitted(lm(log(maxByN)~log(x)))
plot(maxByN,type='p',ylab='Max. character code up to this point in text',xlab='Character order')
points(exp(linFit),type='l',col='blue',lwd=2)
```

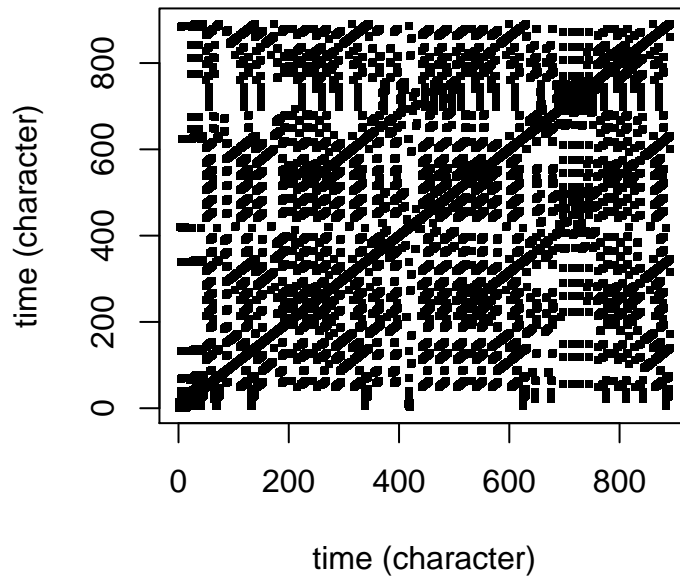


It appears that the text is so short, and lexically simple, that it may be underfit by the basic Heaps approach, though the coefficient is in the range expected by other English corpora of 0.5 or so (see the result of the `lm` function). This sort of thing has been discussed in various places about the Heaps relationship in different kinds of text (e.g., Kubo, 2010).

In any case, note that we convert characters to a series of nominal codes. These numeric codes represent the character types, and converting the characters to numeric codes allows us to utilize all the standard `crqa` library functions for reasons that will become quite clear below.

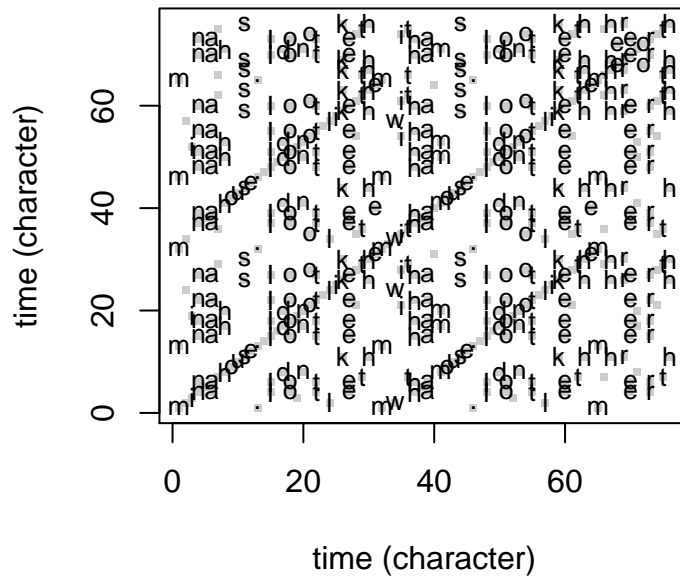
The core data structure that underlies all recurrence quantification is the recurrence plot (RP). Let's define it with respect to our character time series. A recurrence plot (RP) is the set of points  $(i,j)$  such that `charSeries[i]==charSeries[j]`. Building it with the `crqa` library is quite easy.

```
crqaResults = crqa(charSeries,charSeries,1,3,1,.0001,F,2,2,0,F,F) # we'll explain parameters later
RP = as.matrix(crqaResults$RP) # convert into numeric non-sparse matrix
ij = which(RP==1,arr.ind=T) # get coordinates
plot(ij[,1],ij[,2],
      xlab='time (character)',ylab='time (character)',pch=15,cex=.5)
```



So the RP is just a collection of points representing the instances at which the “system” (here, Theodor Geisel, I guess) is revisiting particular states that we are interested in (in this case, characters). To get a sense of how this works, let’s grab the especially repetitive sequencing taking place about midway into Green Eggs and Ham.

