BayesDLMfMRI: Bayesian Matrix-Variate Dynamic Linear Models for Task-based fMRI Modeling in R

Technical Report

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Abstract

This article introduces an R package to perform statistical analysis for task-based fMRI data at both individual and group levels. The analysis to detect brain activation at the individual level is based on modeling the fMRI signal using Matrix-Variate Dynamic Linear Models (MDLM). The analysis for the group stage is based on posterior distributions of the state parameter obtained from the modeling at the individual level. In this way, this package offers several R functions with different algorithms to perform inference on the state parameter to assess brain activation for both individual and group stages. Those functions allow for parallel computation when the analysis is performed for the entire brain as well as analysis at specific voxels when it is required.

Keywords First keyword · Second keyword · More

1 Introduction: fMRI packages with options for Bayesian Analysis

Statistical modeling of processed fMRI data is a challenging problem that has caught the attention of the statistical community in the past two decades. A large number of observations are usually obtained with only one subject in an fMRI session. This high volume of information poses a challenge for the implementation of sophisticated statistical models capable of accounting for the spatiotemporal structures usually present in this type of data. From a Bayesian perspective, there have been published and proposed different types of models to model fMRI data (see, for instance, Zhang et al. [2016], Eklund et al. [2017], Bezener et al. [2018], Yu et al. [2018] and a complete review by Zhang et al. [2015]). Despite those numerous contributions in the field, just a few software implementations of Bayesian methods are available for fMRI data analysis. For instance, the **FSL** software [Jenkinson et al., 2012] offers a Bayesian procedure for group stage analysis. However, this group analysis depends on a Frequentist or Classical output from the individual stage, which means it is not a fully Bayesian procedure. Another popular software among practitioners in the neuroscience community with implementations of Bayesian methods is the **SPM** package [Penny et al., 2011]. It has alternatives for Bayesian analysis to both individual and group stages. Still, as in the case of the **FSL** package, the group analysis depends on a Frequentist output from the individual stage. There is also available a **MATLAB GUI** called **NPBayes-fMRI** [Kook et al., 2019], which is an implementation of the work proposed by Zhang et al. [2016], a fully Bayesian modeling procedure for individual and group stages. In R [R Core Team, 2018], tools for different types of fMRI data analysis are provided in packages like **fmri** [Tabelow and Polzehl, 2011], **oro.nifti** [Whitcher et al., 2011], **neurobase** [Muschelli, 2018], and **neuRosim** [Welvaert et al., 2011]. For fMRI data analysis under a Bayesian approach, there was available a package called **cudaBayesreg** [da Silva et al., 2011], which was removed recently from the CRAN repository. Thus, to our knowledge, the package **BHMSMAfMRI** [Sanyal and Ferreira, 2019] is the only Bayesian option for fMRI data analysis in R to this date.

In this work, we introduce an R package called **BayesDLMfMRI**, which implements the method proposed in Cardona-Jiménez and Pereira [2021]. The **BayesDLMfMRI** permits to perform individual, and group task-based fMRI analysis based on the Matrix-Variate Dynamic Linear Model (MVDLM) proposed by

Quintana [1985]. Given this type of analysis usually involves large amounts of data, we take advantage of the packages **Rcpp** [Eddelbuettel et al., 2011] and **RcppArmadillo** [Eddelbuettel and Sanderson, 2014] in order to speed up the computation time. **BayesDLMfMRI** also depends internally on the package **pbapply** [Solymos and Zawadzki, 2019], which allows the user to visualize a progress bar when the process is executed in either sequence or parallel. In order to run an analysis using our package, the user must provide a 4D array (or a 4D$\times N$ array for a group analysis with N subjects) containing the sequence of processed images and a design matrix whose columns are related to the so-called expected blood-oxygen-Level dependent (**BOLD**) response and (optionally) some other covariates related to particular subjects' characteristics. To process the raw images, we recommend the use of packages such as **FSL** or **SPM**. And to build the expected BOLD response, the user has options like the **fmri** package, which allows defining different types of models to represent the hemodynamic response function (**HRF**). **BayesDLMfMRI** package is intended to be just a complementary well-tested, and assessed tool for researchers and practitioners that run their studies in more popular packages such as **FSL** and **SPM**. In the next section, we give a brief description of the model and methods on which the **BayesDLMfMRI** package is based and present its R functions to perform fMRI data analysis. In section three, we offer some examples to illustrate the use of the package, and in the final section, we give some concluding remarks and mention future lines of work.

2 Methods and software

Table 1: Functions implemented in the **BayesDLMfMRI** package for task-based fMRI individual [group] analysis. LTT stands for Linear Transformation Test, which is the same as the average cluster effect (ACE) distribution defined in Cardona-Jiménez and Pereira [2021].

Function	Description
`ffdEvidenceFETS` [`ffdGroupEvidenceFETS`]	It returns 3D arrays to build individual [group] activation evidence maps [based on outputs from MVDLM] fitting an MVDLM at the individual level and using the FETS algorithm to assess voxel activation. There are two options related to the posterior distribution of $\Theta^{(z)}_{[i,j,k]t}$: LTT and Joint, each of which runs independently and must be set by the user as an input parameter.
`ffdEvidenceFFBS` [`ffdGroupEvidenceFFBS`]	It returns 3D arrays to build individual [group] activation evidence maps [based on outputs from MVDLM] fitting an MVDLM and using the FFBS algorithm to assess voxel activation. The options LTT and Joint related to the posterior distribution of $\Theta^{(z)}_{[i,j,k]t}$ are simultaneously executed in the same run.
`ffdEvidenceFSTS` [`ffdGroupEvidenceFSTS`]	Same features as `ffdEvidenceFFBS` [`ffdGroupEvidenceFFBS`], though using the FSTS algorithm.
`SingleVoxelFETS` [`GroupSingleVoxelFETS`]	Produces some useful outputs from a single voxel analysis related to the FETS algorithm.
`SingleVoxelFFBS` [`GroupSingleVoxelFFBS`]	Same features as `SingleVoxelFETS` [`GroupSingleVoxelFETS`], though using the FFBS algorithm.
`SingleVoxelFSTS` [`GroupSingleVoxelFSTS`]	Same features as `SingleVoxelFETS` [`GroupSingleVoxelFETS`], though using the FSTS algorithm.

