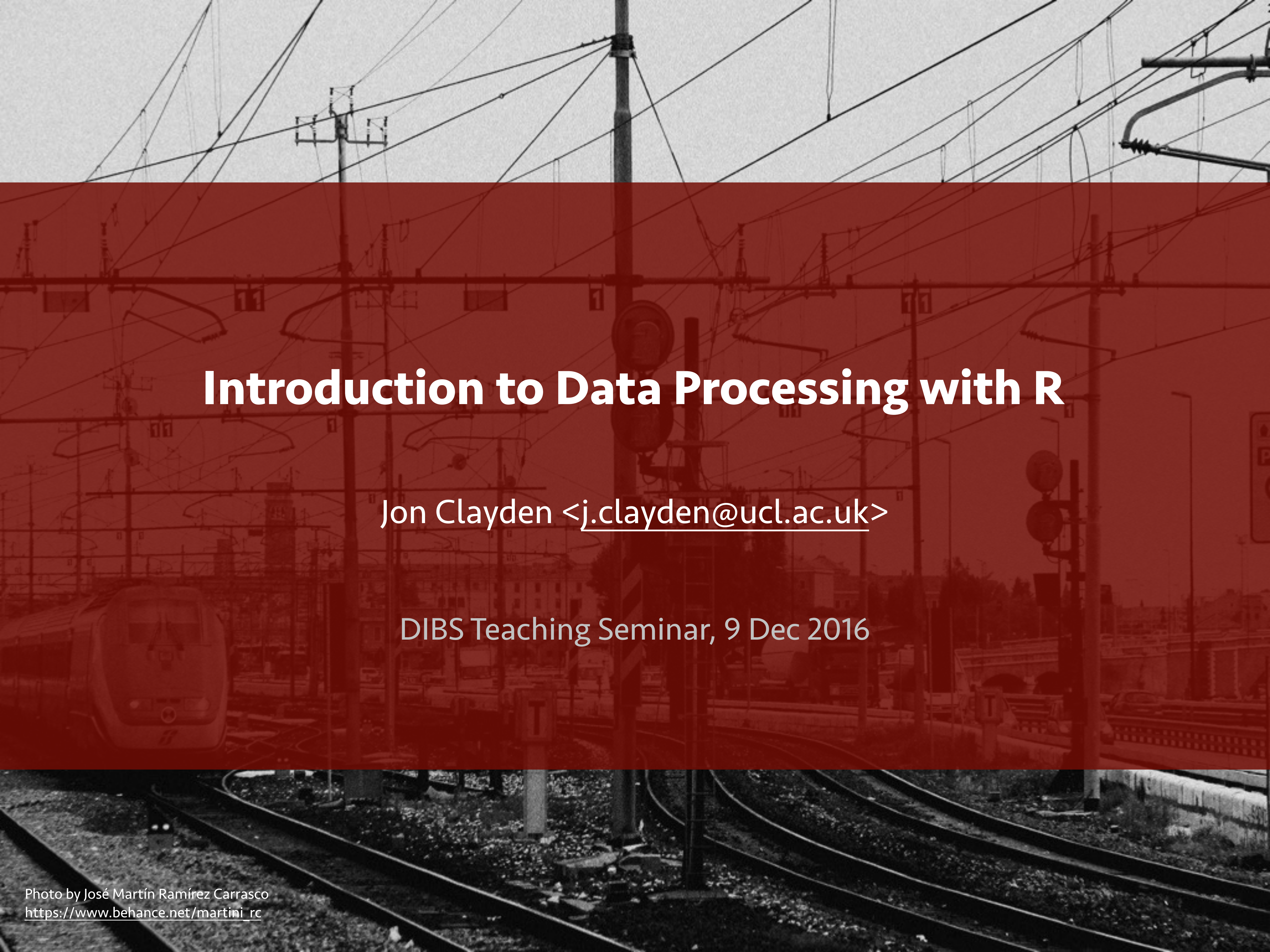

Introduction to Data Processing with R

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DIBS Teaching Seminar, 9 Dec 2016

Photo by José Martín Ramírez Carrasco
https://www.behance.net/martini_rc

R: Background and status

- A free and open-source implementation of S
- Appeared 1993; current version is 3.3.2
- Core strength is statistics, but very good at handling and manipulating data
- Increasingly used by Google, Microsoft, Oracle, etc., for data science applications
- Runs on Windows, Mac OS X, Linux, etc.
- Main contributed code repository (CRAN) contains 9500+ packages; growing supralinearly
- Huge array of statistical methods available
- Annual useR! conference
- About 25 packages currently in the medical imaging "task view"; more for image processing

The language

- High-level; comparable to MATLAB
- Vectorised: you can operate on multiple data elements at once
- A matrix or higher-dimensional array is represented as a vector with a dimension attribute

```
> 1:4
[1] 1 2 3 4
> x <- matrix(1:4,ncol=2)
> x
     [,1] [,2]
[1,]    1    3
[2,]    2    4
> attributes(x)
$dim
[1] 2 2
```

- Index into objects using **[**
- Call functions using **(**
- Assignment can be done with **=**, but usually **<-** or **->** (left or right assign) are used
- Function arguments may be named in a call using **=**
- Default function arguments are also set with **=**
- Commands are separated by **;** or newline

Lists and data frames

- A list can contain (named or unnamed) variables of different types
- Elements are accessed using **[[** or **$** syntax
- A data frame is similar, but elements must be vectors (and will be “recycled”)
- Data frames are typically used to store tabular data, like in a spreadsheet

```
> x <- list(2:3, a="text", b=1)
> x
[[1]]
[1] 2 3

$a
[1] "text"

$b
[1] 1
> x$b
[1] 1
```

```
> y <- data.frame(2:3, a="text", b=1)
> y
  X2.3    a b
1    2 text 1
2    3 text 1
> y$b
[1] 1 1
```

Factors and formulas

- A factor is a vector whose elements can only take certain values (levels)

```
> factor(c(1,2,1,3,1,4))
[1] 1 2 1 3 1 4
Levels: 1 2 3 4
```

```
> factor(c(1,2,1,3,1,4), levels=1:3)
[1] 1    2    1    3    1    <NA>
Levels: 1 2 3
```