```
crqaResults = crqa(charSeries[460:535],charSeries[460:535],1,1,1,.0001,F,2,2,0,F,F) # we'll explain pa
RP = as.matrix(crqaResults$RP) # convert into numeric non-sparse matrix
ij = which(RP==1,arr.ind=T) # get coordinates
plot(ij[,1],ij[,2],
      xlab='time (character)',ylab='time (character)',
      pch=15,cex=.5,col=rgb(.8,.8,.8))
text(ij[,1],ij[,2],chars[ij[,1]+458],cex=.8)
```

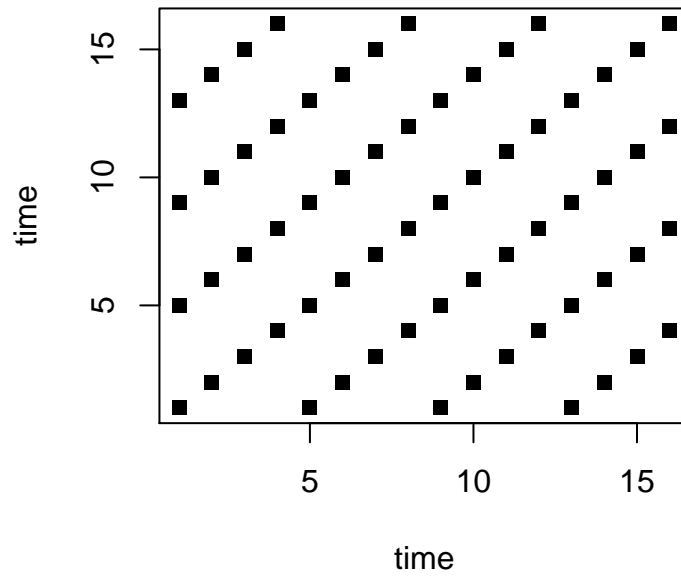


This shows you the specific character sequences that are being revisited by the story (note: grayed points represent spaces). The RP represents these patterns that are repeated as diagonal lines on the plot. Single points would represent single letters being repeated in an isolated fashion. Naturally, there will be a long line up the middle of this plot because by definition ‘charSeries[i]==charSeries[i]’, and so we have what is called the “line of incidence.” This will become crucial later, but in this initial demonstration of “auto-recurrence” – which means we’re building an RP for just one time series compared to itself – it is trivially filled with points. The more interesting points are the off-diagonal lines that show repetition of the system’s character states. In the plot above, you can see a prominent “I do not like them” on either side of the plot. Of course, the story is filled with such repetition. A well-known application of this visualization was conducted by Orsucci et al. (2001), where this poem along with others from other languages are compared.

An RP is also symmetrical, for obvious reasons, because if `charSeries[i]==charSeries[j]` then `charSeries[j]==charSeries[i]`, and so we get these elegant looking Rorschach kind of symmetries. The symmetry will break down when we move beyond recurrence with a single time series (auto-recurrence) and plot the recurrence between two different time series (cross recurrence).

Let's take a quick look at the RP via much shorter time series to build your intuition about the “textures” that emerge on them. To start, let's build a plot that consists of a series of diagonal lines. These would reflect a system that is repeatedly revisiting a prior sequence at various times.

