An example session for analyzing Inversion Recovery MRI and MR Elastography data

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This document illustrates the workflow of analyzing Inversion Recovery Magnetic Resonance Imaging (IRMRI) data. The example uses noisy IR data created from a small sub cube of an artificial IR image (Infinity Inversion Time), a corresponding segmentation image and MR Elastography data. For neuroimaging bacckground we refer to (**MNRLilai21b**) (IRMRI) and (**MNRLilai21a**) (MRE).

For an more extended introduction we refer to **MRBIbook2** Chapter 6.

1 Generating the IR MRI data

First, we specify the directory where the data are stored within the package

```
> dataDir0 <- system.file("extdataIR", package = "qMRI")
> dataDir <- tempdir()
> library(oro.nifti)
```

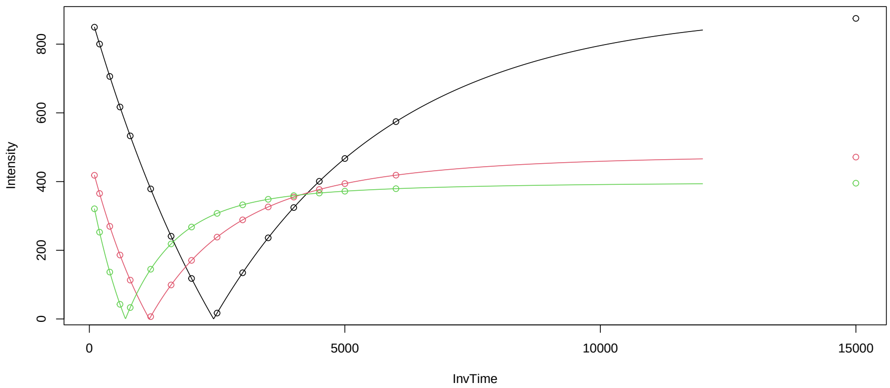
We now generate IRMRI data following a model that assumes voxel to contain a mixture of a solid tissue (either DM or WM) and fluid.

```
> library(qMRI)
> segm <- readNIfTI(file.path(dataDir0,"Brainweb_segm"))
> Sf <- 900
> Rf <- 0.000285
> Sgm <- 400
> Rgm <- 0.00075
> fgm <- .15
> Swm <- 370
> Rwm <- 0.0011
> fwm <- .05
> InvTimes <- c(100, 200, 400, 600, 800, 1200, 1600, 2000, 2500, 3000,
+               3500, 4000, 4500, 5000, 6000, Inf)
> InvTimes0 <- c(100, 200, 400, 600, 800, 1200, 1600, 2000, 2500, 3000,
+               3500, 4000, 4500, 5000, 6000, 15000)
```

Typical intensities as functions of inversion times an tissue type (black for CSF, red for GM and green for WM) are illustrated in Figure **??**

```
> x <- seq(100,12000,10)
> fintCSF <- qMRI:::IRhomogen(c(Sf,Rf),InvTimes0)
```

```
> fintGM <- qMRI:::IRmix2(c(fgm,Rgm,Sgm),InvTimes0,Sf,Rf)
> fintWM <- qMRI:::IRmix2(c(fwm,Rwm,Swm),InvTimes0,Sf,Rf)
> plot(InvTimes0,fintCSF,xlab="InvTime",ylab="Intensity")
> points(InvTimes0,fintGM,col=2)
> points(InvTimes0,fintWM,col=3)
> lines(x,qMRI:::IRhomogen(c(Sf,Rf),x))
> lines(x,qMRI:::IRmix2(c(fgm,Rgm,Sgm),x,Sf,Rf),col=2)
> lines(x,qMRI:::IRmix2(c(fwm,Rwm,Swm),x,Sf,Rf),col=3)
```



We generate artificial Rician distributed data with standard deviation $\sigma = 40$

```
> sigma <- 40
> nTimes <- length(InvTimes0)
> nCSF <- sum(segm==1)
> nGM <- sum(segm==2)
> nWM <- sum(segm==3)
> IRdata <- array(0,c(nTimes,prod(dim(segm))))
> IRdata[,segm==1] <- sqrt(rnorm(nTimes*nCSF,fintCSF,sigma)^2+
+                          rnorm(nTimes*nCSF,0,sigma)^2)
> IRdata[,segm==2] <- sqrt(rnorm(nTimes*nGM,fintGM,sigma)^2+
+                          rnorm(nTimes*nGM,0,sigma)^2)
> IRdata[,segm==3] <- sqrt(rnorm(nTimes*nWM,fintWM,sigma)^2+
+                          rnorm(nTimes*nWM,0,sigma)^2)
> dim(IRdata) <- c(nTimes,dim(segm))
> for(i in 1:9) writeNIfTI(as.nifti(IRdata[i,,,]),
+                          file.path(dataDir,paste0("IR0",i)))
> for(i in 10:nTimes) writeNIfTI(as.nifti(IRdata[i,,,]),
+                          file.path(dataDir,paste0("IR",i)))
```