The type of MVDLM which this package relies on is the version developed initially by Quintana [1985] and Quintana [1987]. Here, we just give a brief description of the model and methods. For a better understanding of the method implemented in this package for the individual and group stage, see Cardona-Jiménez and

Pereira [2021]. Let $\mathbf{Y}^{(z)}_{[i,j,k]t}$ be a $q \times 1$ random vector representing the cluster of observed BOLD responses at position (i, j, k) in the brain image, time t and subject z, for $i = 1, \ldots, d_1$, $j = 1, \ldots, d_2$, $k = 1, \ldots, d_3$, $t = 1, \ldots, T$ and $z = 1 \ldots, N$. Thus, the cluster of BOLD signals is modeled as

$$\begin{array}{lrcl} \text{Observation:} & \mathbf{Y}^{(z)}_{[i,j,k]t} & = & \mathbf{F}_t^{'}\Theta^{(z)}_{[i,j,k]t} + \boldsymbol{\nu}^{'(z)}_{[i,j,k]t} \\ \text{Evolution:} & \Theta^{(z)}_{[i,j,k]t} & = & \mathbf{G}_t\Theta^{(z)}_{[i,j,k]t-1} + \Omega^{(z)}_{[i,j,k]t}, \end{array} \tag{1}$$

where, for each t we have a $q \times 1$ vector $\boldsymbol{\nu}^{'(z)}_{[i,j,k]t}$ of observational errors, a $p \times q$ matrix $\Theta_{[i,j,k]t}$ of state parameters, a $p \times q$ matrix $\Omega^{(z)}_{[i,j,k]t}$ of evolution errors. The $1 \times p$ and $p \times p$ matrices $\mathbf{F}_t^{'}$ and $\mathbf{G}_t$ respectively are common to each of the q univariate DLMs. The covariates related to the design being used, either a block or an event-related design as well as other characteristics of the subjects, can be included in the columns of $\mathbf{F}_t^{'}$. For individual analysis, the model (1) is fitted to every cluster of voxels related to each position $[i, j, k]$ in the brain image, and the cluster size depends on the r distance, which is a parameter defined by the user. To identify whether or not there is significant evidence of cluster activation at location $[i, j, k]$, three different algorithms (FETS, FSTS, and FFBS) proposed in Cardona-Jiménez and Pereira [2021] are implemented. Those algorithms are sampling schemes that allow drawing on-line trajectory curves related to the state parameter $\Theta^{(z)}_{[i,j,k]t}$, and with those resulting simulated samples a Monte Carlo evidence related to the event of cluster activation is computed. The information obtained from the individual stage can be combined in different ways to produce several measures of evidence for group activation. For a better understanding of the method implemented in this package for the group stage, see Cardona-Jiménez and Pereira [2021]. In table 1, the package's functions for individual and group analysis, along with a brief description, are presented.

3 Illustrations

In order to show some practical illustrations about the use of the **BayesDLMfMRI** package, we use data related to an fMRI experiment where a sound stimulus is presented. That experiment is intended to offer a "voice localizer" scan, which allows rapid and reliable localization of the voice-sensitive "temporal voice areas" (TVA) of the human auditory cortex [Pernet et al., 2015]. The data of this "voice localizer" scan is freely available on the online platform OpenNEURO [Gorgolewski et al., 2017]. In the original experiment, the voice and non-voice sounds are separately analyzed, but here we merge both sounds in one block as if it were just one stimulus (see figure 1). For the individual analysis, we select one from the 217 subjects whose data are available on OpenNEURO; specifically, we take the data from sub-007. To illustrate the group analysis functions, we take 20 subjects (sub-001:sub-021). The raw fMRI data is preprocessed using the standard processing pipelines implemented on the **FSL** software for motion correction, spatial smoothing, and other necessary procedures to perform statistical analysis for both individual and group stages.