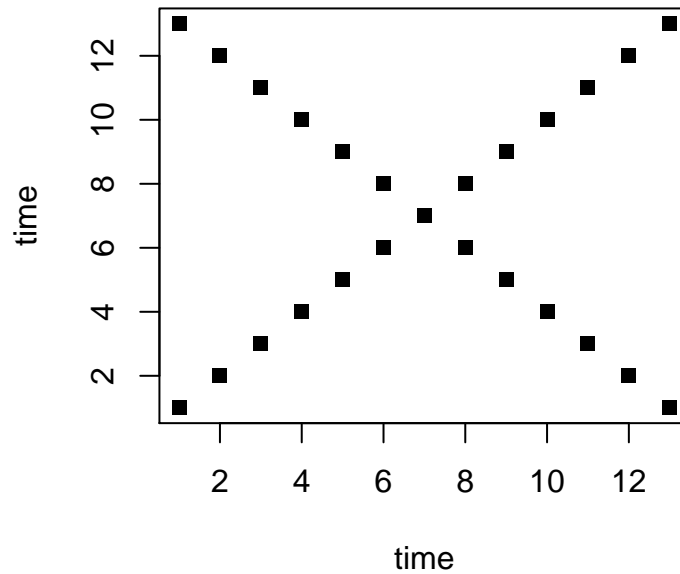
```
charSeries = c(1,2,3,4,1,2,3,4,1,2,3,4,1,2,3,4)
crqaResults = crqa(charSeries,charSeries,1,1,1,.0001,F,2,2,0,F,F) # we'll explain parameters later
RP = as.matrix(crqaResults$RP) # convert into numeric non-sparse matrix
ij = which(RP==1,arr.ind=T) # get coordinates
plot(ij[,1],ij[,2],
      xlab='time',ylab='time',pch=15,cex=1)
```



If we have “palindromic” patterns – a system that is reversing direction in its dynamics – this shows up as perpendicular lines in the plot. A palindrome itself looks like this:

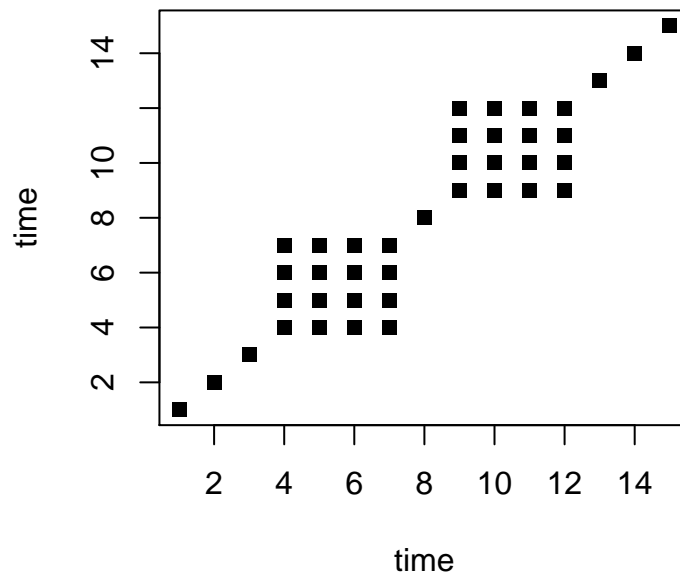
```
charSeries = c(1,2,3,4,5,6,7,6,5,4,3,2,1)
crqaResults = crqa(charSeries,charSeries,1,1,1,.0001,F,2,2,0,F,F) # we'll explain parameters later
RP = as.matrix(crqaResults$RP) # convert into numeric non-sparse matrix
ij = which(RP==1,arr.ind=T) # get coordinates
plot(ij[,1],ij[,2],
      xlab='time',ylab='time',pch=15,cex=1)
```





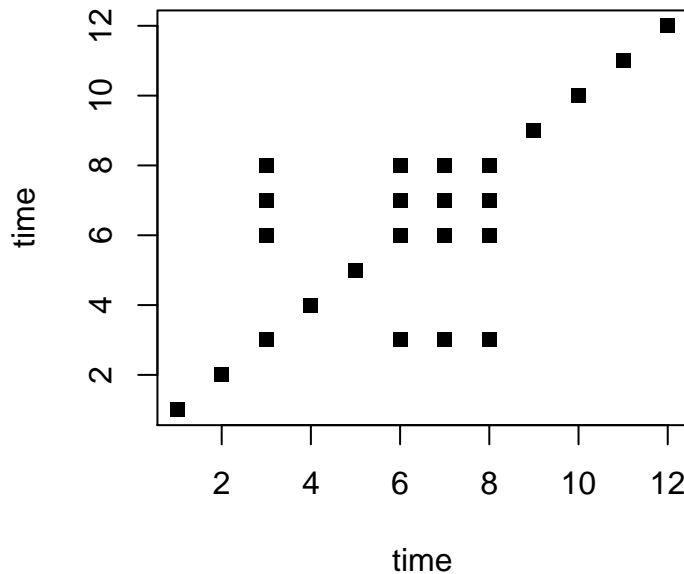
Plots that have “blocks,” wide swaths of points, reflect a system which is “trapped” in one state. This may reflect a stable state of the system that may be describable as a temporary point attractor – one fixed state in which the system has become stable (or, really meta-stable) – before moving on. This can be useful, for example, when looking at eye movements and attention. Focal spots of interest in a visual scene, for example, can be visualized in these plots as large swaths of rectangular regions. This would mean that the focal object of interest was fixated for a sequence of time in a stable way. As a very simple demonstration of this, consider this toy time series.