- Note that the element which is not a valid level is set to **NA**, which is used by R to denote missing values

- Because of R’s statistical heritage, formulas describing relationships between variables are important

```
> y ~ x
y ~ x
> class(y ~ x)
[1] "formula"
```

- More on this later

Data manipulation

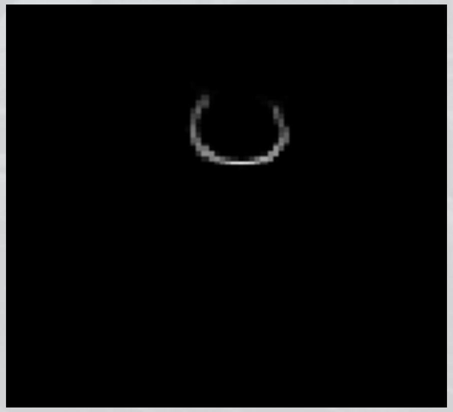
- As in most vectorised languages, widespread use of **for** loops is inefficient and unnecessary
- The **apply** function allows another function to be applied along one or more dimensions of an array

```
> # Find the mean value along each row
> x <- matrix(1:4,ncol=2)
> apply(x, 1, mean)
[1] 2 3
```

- **lapply** is used for applying a function to elements of a list, and returning a list containing the results

```
> y <- readImageFile("genu.nii")
> image(y[,,35], col=grey(0:100/100))
```

```
> z <- apply(y, 1:2, max)
> image(z, col=grey(0:100/100))
```



tapply

- **tapply** lets you apply a function to subsets of a vector defined by the levels of a factor

```
> gender <- factor(c("male","female","male","male","female"))
> age <- c(28,31,30,29,32)
> tapply(age, gender, mean)
female   male
  31.5   29.0
> tapply(age, gender, sd)
   female      male
0.7071068 1.0000000
```

Simple statistics

```
> a <- rnorm(10); b <- rnorm(10)  # Generate random data
> t.test(a,b)  # Do the means of “a” and “b” differ?

   Welch Two Sample t-test

data:  a and b
t = 0.5343, df = 16.344, p-value = 0.6003
alternative hypothesis: true difference in means is not
equal to 0
95 percent confidence interval:
 -0.6769035  1.1341339
sample estimates:
  mean of x   mean of y
 0.15810667 -0.07050854

> cor.test(a,b)  # Are “a” and “b” correlated?
(output removed)
```

Using a data frame and formula

- A formula is used to define a simple (ANCOVA) model

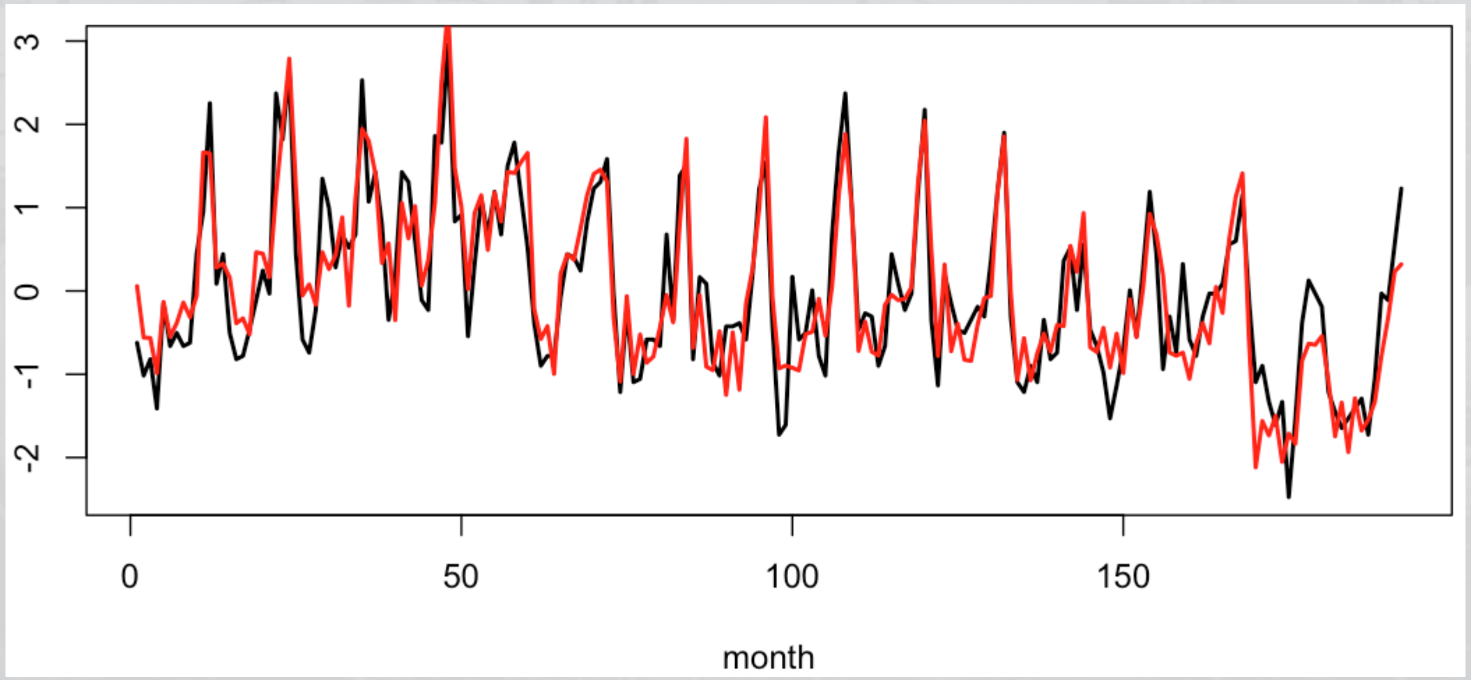
- We are assuming that the response (*DriversKilled*) may be modelled using a linear combination of *drivers* and *law*

```
> data(Seatbelts)
> s <- as.data.frame(Seatbelts)
> head(s)
  DriversKilled drivers front rear   kms PetrolPrice VanKilled law
1           107    1687   867  269  9059   0.1029718        12   0
2            97    1508   825  265  7685   0.1023630         6   0
3           102    1507   806  319  9963   0.1020625        12   0
4            87    1385   814  407 10955   0.1008733         8   0
5           119    1632   991  454 11823   0.1010197        10   0
6           106    1511   945  427 12391   0.1005812        13   0
> anova(lm(DriversKilled ~ drivers * law, data=s))
Analysis of Variance Table

Response: DriversKilled
             Df Sum Sq Mean Sq  F value Pr(>F)
drivers       1  97196   97196 734.2697 <2e-16 ***
law           1    693     693   5.2387 0.0232 *
drivers:law   1    256     256   1.9324 0.1661
Residuals   188  24886     132
```