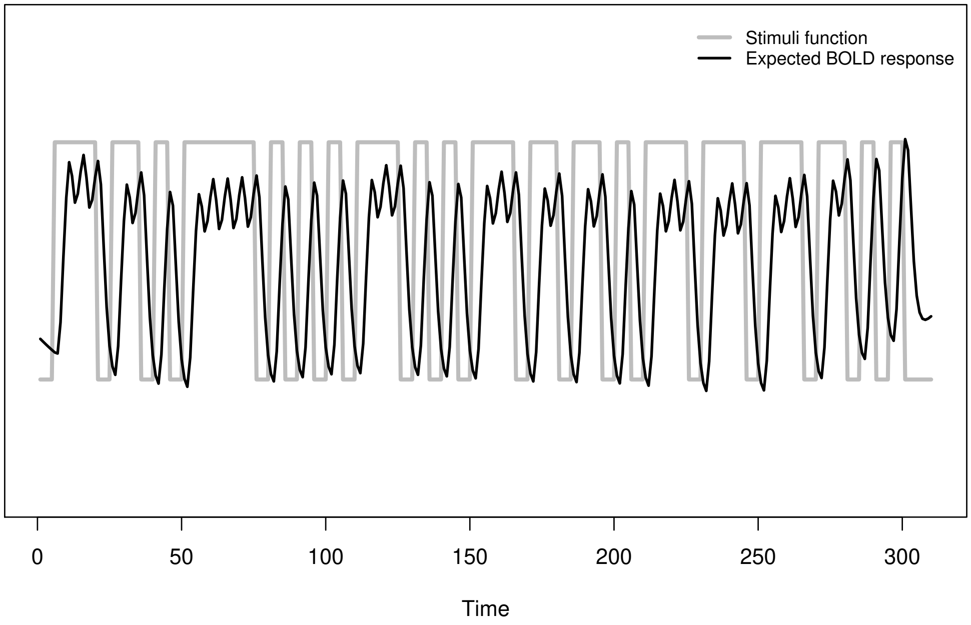


Figure 1: Merged stimuli function for voice and non-voice sounds with its related expected BOLD response function for the "voice localizer" example.

Individual analysis

To run any of the functions related to individual analysis, the user must provide two inputs: an array of four dimensions containing the sequence of MRI images and a matrix whose columns have the covariates to model the observed BOLD response. Thus, we read the sub-007.nii.qz file, which contains the MRI images, using the function `readNIFTI` from the package **oro.nifti**. The covariates, specifically, the expected BOLD response (shown in figure 1) and its derivative, are contained in the covariates.cvs file. The rationale for including the temporal derivative is that this basis can capture small offsets in the time to peak of the hemodynamic response [Poldrack et al., 2011].

```
R> library("oro.nifti")
R> fMRI.data <- readNIfTI("./fMRIData/sub-007.nii.gz", reorient=FALSE)
R> fMRI.data <- fMRI.data@.Data
R> dim(fMRI.data)

[1]  91 109  91 310

R> Covariates <- read.csv("./covariates.csv", header=FALSE, sep="")
R> dim(Covariates)

[1] 310   2
```

To perform an individual voxel-wise analysis and consequently obtain a 3D array of measurements of activation, the user can choose among three different functions: `ffdEvidenceFETS`, `ffdEvidenceFFBS` and `ffdEvidenceFSTS`. These functions can yield three types of evidence measurements for voxel activation: Marginal effect, Average cluster effect, and Joint effect. To illustrate their use and functionality, we run an example from the "voice localizer" data.

```
R> library(devtools)
R> install_github("JohnatanLAB/BayesDLMfMRI")
```

```
R> library(BayesDLMfMRI)
R> res <- ffdEvidenceFEST(ffdc = fMRI.data, covariates = Covariates,
+ m0 = 0, Cova = 100, delta = 0.95, S0 = 1, n0 = 1, Nsimu1 = 100, Cutpos1 = 30,
+ r1 = 1, Test = "LTT",  Ncores = 15)

  |++++++++++++++++++++++++++++++++++++++++++++++++++| 100% elapsed = 05m 36s
```

The arguments m0, Cova, S0 and n0 are the hyper-parameters related to the joint prior distribution of $(\Theta^{(z)}_{[i,j,k]t}, \Sigma^{(z)}_{[i,j,k]t})$. For this example, we are setting a "vague" prior distribution according to Quintana and West [1987], where m0 = 0 define a null matrix with zero values in all its entries. And both Cova = 100 and S0 = 1 define respectively the values for the diagonal matrices C_0 and S_0 as defined in Cardona-Jiménez and Pereira [2021]. r1 is the euclidean distance, which defines the size of the cluster of voxels jointly modeled. Test is the parameter related to the test selected by the user, for which there are two options: "LTT" and "Joint". "Ncores" is the argument related to the number of cores when the process is executed in parallel. Nsimu1 is the number of simulated on-line trajectories related to the state parameter $\Theta^{(z)}_{[i,j,k]t}$. From our own experience dealing with different sets of fMRI data, we recommend Nsimu1 = 100 as a good number of draws to obtain reliable results. Cutpos1 is the time up from where the on-line trajectories are considered in order to compute the activation evidence, and delta is the value of the discount factor. For a better understanding about the setting of these two last arguments, see Cardona-Jiménez and Pereira [2021].

```
R> str(res)

List of 2
 $ : num [1:91, 1:109, 1:91] 0 0 0 0 0 0 0 0 0 0 ...
 $ : num [1:91, 1:109, 1:91] 0 0 0 0 0 0 0 0 0 0 ...

R> dim(res[[1]])

[1]  91 109  91
```

The output for the ffdEvidenceFEST function depends on the type of Test set by the user. For Test = "LTT" the function returns a list of the type res[[p]][x,y,z], where p represents the column position in the covariates matrix and [x,y,z] represent the voxel position in the brain image. Thus, for the "voice localizer" example res[[1]] and res[[2]] are the 3D arrays related to the evidence for brain activation related to the BOLD response for the auditory stimuli and its derivative respectively. When Test = Joint the output returned is an array of the type res[[2*p]][x,y,z], with the first p elements of the array related to the Joint effect and the rest of it to the Marginal effect.

```
R> library(neurobase)
R> res.auxi <- res[[1]]
R> ffd <- readNIfTI("./standard.nii.gz")
R> Z.visual.c <- nifti(res.auxi, datatype=16)
R> ortho2(ffd, ifelse(Z.visual.c > 0.95, Z.visual.c, NA),
+  col.y = heat.colors(50), ycolorbar = TRUE, ybreaks = seq(0.95, 1, by = 0.001))
```

