This exercise is intended to introduce you to some of the Time Series functions in R.

As you come across each new command, read the help file. While this may not help immediately, it will in the long term. Usually several readings are required before it all becomes more apparent!

To obtain the data for this session enter R and type library(ts).

We will use the dataset UKLungDeaths so type data (UKLungDeaths).

The help(UKLungDeaths) file in R is as follows:

UKLungDeaths {ts} R Documentation
Monthly Deaths from Lung Diseases in
the UK
Description
Three time series giving the monthly deaths from bronchitis,
emphysema and asthma in the UK, 1974–1979, both sexes
(ldeaths), males (mdeaths) and females (fdeaths).
Usage
data(UKLungDeaths)
Source

P. J. Diggle (1990) *Time Series: A Biostatistical Introduction*. Oxford, table A.3

Set up the on-line help in R now.

1. Note that the data are given as a *time series structure*, not as a dataframe.

We will consider the male death rates because there is a small trend present. Have a look at the data by typing mdeaths. Have a look at the two other time series.

To investigate the time series structure, type

```
class(mdeaths)
attributes(mdeaths)
```

There are several functions which extract aspects of the time base. Have a look at

```
tsp(mdeaths)
start(mdeaths)
end(mdeaths)
frequency(mdeaths)
deltat(mdeaths)
cycle(mdeaths)
```

- 2. There is a function time which takes a time series as its argument. Type in this command using mdeaths as its argument. What do you obtain?
- 3. The first thing to do with a time series is plot it. For a single series, you can type

plot(mdeaths)

There is also a special command ts.plot() for plotting a time series. Use this now to plot mdeaths.

What is the clear message in the data, and why?

4. * ts.plot can plot several series simultaneously: try

ts.plot(mdeaths, fdeaths, ldeaths)

Obtain a better plot with

```
ts.plot(mdeaths, fdeaths, ldeaths,
  gpars=list(xlab="year", ylab="deaths", lty=c(1:3)))
```

Describe the main features of each time series.

Add your name and a title, for example, by

title("<your name> : deaths from lung diseases in the UK")

and hand in your plot and description as part of Assignment 1.

5. Plot the male deaths data again but using points. This can be achieved by

```
par(pch="*")
ts.plot(mdeaths, type="p")
```

6. We shall smooth these data in various ways. Firstly, we use a simple moving average of order 3:

```
m.ma3 <- filter(mdeaths, rep(1,3)/3)</pre>
```

(Remember to keep reading the help files.) Add the smoothed series to the plot by

```
lines(m.ma3, col="cyan")
```

7. * Repeat the above but with a moving average of order 13, as discussed in lectures. You could do this with

m.ma13 <- filter(mdeaths, c(1/24, rep(1, 11)/12, 1/24))</pre>

Plot the 13-point moving average and the three-point moving average on the same plot, comment on any interesting features that you observe, and hand in the plot and comments as part of Assignment 1.

Now plot the 13-point moving average on its own: notice how important the scaling can be in interpretation. (Don't hand in this plot.)

8. Calculate the differences between the original series and the two smoothed versions and plot both sets of differences. This is how to find the differences (i.e., the residuals) from the three-point moving average:

m.res3 <- mdeaths - m.ma3
plot(m.res3)</pre>

Now find and plot the residuals after subtracting the 13-point moving average.

What do you see?

9. Finally in smoothing, we use the spline smoothing approach. Load the modreg library, then type

males.ss <- smooth.spline(mdeaths)</pre>

smooth.spline fits a cubic smoothing spline to the data. Again plot the series as points and add the fitted spline using lines. What does it resemble?

Repeat the exercise for the three-point moving average residuals. There is a problem here because some of the time points do not have a smoothed value. To overcome this enter

```
ma3.res <- window(m.res3,start=c(1974,2),end=c(1979,11))
ma3.res <- as.ts(ma3.res)</pre>
```

Now plot the residuals and fit the smoothing spline, adding the fit to the plot. What do you see?

Note that males.ss and res.ss are not time series - you can check this by typing is.ts(males.ss).

10. To remove a seasonal effect, we could take differences of lag 12:

```
males.diff <- diff(mdeaths, lag=12)</pre>
```

Plot the resultant series, and also the difference between this and the original series. What do you see?

11. For each time series found in this exercise (including the original mdeaths)

acf(<name of series>)

calculates the correlogram and plots it. Do this now. Comment on the shape for each series and think about what each plot indicates.

Questions 4 and 7 above are part of Assignment 1.

Assignment 1 is due by noon on Friday 27 August (end of Week 5).

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