Graphics

- **plot** creates a standard scatter plot; additions can be made with **lines** or **points**

```
> plot(scale(s$DriversKilled),
type="l", lwd=2, xlab="month", ylab="")
> lines(scale(s$drivers), col="red",
lwd=2)
```



- Other useful plots include histograms (**hist**), box-and-whisker plots (**boxplot**) and 3D surface plots (**persp**)
- Also many more specialised ones

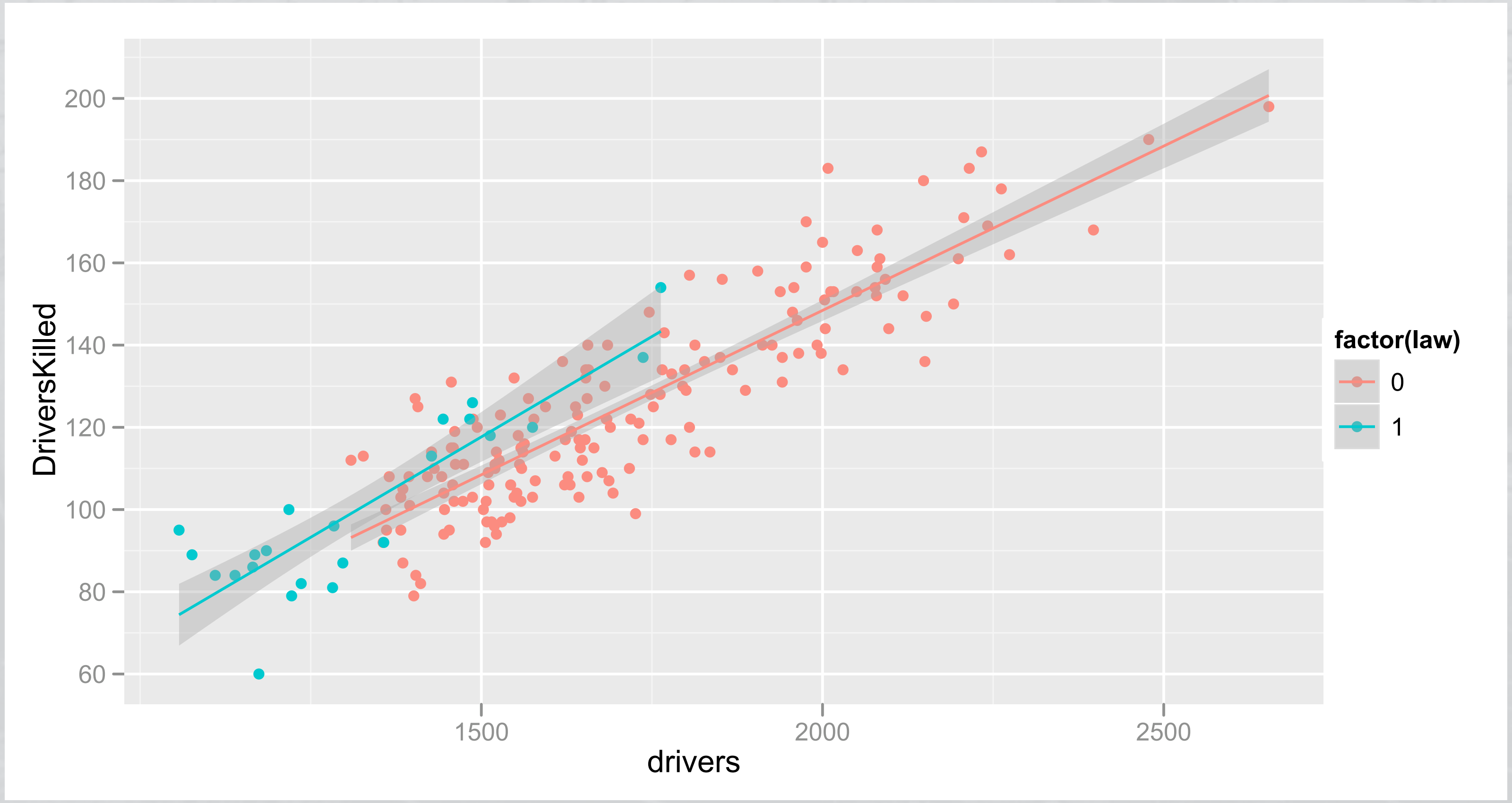
The “Hadleyverse”

- The packages of one very productive R contributor: Hadley Wickham
- Getting data into R: readr, haven, readxl, rvest
- Data manipulation: plyr, dplyr, tidyr
- Working with particular data types: httr, stringr, lubridate
- Visualisation: ggplot2, ggvis, rggobi
- Tools for package developers: devtools, testthat, roxygen2

The ggplot2 package

- Highly recommended; provides a neat mechanism for mapping graphical aesthetics to variables

```
> library(ggplot2)
> qplot(drivers, DriversKilled, colour=factor(law), data=s) +
geom_smooth(method="lm")
```



The dplyr package

- Provides a set of simple, chainable operations which can be applied to data frames

```
> library(dplyr)
# How many drivers were killed on average with and without the seatbelt law?
> s %>% group_by(law) %>% summarise(AverageDriversKilled=mean(DriversKilled))
Source: local data frame [2 x 2]

    law AverageDriversKilled
  (dbl)                (dbl)
1     0             125.8698
2     1             100.2609

# Was the law in place during the worst months?
> s %>% filter(DriversKilled > 180) %>% select(law)
  law
1   0
2   0
3   0
4   0
5   0
```