```
charSeries = c(1,2,3,4,4,4,4,5,6,6,6,6,7,8,9)
crqaResults = crqa(charSeries,charSeries,1,1,1,.0001,F,2,2,0,F,F) # we'll explain parameters later
RP = as.matrix(crqaResults$RP) # convert into numeric non-sparse matrix
ij = which(RP==1,arr.ind=T) # get coordinates
plot(ij[,1],ij[,2],
      xlab='time',ylab='time',pch=15,cex=1)
```



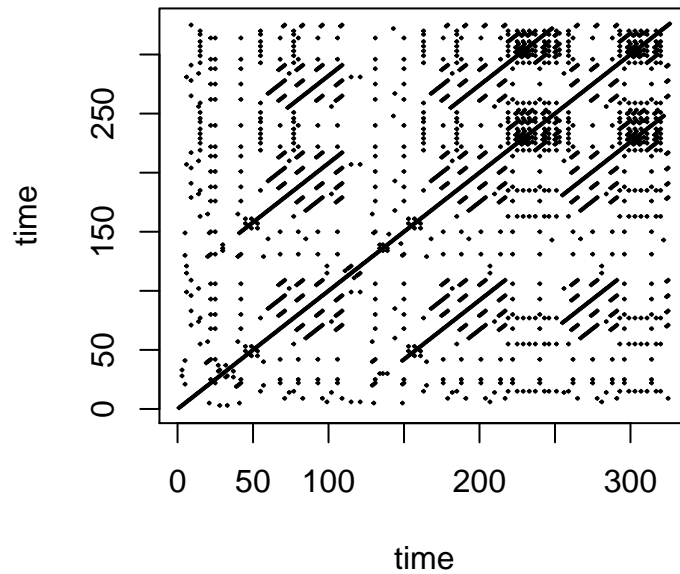
Horizontal and vertical lines connote the same sort of thing: The system is, for a time, stable in some sequence of the same state. Lines occur because the system, relative to another point in time, has “moved on” from that particular state.

```
charSeries = c(1,2,3,4,5,3,3,3,6,7,8,9)
crqaResults = crqa(charSeries,charSeries,1,1,1,.0001,F,2,2,0,F,F) # we'll explain parameters later
RP = as.matrix(crqaResults$RP) # convert into numeric non-sparse matrix
ij = which(RP==1,arr.ind=T) # get coordinates
plot(ij[,1],ij[,2],
      xlab='time',ylab='time',pch=15,cex=1)
```



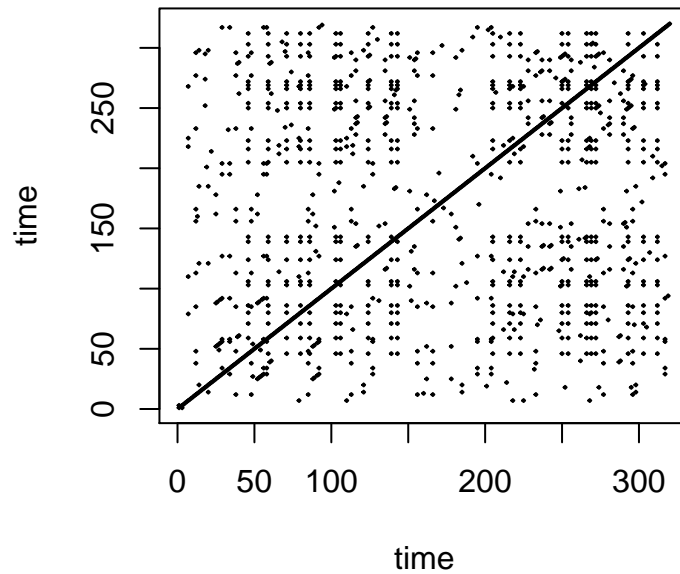
So what is this good for? Well, Orsucci et al. (2001) compared different poetry and proposed some theories of poetic change and cross-cultural patterns. In fact, any hypothesis for which one might use simple n-gram models to explore the structure of text (e.g., compressibility, entropy, etc.) can be embedded in a recurrence analysis context. As we'll see in the next section, a wide variety of measures can be extracted from these plots to quantify the diagonal and horizontal line textures in various ways. A very simple demonstration of this can be done by comparing different kinds of text. Human beings engage in qualitatively different “linguistic modes.” For example, poetry or lyrical composition have fundamentally different structural expectations than, say, an off-the-cuff speech or statement. We would expect their visualization in recurrence to be quite different. Let's start with an example of this here. Carly Rae Jepsen's “Call Me Maybe,” a rivetting cultural commentary on teenagers calling each other on a cell phone, shows considerable regularity in its lyrical patterns.