The **neurobase** package is one option available in R to visualize MRI images. In this example, we use its ortho2() function to plot the evidence activation map. The standar.nii.gz file contains the MNI brain atlas, which is used in this example as a reference space for individual and group analysis. For a better understanding of the use of brain atlas, see Brett et al. [2002].

```
R> res <- ffdEvidenceFEST(ffdc = fMRI.data, covariates = Covariates,
+  m0 = 0, Cova = 100, delta = 0.95, S0 = 1, n0 = 1, Nsimu1 = 100, Cutpos1 = 30,
+  r1 = 2, Test = "JointTest",  Ncores = 15)

 |++++++++++++++++++++++++++++++++++++++++++++++++++| 100% elapsed = 28m 57s

R> str(res)

List of 4
 $ : num [1:91, 1:109, 1:91] 0 0 0 0 0 0 0 0 0 0 ...
 $ : num [1:91, 1:109, 1:91] 0 0 0 0 0 0 0 0 0 0 ...
 $ : num [1:91, 1:109, 1:91] 0 0 0 0 0 0 0 0 0 0 ...
```

For both `ffdEvidenceFFBS` and `ffdEvidenceFSTS` the input arguments and output structures are the same. Below we run the "voice localizer" example using the `ffdEvidenceFFBS` function. It returns a list of the form `res[[T]][p,x,y,z]`, where `T` defines the type of test (`T = 1` for Marginal effect, `T = 2` for Joint effect, and `T = 3` for Average cluster effect), `p` represents the column position in the `covariates` matrix and `x,y,z` represent the voxel position in the brain image.

```
#Change JointTest for Joint
R> res <- ffdEvidenceFFBS(ffdc = fMRI.data, covariates = Covariates, m0 = 0,
+  Cova = 100, delta = 0.95, S0 = 1,n0 = 1, Nsimu1 = 100, Cutpos1 = 30,
+  r1 = 1,  Ncores = 15)

 |++++++++++++++++++++++++++++++++++++++++++++++++++| 100% elapsed = 19m 08s

R> str(res)

List of 3
 $ : num [1:2, 1:91, 1:109, 1:91] 0 0 0 0 0 0 0 0 0 0 ...
 $ : num [1:2, 1:91, 1:109, 1:91] 0 0 0 0 0 0 0 0 0 0 ...
 $ : num [1:2, 1:91, 1:109, 1:91] 0 0 0 0 0 0 0 0 0 0 ...$

R> library(neurobase)
R> res.auxi <- res[[3]][1,,,]
R> ffd <- readNIfTI("standard.nii.gz")
R> Z.visual.c <- nifti(res.auxi, datatype=16)
R> ortho2(ffd, ifelse(Z.visual.c > 0.95, Z.visual.c, NA),
+  col.y = heat.colors(50), ycolorbar = TRUE, ybreaks = seq(0.95, 1, by = 0.001))
```

The **BayesDLMfMRI** package also has functions that allow performing analysis at specific voxels defined by the user. For instance, let us suppose we are interested to see some of the output elements related to the FETS algorithm for an active voxel when using the LTT test.

```
R> #Identifying active voxels for a probability threshold of 0.99
R> active.voxels = which(res[[1]] > 0.99, arr.ind = TRUE)
R> head(active.voxels)

     dim1 dim2 dim3
[1,]   28   75   22
[2,]   22   71   24
[3,]   22   72   24
[4,]   23   72   24
[5,]   23   73   24
[6,]   24   73   24

R> N1 <- dim(covariables)[1]
R> res.indi <- SingleVoxelFEST(posi.ffd = c(14, 56, 40), covariates
+  = Covariates, ffdc =  fMRI.data, m0 = 0, Cova = 100, delta = 0.95, S0 = 1,
+  n0 = 1, Nsimu1 = 100, N1 = N1, Cutpos1 = 30, Min.vol = 0.10, r1 = 1,
+  Test = "LTT")
R> str(res.indi)

List of 4
$ Eviden      : num [1, 1:2] 0.98 0
$ Online_theta: num [1:280, 1:2, 1:100] 2.57 2.52 2.54 2.62 2.46 ...
$ Y_simu      : num [1:280, 1:100] 1.785 0.521 0.624 1.028 -0.165 ...
$ FitnessV    : num 0.762
```

The function `SingleVoxelFEST` requires just a few additional input arguments: the position of the voxel in the brain image (`posi.ffd`), the last period of time of the temporal series ($\mathbf{Y}_{[i,j,k]t=1} : \mathbf{Y}_{[i,j,k]t=N1}$) that are used in the analysis (`N1`) and `Min.vol`, which helps to define a threshold for the voxels that are considered in the analysis. For example, `Min.vol = 0.10` means that all the voxels with values below to `max(fMRI.data) * Min.vol` are discarted from the analysis. The output is a list containing the following elements: a vector with the evidence measure of activation for each one of the `p` covariates considered in the model (`Eviden`), the simulated online trajectories of $\Theta^{(z)}_{[i,j,k]t}$ (`Online_theta`), the simulated BOLD responses (`Y_simu`) and a measure to examine the goodnes of fit of the model ($100 * |\mathbf{Y}_{[i,j,k]t} - \hat{\mathbf{Y}}_{[i,j,k]t}|/\hat{\mathbf{Y}}_{[i,j,k]t}$) for that particular cluster of voxels (`FitnessV`).

```
R> res.indi2 <- singleVoxelFEST(posi.ffd = c(14, 56, 40),
+  covariates = covariates, ffdc =  fMRI.data, m0 = 0, Cova = 100,
+  delta = 0.95, S0 = 1,n0 = 1, Nsimu1 = 100, N1=N1, Cutpos1 = 30, Min.vol=0.10,
+  r1 = 1, Test = "JointTest")
R> str(res.indi2)

List of 5
$ EvidenMultivariate: num [1, 1:2] 0.81 0
$ EvidenMarginal    : num [1, 1:2] 0.98 0
$ Online_theta      : num [1:2, 1:280, 1:100] 2.38 -1.7 2.42 -1.77 2.35 ...
$ Y_simu            : num [1:100, 1:7, 1:280] 0.597 0.883 1.716 0.11 0.344 ...
$ FitnessV          : num 0.805$
```