The mmand and RNiftyReg packages

- Standalone packages which are also used by TractoR
- mmand is for mathematical morphology and resampling
- RNiftyReg is for registration; also has fast functions for reading and writing NIfTI files

- Affine (linear) and nonlinear registration
- 2D or 3D (target may also be 4D)
- Control over cost function, resampling scheme
- Can apply transformations to other images or points, construct affine matrices from scratch

Mathematical morphology

- Basis of morphological image processing
- Erosion/dilation: region growing/ shrinking
- Opening/closing: e.g., removing "holes"
- Additional composite processes
- A kernel, or "structuring element", acts like a brush
- The mmand package can work in any number of dimensions, with arbitrary kernels

Wikipedia/Renato Keshet

Binary morphology in 1D

```
library(mmand)
x <- c(0,0,1,0,0,0,1,1,1,0,0)
```

0	0	1	0	0	0	1	1	1	0	0

```
kernel <- c(1,1,1)
```

1	1	1

```
erode(x,kernel)
```

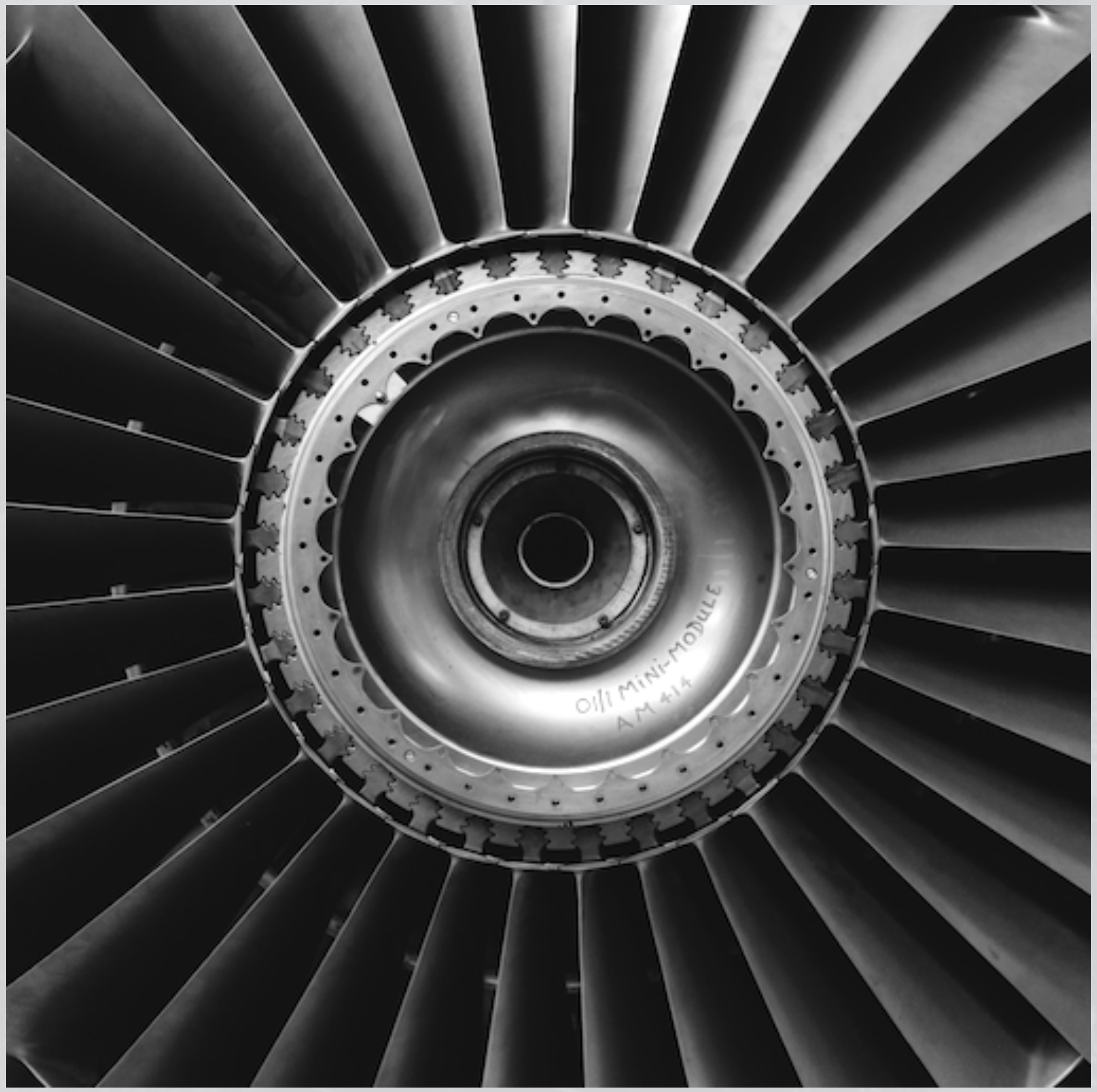
0	0	0	0	0	0	0	1	0	0	0

```
dilate(x,kernel)
```