```
rawText = readChar('data/callmemaybe.txt',
  file.info('data/callmemaybe.txt')$size)
chars = unlist(strsplit(rawText, " ")) # words
uniqChars = unique(chars)
charSeries = as.vector(sapply(chars,function(x) {
  which(x == uniqChars)
}))
crqaResults = crqa(charSeries,charSeries,1,1,1,.0001,F,2,2,0,F,F) # we'll explain parameters later
RP = as.matrix(crqaResults$RP) # convert into numeric non-sparse matrix
ij = which(RP==1,arr.ind=T) # get coordinates
plot(ij[,1],ij[,2],
  xlab='time',ylab='time',pch=5,cex=.15)
```



A speech, however, such as Barack Obama's 2014 State of the Union exhibits quite different structure. There are, of course, many patterns of repetition, but they are considerably less regular, and appear sparser.

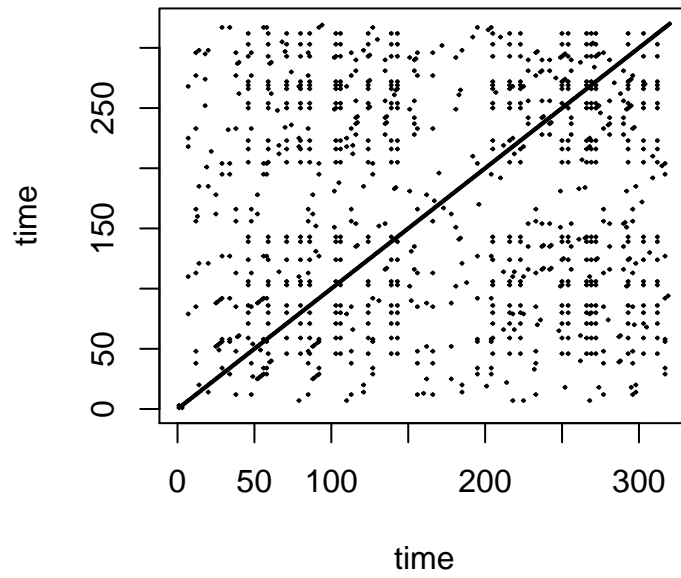
```
rawText = readChar('data/obama.txt',
  file.info('data/obama.txt')$size) # portion of SoU
chars = unlist(strsplit(rawText, " ")) # words
uniqChars = unique(chars)
charSeries = as.vector(sapply(chars,function(x) {
  which(x == uniqChars)
}))
crqaResults = crqa(charSeries,charSeries,1,1,1,.0001,F,2,2,0,F,F) # we'll explain parameters later
RP = as.matrix(crqaResults$RP) # convert into numeric non-sparse matrix
ij = which(RP==1,arr.ind=T) # get coordinates
plot(ij[,1],ij[,2],
  xlab='time',ylab='time',pch=5,cex=.15)
```



Do we have to run this code each time we want to build an RP? We can design our own function. It's easy to do this on top of the 'crqa' library. It might work like this.

```
plotRP = function(fileName) {
  rawText = readChar(fileName,
    file.info(fileName)$size) # portion of SoU
  chars = unlist(strsplit(rawText, " ")) # words
  uniqChars = unique(chars)
  charSeries = as.vector(sapply(chars,function(x) {
    which(x == uniqChars)
  }))
  crqaResults = crqa(charSeries,charSeries,1,1,1,.0001,F,2,2,0,F,F) # we'll explain parameters later
  RP = as.matrix(crqaResults$RP) # convert into numeric non-sparse matrix
  ij = which(RP==1,arr.ind=T) # get coordinates
  plot(ij[,1],ij[,2],
    xlab='time',ylab='time',pch=5,cex=.15)
}

plotRP('data/obama.txt')
```



```
plotRP('data/callmemaybe.txt')
```