When `Test = "JointTest"`, the function `IndividualVoxelFETS` returns two measures of voxel activation related to the Joint and Marginal effects along with the remaining list elements explained above.

```
R> res.indi3 <- SingleVoxelFFBS(posi.ffd = c(14, 56, 40), covariates = covariates,
+  ffdc = fMRI.data, m0 = 0, Cova = 100, delta = 0.95, S0 = 1, n0 = 1,
+  Nsimu1 = 100, N1 = N1, Cutpos1 = 30, Min.vol=0.10, r1 = 1)
R> str(res.indi3)

List of 5
 $ Eviden_joint     : num [1, 1:2] 0.94 0.03
 $ Eviden_margin    : num [1, 1:2] 1 0.08
 $ eviden_lt        : num [1, 1:2] 1 0.08
 $ Online_theta     : num [1:310, 1:2, 1:100] 0 0 0 0 0 0 0 0 0 0 ...
 $ Online_theta_mean: num [1:310, 1:2, 1:100] 0 0 0 0 0 0 0 0 0 0 ...$
```

For both functions `SingleVoxelFFBS` and `SingleVoxelFSTS` the input arguments and output estructures are exactly the same. Three measures of evidence related to the Joint effect, Marginal effect, and Average cluster effect are generated in the same run. There are also two additional elements related to the online simulated trajectories of the state parameter. `Online_theta` are the draws from the Marginal effect distribution and `Online_theta_mean` are the average on-line simulated trajectories obtained from the joint effect distribution.

```
R> frame()
R> plot.window(xlim=c(30, 311), ylim=c(-5, 5))
axis(1, at=seq(30, 310, by = 20), lwd = 2, xlab = "Time")
R> box(lwd = 2)
R> for(i in 1:dim(res.indi$Y_simu)[2]){lines(31:dim(covariates)[1],
+ res.indi$Y_simu[, i])}
R> lines(31:dim(covariates)[1], covariates[31:dim(covariates)[1], 1],
+ col = "red", lwd = 2)

R> frame()
R> plot.window(xlim=c(30, 311), ylim=c(-0.5, 4.5), ylab = expression(theta))
R> axis(1, at=seq(30, 310, by = 20), lwd = 2, xlab = "Time")
R> axis(2, at=-1:4, lwd=2)
R> box(lwd = 2)
R> for(i in 1:dim(res.indi$Online_theta)[2]){lines(31:dim(covariates)[1],
+ res.indi$Online_theta[, i])}
R> abline(h = 0, col = "red" , lwd = 2)
```

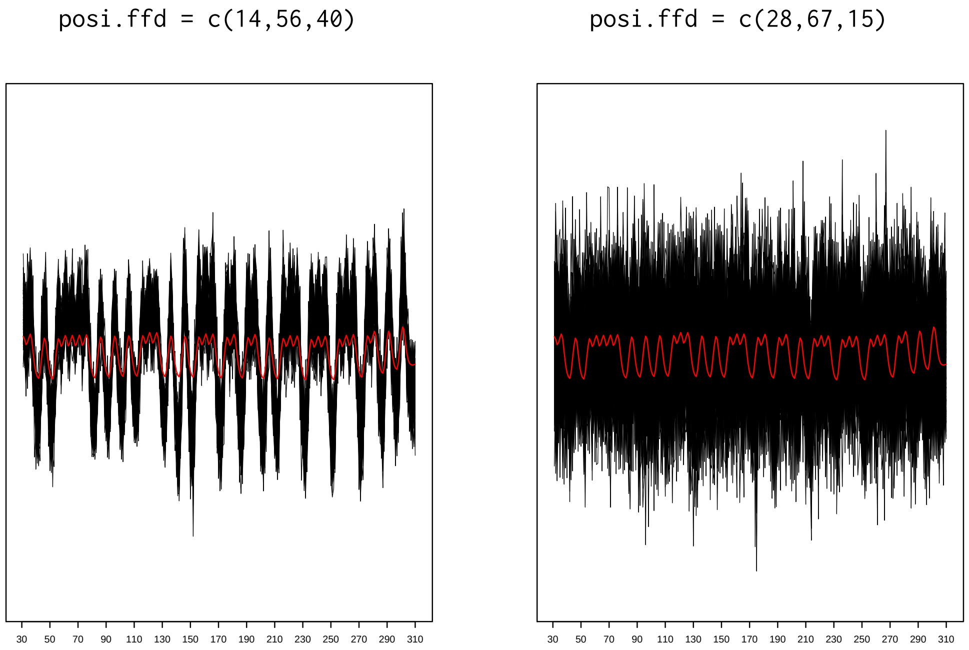


Figure 4: Simulated Bold response (black lines) and expected Bold response (red line) for an active (left) and non-active (right) voxel respectively.