0	1	1	1	0	1	1	1	1	1	0

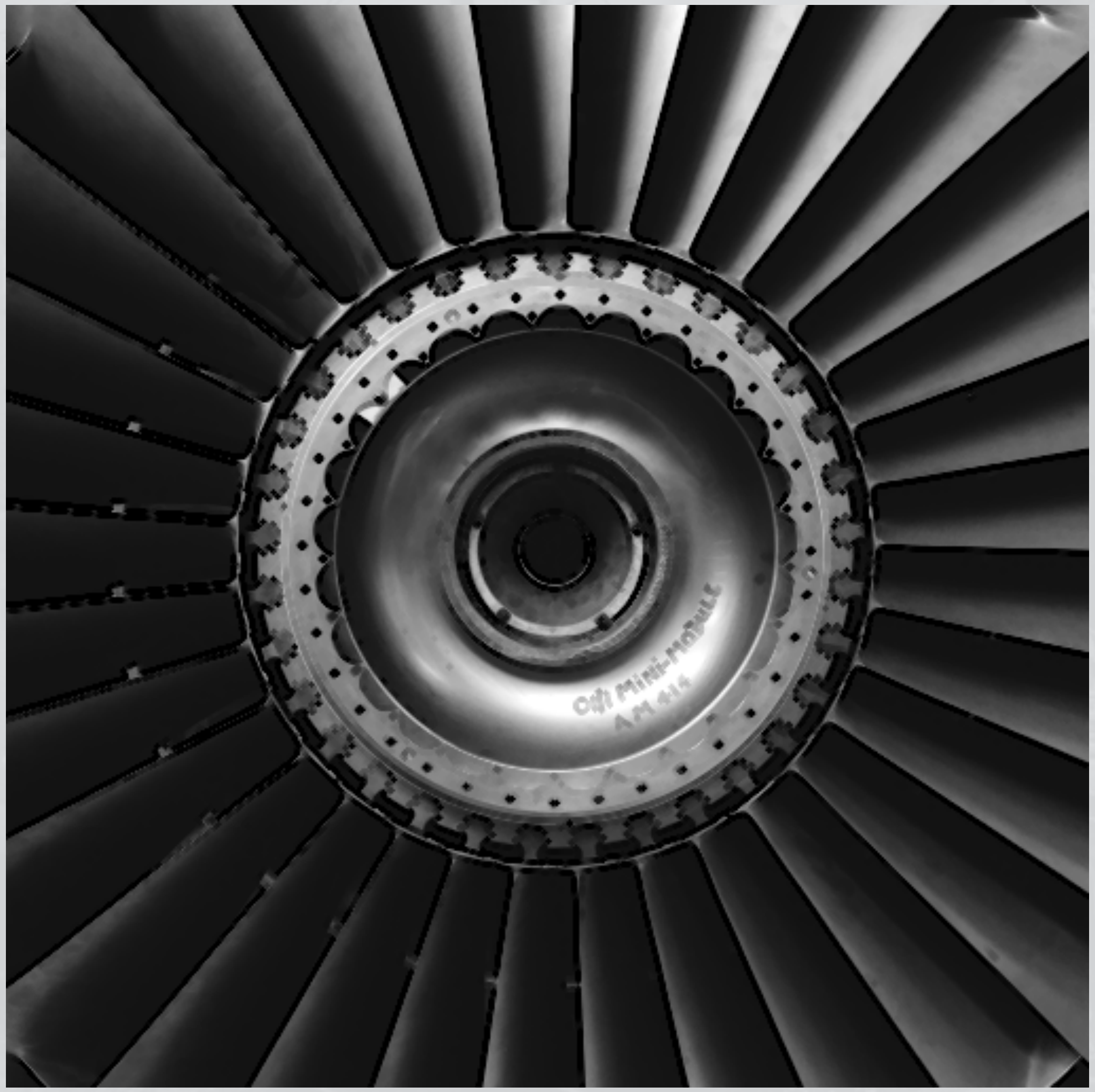
Two dimensions

```
library(png); library(mmand)
fan <- readPNG(system.file("images", "fan.png", package="mmand"))
display(fan)
```



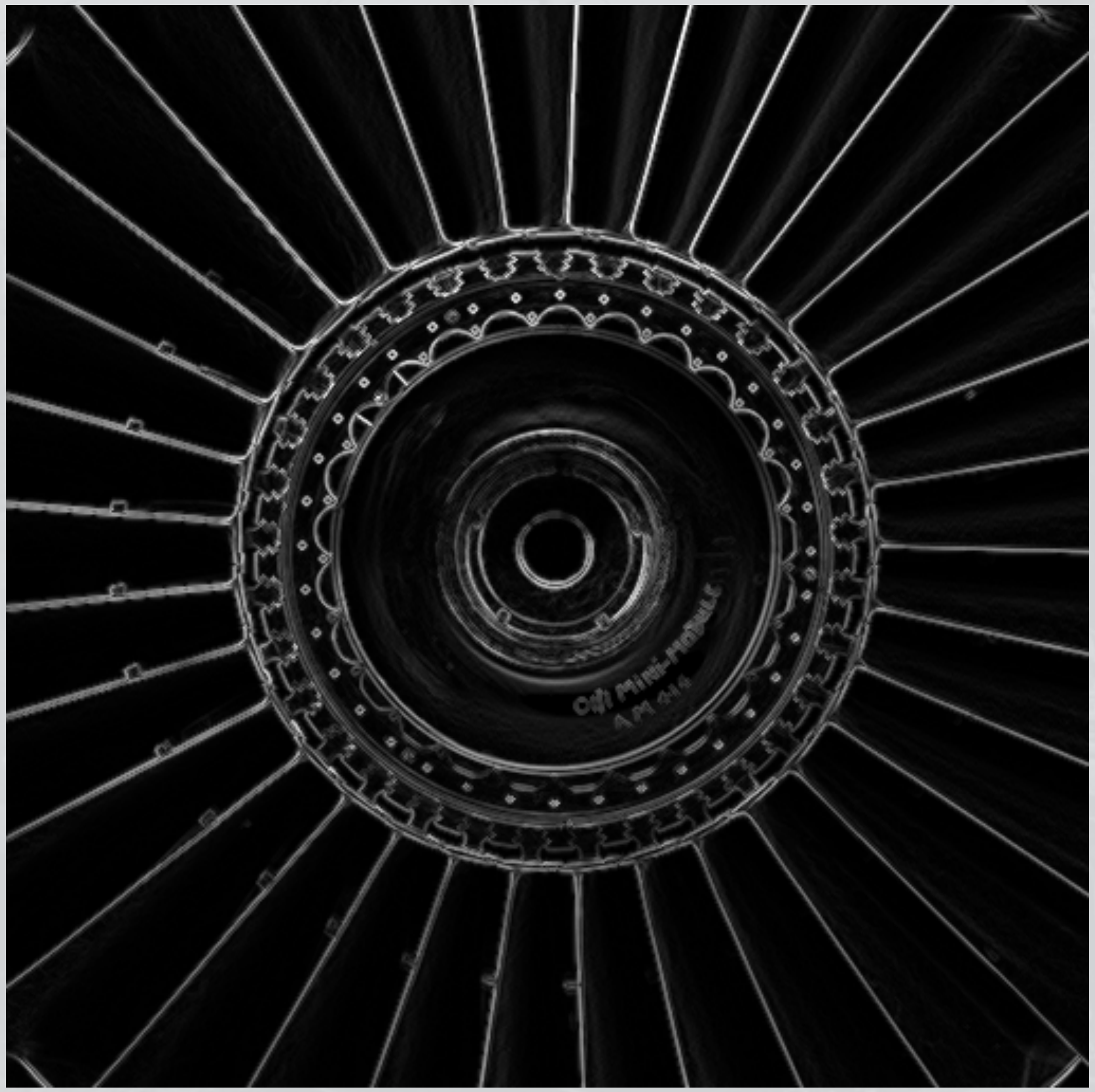
Greyscale morphology in 2D

```
kernel <- shapeKernel(c(3,3), type="diamond")
display(erode(fan,kernel))
```



