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Date: 31-01-2020

#README

This document gives some additional information on two scripts that are part of:

***Perivascular fibroblasts contribute to sporadic ALS neurodegeneration***

Scripts:

**Cutpoint\_Analyses\_Publ.R**

Performs the cut-point analyses of figure 3A, B and C.

**CoxOutput.R**

Produces Cox models of figure 3D.

Both scripts can be used after loading the data object into Rs global environment.

Data object:

**Combined\_Cohort\_Dataframes.RData**

Includes two dataframes:

**cohorts**

Consists of protein readouts from all three cohorts (Leuven, Ulm and Utrecht) and necessary patient information, including controls.

**combinedALS**

Same data excluding controls and including sampling delay information.

Column names that might be unclear are:

**Survobj**

Data created by Surv() function from the survival package. It includes both survival time and if the particular patient is censored. In case of the latter, the cell will include a + symbol.

**RawB.53, RawB.123 and RawB.193**

These are the log normalized MFI values where;

* 53 is SPP1
* 123 is COL6A1
* 193 NEFL

**gap** (only in the combinedALS dataframe)

* Gap time between onset and taking the sample. Determined by looking at sampling age and age of onset. It is used to correct for sampling delay in the Cox models.

For explanations of the methods used see ‘Materials and Methods’ section of the paper. All analyses were done with R in Rstudio.