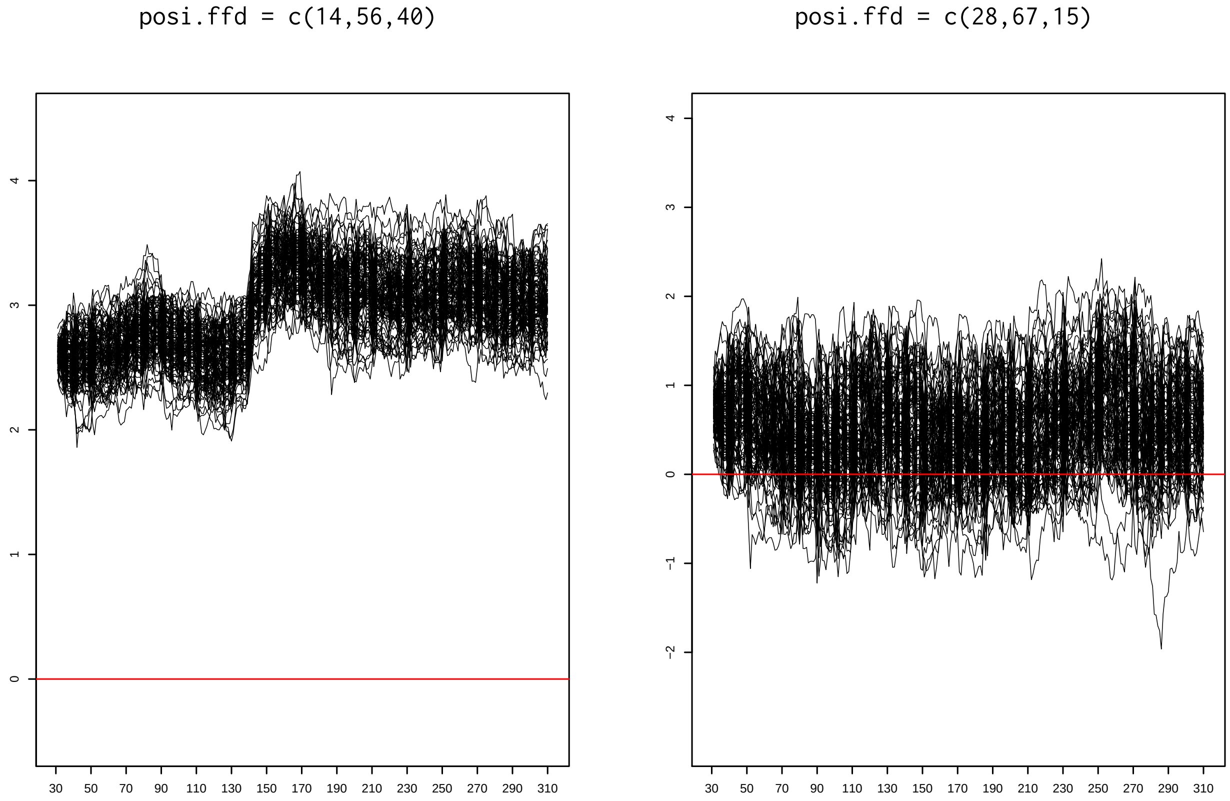


Figure 5: Simulated online trajectories of the state parameter for an active (left) and nonactive (right) volxel respectively.

Group analysis

Now we illustrate how to run an fMRI group analysis as described in Cardona-Jiménez and Pereira [2021]. In this first version of the **BayesDLMfMRI** package, we implement functions to detect brain activation for single groups. The comparison analysis between groups is under development and will be offered in future versions of the package. First, we read the fMRI images of 21 subjects taken from the "voice-localizer" example:

```
R> names <- list.files("~/fMRIData/")
R> names

 [1] "sub-001.nii.gz" "sub-002.nii.gz" "sub-003.nii.gz"
 [4] "sub-004.nii.gz" "sub-005.nii.gz" "sub-006.nii.gz"
 [7] "sub-007.nii.gz" "sub-008.nii.gz" "sub-009.nii.gz"
[10] "sub-010.nii.gz" "sub-011.nii.gz" "sub-012.nii.gz"
[13] "sub-013.nii.gz" "sub-014.nii.gz" "sub-015.nii.gz"
[16] "sub-016.nii.gz" "sub-017.nii.gz" "sub-018.nii.gz"
[19] "sub-019.nii.gz" "sub-020.nii.gz" "sub-021.nii.gz"

R> DataGroups <- function(x){
+   ffd.c2 <- readNIfTI(paste("~/fMRIParietal/",x, sep=""), reorient = FALSE)
+   ffd.c <- ffd.c2@.Data
+   return(ffd.c)
+ }
```

```
R> system.time(DatabaseGroup <- parLapply(names, DataGroups, cl = 7))
   user  system elapsed
637.016 923.008 400.528
R> str(DatabaseGroup)

List of 21
 $ : num [1:91, 1:109, 1:91, 1:310] 0 0 0 0 0 0 0 0 0 0 ...
 $ : num [1:91, 1:109, 1:91, 1:310] 0 0 0 0 0 0 0 0 0 0 ...
 $ : num [1:91, 1:109, 1:91, 1:310] 0 0 0 0 0 0 0 0 0 0 ...
 $ : num [1:91, 1:109, 1:91, 1:310] 0 0 0 0 0 0 0 0 0 0 ...
 $ : num [1:91, 1:109, 1:91, 1:310] 0 0 0 0 0 0 0 0 0 0 ...
 $ : num [1:91, 1:109, 1:91, 1:310] 0 0 0 0 0 0 0 0 0 0 ...
 $ : num [1:91, 1:109, 1:91, 1:310] 0 0 0 0 0 0 0 0 0 0 ...
 $ : num [1:91, 1:109, 1:91, 1:310] 0 0 0 0 0 0 0 0 0 0 ...
```