Morphological gradient

```
kernel <- shapeKernel(c(3,3), type="diamond")
display(dilate(fan,kernel) - erode(fan,kernel))
```



Resampling

- Indexing between elements

```
x <- c(0,0,1,0,0)
x[2.5]
[1] 0
```

- R truncates 2.5 to 2 and returns the second element
- In some cases there is conceptually a value at location 2.5 but we don't know it
- Best guess is probably that it's 0, or 1, something in between
- Using mmand we can interpolate using different sampling kernels

```
# "Nearest neighbour"
resample(x, 2.5, boxKernel())
[1] 1

# Linear interpolation
resample(x, 2.5, triangleKernel())
[1] 0.5

# Mitchell-Netravali cubic spline
resample(x, 2.5,
  mitchellNetravaliKernel(1/3,1/3))
[1] 0.5708661
```

- An entire image of any dimensionality can be resampled similarly
- Allows regridding, upsampling and downsampling

Upsampling a smaller image

```r
fan_small <- readPNG(system.file("images", "fan-small.png", package="mmand"))
display(rescale(fan_small, 4, mnKernel()))
```

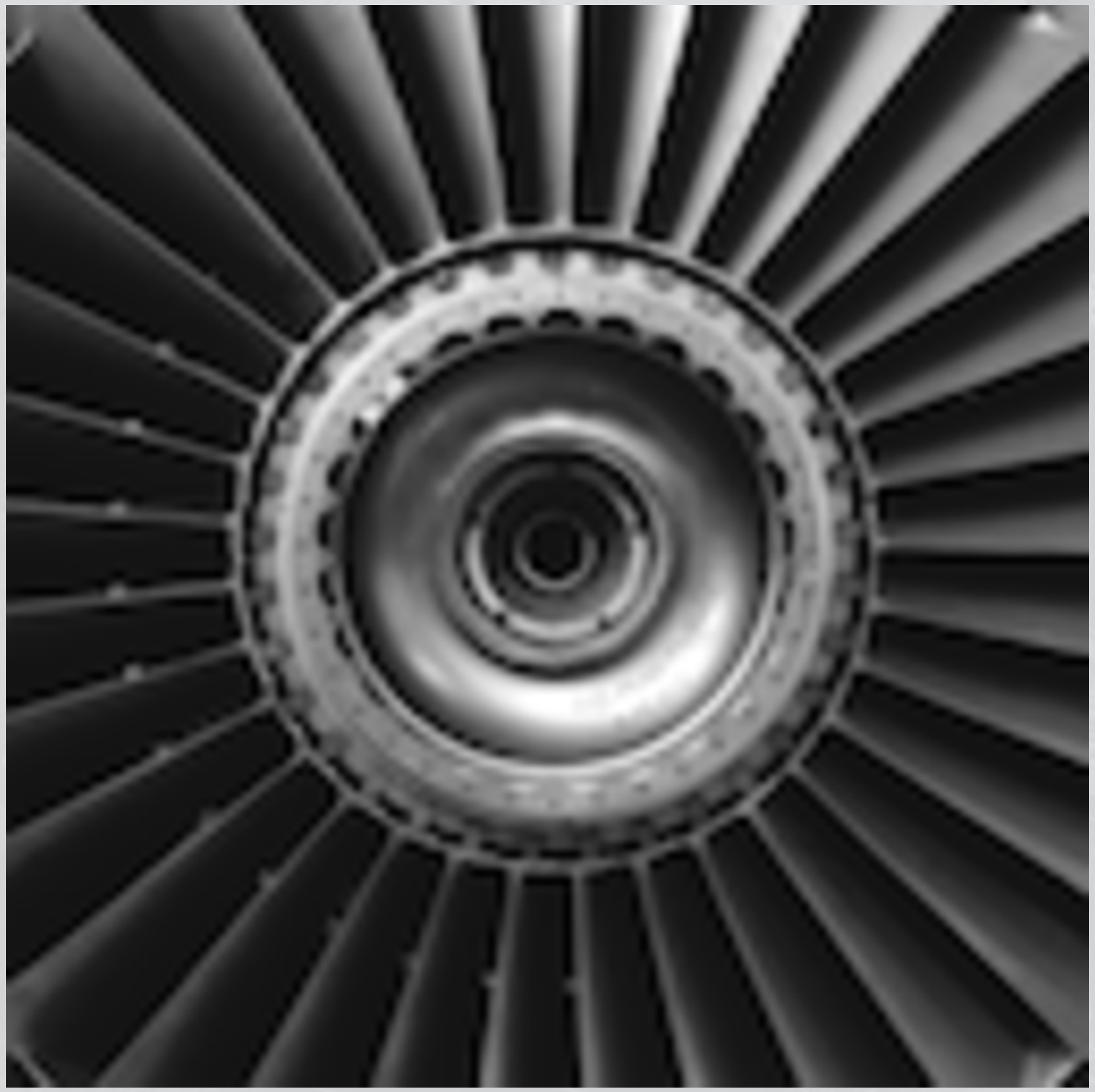
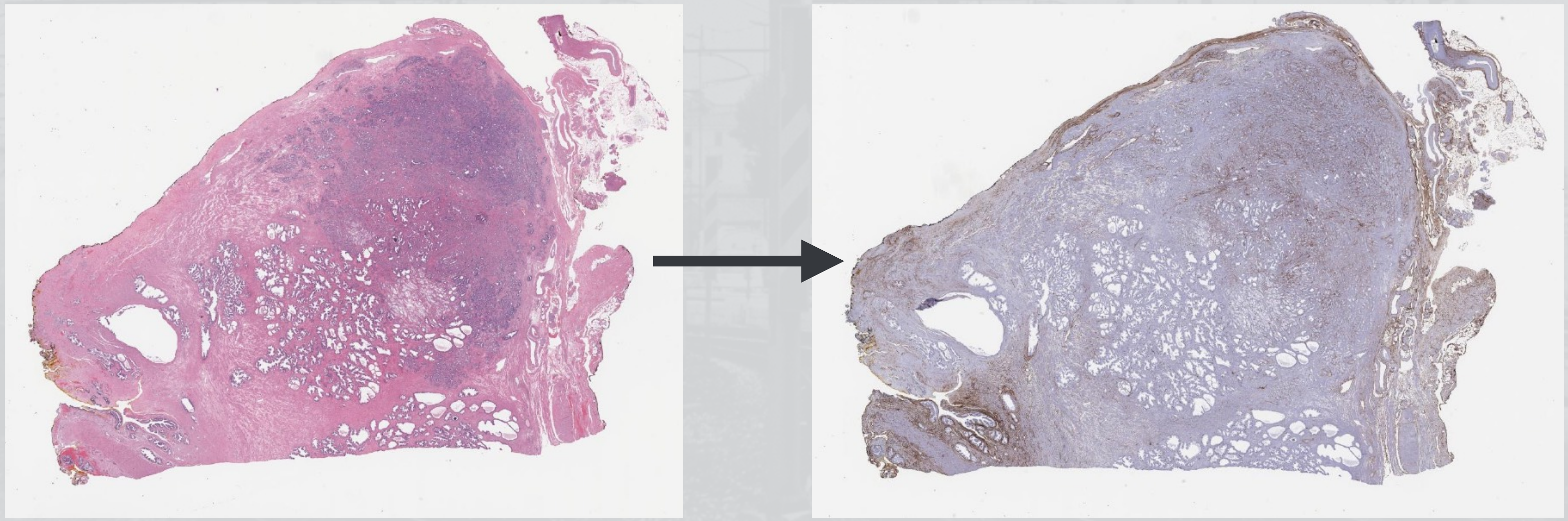