2 Analysis of IR MRI data

We now illustrate the analysis pipeline for IRMRI data. First we generate an IRdata object

```
> library(qMRI)
> t1Files <- list.files(dataDir,"*.nii.gz",full.names=TRUE)
```

```
> segmFile <- file.path(dataDir0,"Brainweb_segm")
> IRdata <- readIRData(t1Files, InvTimes0, segmFile, sigma=sigma,
+                          L=1, segmCodes=c("CSF","GM","WM"))
```

In a first analysis step parameters S_f and R_f characterizing fluid are obtained from voxel that are classified as CSF using the model

$$\xi(TI; S^f, R_1^f) = |S^f \left(1 - 2\mathrm{e}^{-TI \cdot R_1^f}\right)| \tag{1}$$

with data for inversion time TI distributed as $Rician(\xi(TI; S_f, R_1^f), \sigma)$.

The parameters S_f and R_1^f are assumed not to vary within CSF.

```
> setCores(2) # parallel mode using 2 threads
> IRfluid <- estimateIRfluid(IRdata, method="NLR", verbose=FALSE)
> cat("Estimated parameters Sf:", IRfluid$Sf,
+                             " Rf:", IRfluid$Rf, "\n")

Estimated parameters Sf: 902.0022  Rf: 0.0002862264
```

We here use nonlinear regression instead of the more adequate quasi-likelihood method (`method="QL"`) In the next step we evaluate a mixture model

$$\xi(TI; f, S^f, R_1^f, S^s, R_1^s) = |(1-f)S^f \left(1 - 2\mathrm{e}^{-TI \cdot R_1^f}\right) + fS^s \left(1 - 2\mathrm{e}^{-TI \cdot R_1^s}\right)|, \tag{2}$$

for voxel classified as GM or WM with parameters S_f and R_1^f plugged in.

```
> IRmix <- estimateIRsolid(IRfluid, verbose=FALSE)
```

Parameters S^s and R_1^s characterizing solid material in GM and WM can be assumed to be spatially smooth within the respective tissue types. Parameter f characterizes the proportion of fluid within a voxel. This parameter is difficult to estimate in model 2. We therefor apply an adaptive smoothing procedure within segments characterizing GM and WM to reduce the variance of the estimates of S^s and R_1^s

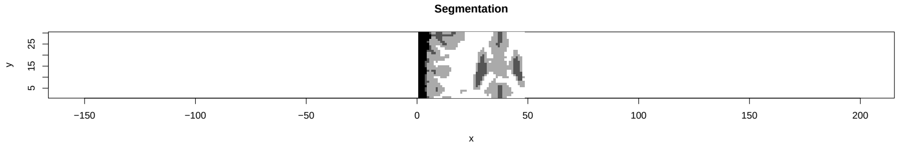
```
> sIRmix <- smoothIRSolid(IRmix, alpha=1e-4, verbose=FALSE,partial=FALSE)
```

and then re-estimate the fluid proportion f

```
> sIRmix <- estimateIRsolidfixed(sIRmix, verbose=FALSE)
```

We shortly illustrate the estimated maps (central slice) that we gain

```
> oldpar <- par(mfrow=c(1,4),mar=c(3,3,3,.5),mgp=c(2,1,0))
> on.exit(par(oldpar))
> library(adimpro)
> rimage(segm[,,2])
> title("Segmentation")
> rimage(sIRmix$Sx[,,2],zlim=c(250,500))
> title("solid intensity map")
> rimage(sIRmix$Rx[,,2],zlim=c(0,.0015))
> title("solid relaxation rate map")
> rimage(sIRmix$fx[,,2],zlim=c(0,.4))
> title("fluid proportion map")
```



All analysis steps can be combined, in this case using quasi-likelihood, simply calling

```
> sIRmix <- estimateIR(IRdata, method="QL")
```