In order to run any of the functions available in this package to perform fMRI group analysis, the data sets or sets of images from each subject must be stored on a list object as it is shown above. To deal with this massive amount of information, the user must have a big RAM capacity available on the machine where this process will be run. It is also recommended to have a multi-core processor available in order to speed up computation time. The arguments or input parameters for any functions offered in this package to run group analysis are almost identical to those required for individual analysis. There is only an additional argument needed (`mask`), which adds a 3D array that works as a brain of reference (MNI atlas) for the group analysis.

```
R> MASK <- readNIfTI(”~/mask.nii.gz”)

R> res <- ffdGroupEvidenceFEST(ffdGroup = DatabaseGroup,
+ covariates = Covariates, m0 = 0, Cova = 100, delta = 0.95, S0 = 1,
+ n0 = 1, N1 = FALSE, Nsimu1 = 100, Cutpos=30, r1 = 1, Test = "Joint",
+ mask = MASK, Ncores = 7)

 |++++++++++++++++++++++++++++++++++++++++++++++++++| 100% elapsed = 53m 45s

R> str(res)

List of 4
 $ : num [1:91, 1:109, 1:91] 0 0 0 0 0 0 0 0 0 0 ...
 $ : num [1:91, 1:109, 1:91] 0 0 0 0 0 0 0 0 0 0 ...
 $ : num [1:91, 1:109, 1:91] 0 0 0 0 0 0 0 0 0 0 ...
 $ : num [1:91, 1:109, 1:91] 0 0 0 0 0 0 0 0 0 0 ...
```

`ffdGroupEvidenceFETS` returns an array of dimension $2 \times p$ elements, where p is the number of covariates and 2 is the number of options evaluated as sampler distributions: Average cluster effect and Marginal effect (when `Test=="LTT"`) or Joint effect and Marginal effect (when `Test=="JointTest"`). The first p elements from the list are the activation maps related to each column of the covariates matrix respectively when computing the activation evidence using either `Test=="LTT"` or `Test=="JointTest"`. The remaining activation maps are those associated with the marginal distribution.

```
R> res2 <- ffdGroupEvidenceFFBS(ffdGroup = DatabaseGroup, covariates = Covariates,
+ m0=0, Cova=100, delta = 0.95, S0 = 1, n0 = 1, N1 = FALSE, Nsimu1 = 100,
+ Cutpos = 30, r1 = 1, mask = MASK, Ncores = 7)

 |++++++++++++++++++++++++++++++++++++++++++++++++++| 100% elapsed = 44m 49s

R> str(res2)

List of 3
 $ : num [1:2, 1:91, 1:109, 1:91] 0 0 0 0 0 0 0 0 0 0 ...
 $ : num [1:2, 1:91, 1:109, 1:91] 0 0 0 0 0 0 0 0 0 0 ...
 $ : num [1:2, 1:91, 1:109, 1:91] 0 0 0 0 0 0 0 0 0 0$ ...
```

`ffdGroupEvidenceFFBS` returns an 3D array with the same structure and characteristics as its individual counterpart.

```
R> library(neurobase)
R> res.auxi <- res2[[1]][1,,,]
R> ffd <- readNIfTI(”standard.nii.gz”)
R> Z.visual.c <- nifti(res.auxi, datatype=16)
R> ortho2(ffd, ifelse(Z.visual.c > 0.95, Z.visual.c, NA),
+  col.y = heat.colors(50), ycolorbar = TRUE, ybreaks = seq(0.95, 1, by = 0.001))
```

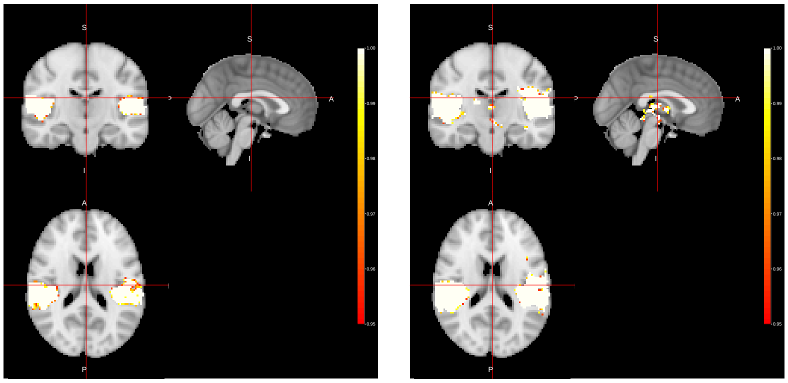
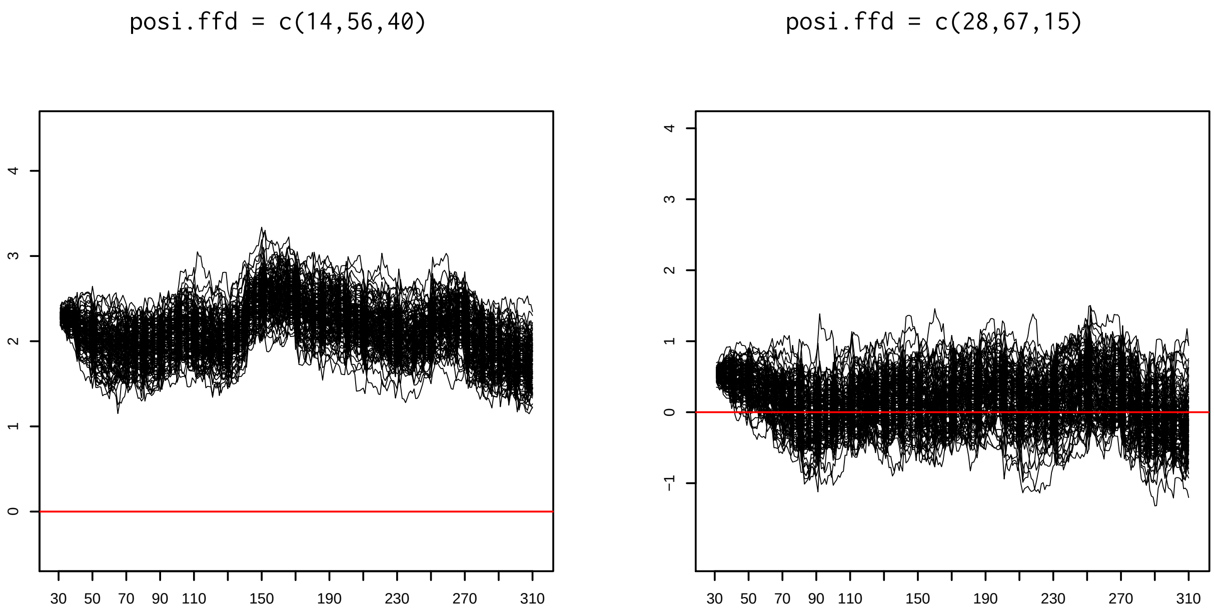