Image registration

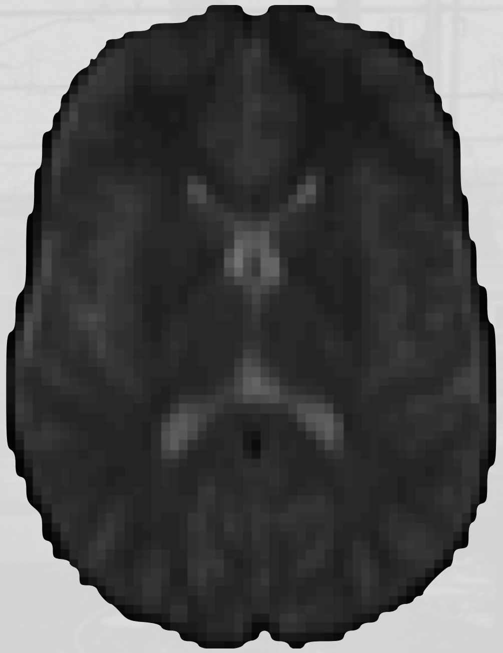
- Aligning two related images
- Contrasts may be similar or different
- Pixel information may be combined
- Optimisation over a space of transformations (global/linear or local/nonlinear)
- Resampling to match the target image

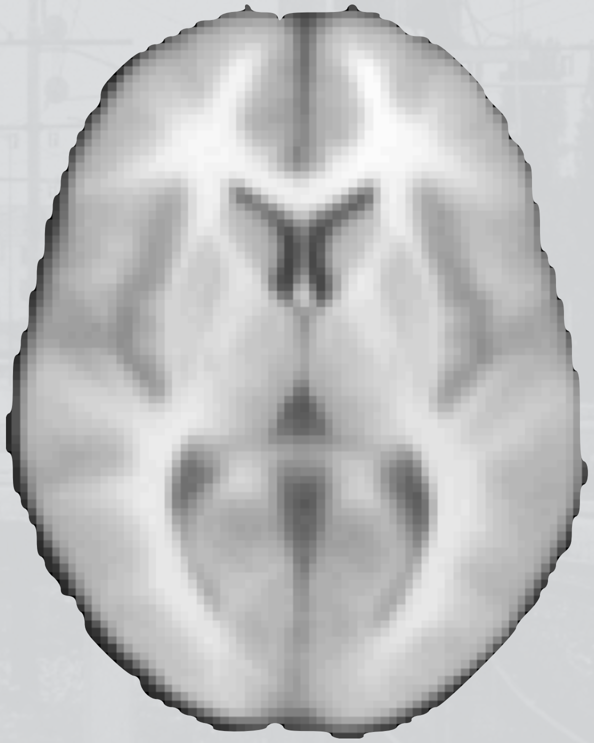


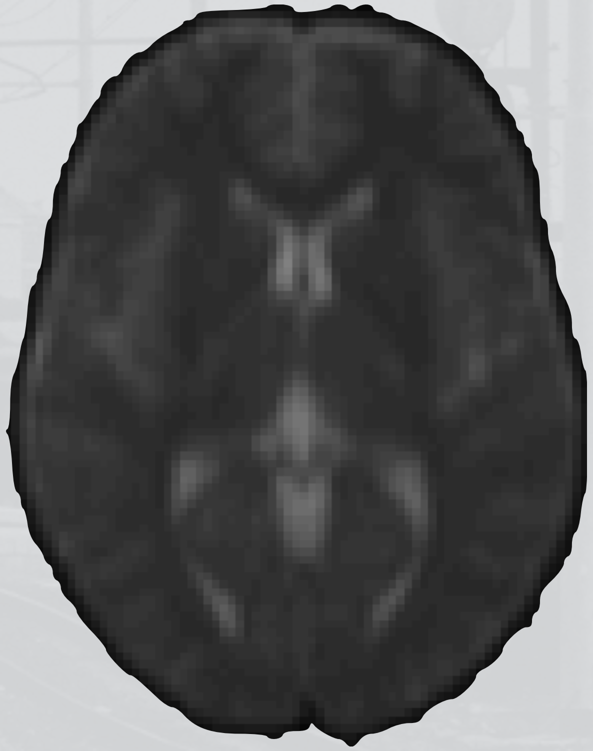
Courtesy of Jiří Borovec, Czech Technical University, Prague

RNiftyReg usage (3D)

```
library(RNiftyReg)
source <- readNifti(system.file("extdata","epi_t2.nii.gz",package="RNiftyReg"))
target <- readNifti(system.file("extdata","mni_brain.nii.gz",package="RNiftyReg"))

linear <- niftyreg(source, target, scope="affine")
nonlinear <- niftyreg(source, target, scope="nonlinear", init=forward(linear))
```


source

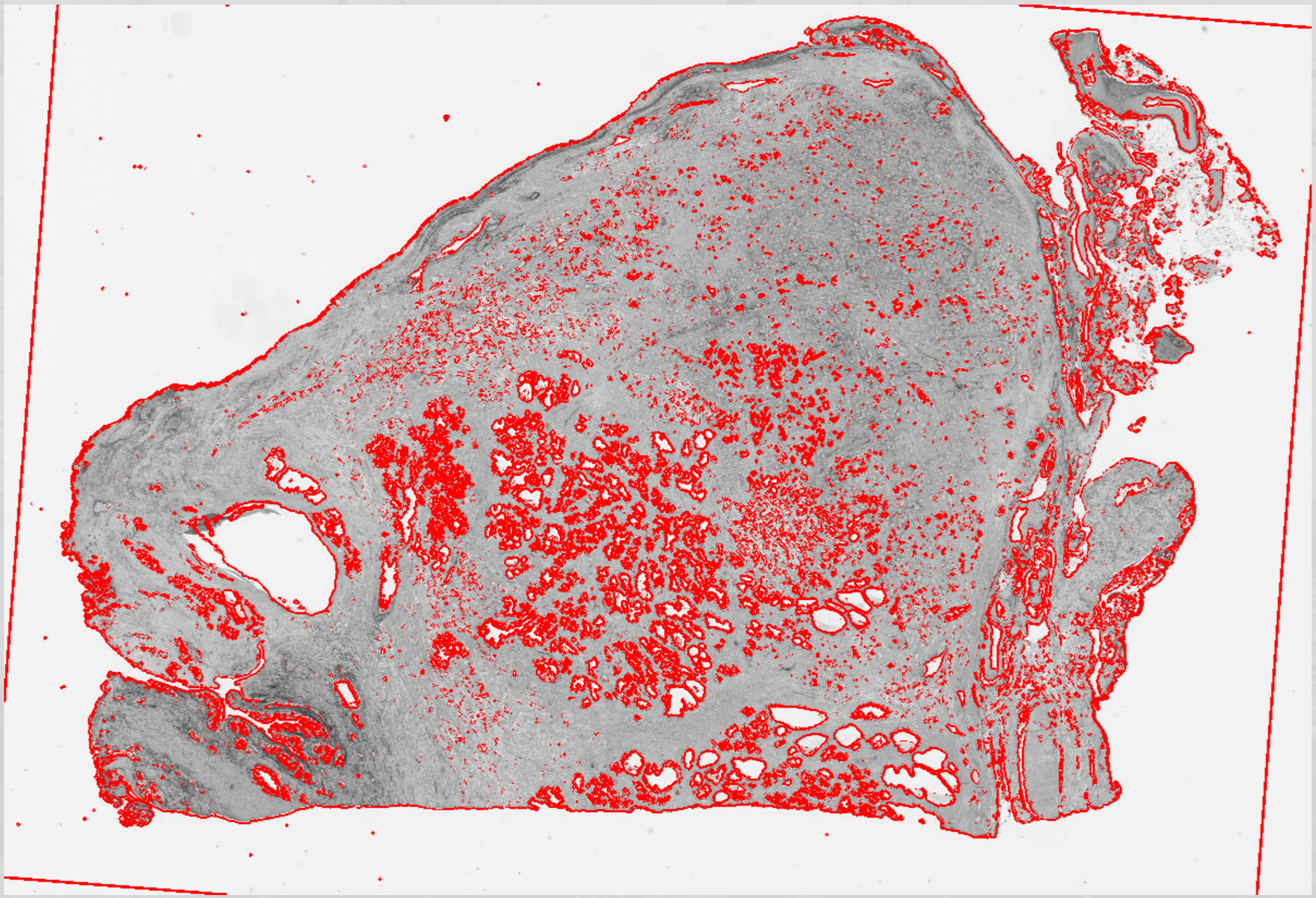

target


result (nonlinear)

Combining the packages: checking registration

```r
library(jpeg)
library(mmand)
library(RNiftyReg)

# Read images and convert to greyscale
source <- readJPEG("source.jpg")
target <- readJPEG("target.jpg")
source <- apply(source, 1:2, mean)
target <- apply(target, 1:2, mean)

# Register images
result <- niftyreg(source, target)

# Calculate morphological gradient
kernel <- shapeKernel(c(3,3), type="diamond")
gradient <- dilate(result$image,kernel) - erode(result$image,kernel)

# Display the results
display(target)
display(threshold(gradient,method="kmeans"), add=TRUE, col="red")
```

Combining the packages: checking registration



Other tools I have written and/or found useful

- The multiplatform RStudio IDE
- car for better AN(C)OVA
- divest for DICOM-to-NIfTI conversion
- lme4 for random/mixed effects models
- igraph for graph theory
- pcaMethods for PCA
- png and jpeg for working with image formats
- R.matlab for reading .mat files
- soma for nonlinear optimisation
- ore for text processing
- shades for simple colour manipulation
- TractoR, of course!
- See also http://www.statmethods.net for other applications

Why use R?

- Very strong on stats
- Scripted analyses for reproducibility; explicit tests
- Quick development due to high-level code
- Good performance in vectorised code
- Very easy to link in bits of C/C++/ FORTRAN code for improved speed where needed
- Pretty, publication-ready graphics
- Free and open source: install it wherever you like
- Even modify it if you want!
- A strong platform for (image) data analysis
- Usage and awareness in imaging groups is growing (cf. Tabelow, Clayden et al., *NeuroImage*, 2011)