Figure 6: Activations maps obtained with the functions `ffdGroupEvidenceFEST` (left) and `ffdGroupEvidenceFFBS` (right) using the "Joint" as sampler distribution.

The functioning of the functions for single-voxel analysis at the group stage is the same as their counterparts at the individual stage.

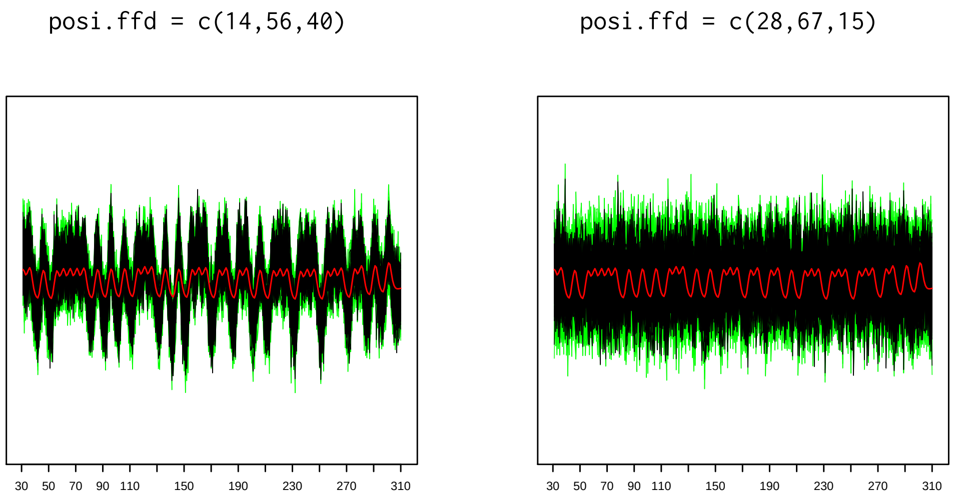
```
R> resSingle <- GroupSingleVoxelFEST(posi.ffd = c(14, 56, 40), DatabaseGroup,
+ covariates = Covariates, m0 = 0, Cova = 100, delta = 0.95, S0 = 1, n0 = 1,
+ N1 = FALSE, Nsimu1 = 100, r1 = 1, Test = ”Joint”, Cutpos = 30)
```

```
R> frame()
R> plot.window(xlim=c(30, 311), ylim = c(-5, 5))
axis(1, at=seq(30, 310, by = 20), lwd = 2, xlab = ”Time”)
R> box(lwd = 2)
R> for(j in 2:7){for(i in 1:dim(resSingle[[4]])[1]){lines(31:dim(covariates)[1],
+ resSingle[[4]][i, j,], col = ”green”)}}
R> for(i in 1:dim(resSingle[[4]])[1]){lines(31:dim(covariates)[1],
+ resSingle[[4]][i, 1,], col = ”black”)}
lines(31:dim(covariates)[1], covariates[31:dim(covariates)[1], 1],
+ col = ”red”, lwd = 2)
```


posi.ffd = c(14,56,40)

posi.ffd = c(28,67,15)

Figure 7: Simulated online trajectories of the state parameter for active (left) and nonactive (right) voxels, respectively.


posi.ffd = c(14,56,40)

posi.ffd = c(28,67,15)

Figure 8: The black curves are simulated BOLD responses for voxel at position `posi.ffd` and the green curves are the BOLD responses related to its neighbors. The red curve is the expected BOLD response for the "voice localizer" experiment.

```
R> frame()
R> plot.window(xlim=c(30, 311), ylim=c(-0.5, 4.5), ylab = expression(theta))
R> axis(1, at=seq(30, 310, by = 20), lwd = 2, xlab = "Time")
```

```
R> axis(2, at=-1:4, lwd=2)
R> box(lwd = 2)
R> for(i in 1:dim(resSingle[[3]])[3]){lines(31:dim(covariates)[1],
resSingle[[3]][1, , i])}
R> abline(h = 0, col = "red" , lwd = 2)
```

4 Conclusions and future work

In this work, we present the **BayesDLMfMRI** package, which allows performing statistical analysis for task-based fMRI data at individual and group stages. It offers different options to assess brain activation for single voxels as well as the entire brain. The low-level functions are written in C++, and options for parallel computation are available in some of the functions. Currently, some extensions for this package related to comparisons between groups and comparisons between tasks, as well as other relevant features, are being developed and will be implemented in future versions of the package.

Computational details

The results in this paper were obtained using **R** 3.4.4 with the **Rcpp** 1.0.2, **RcppArmadillo** 0.9.200.5.0 and **pbapply** 1.4.2 packages on a computer with Linux-Ubuntu, 32 CPUs and 188GB of RAM. **R** itself and all packages used are available from the Comprehensive **R** Archive Network (CRAN) at https://CRAN.R-project.org/.

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