The Matlab code in this folder aims to analysis pairs of experiments with regards to changes in

- spike rates
- spiking variability
- spiking co-variability between single and multiunit activity
- spike waveform
- tuning
- response dynamics

Before you start, update your Matlab version to MatlabR2017a or later. Next create a folder where you can clone https://github.com/Corinna504/SpkAlys5HT_Code into.

Consider initExinfo.m and runExinfoAnalysis.m and adapt the directories added to the matlab path accordingly. For me this was

```
addpath(genpath(pwd)); % all subfolders within this path
addpath(genpath('Z:\Corinna\SharedCode\File Exchange Code'));
addpath(genpath('C:\Users\Corinna\Documents\CODE\GenAlyz_Code')
```

Code that was not written by me is saved on the network and need to be added. The more generic files that I wrote can be cloned from https://github.com/Corinna504/GenAlyz_Code – the files are needed for fitting and plotting functions.

To start, call

```
exinfo =runExinfoAnalysis('all', 'plot');
```

It initializes and fills the result structure while plotting and saving the analytical results as figures in a folder called *Figures.* This folder is created in the parent folder.

The rationale of the program architecture that creates the result structure `exinfo.mat` is as follows:

1. Generate a text file with the full names of all considered ex files. Always use pairs of experiment where the baseline is followed by the drug experiment. Your document should then look like this:

   Z:\data\mango\0014\ma_0014_c1_sortLH_5.30PM.grating.ORxM.mat
   Z:\data\mango\0014\ma_0014_c1_sortLH_5.34PM.grating.ORxM_5HT.mat
   Z:\data\mango\0014\ma_0014_c1_sortLH_5.44PM.grating.ORxRC.mat
   Z:\data\mango\0014\ma_0014_c1_sortLH_5.37PM.grating.ORxRC_5HT.mat
   Z:\data\mango\0015\ma_0015_c1_sortHN_5.30PM.grating.ORxM.mat
   Z:\data\mango\0015\ma_0015_c1_sortHN_5.24PM.grating.ORxM_5HT.mat

   I colored pairs of experiments to emphasize the order and the fact that pairs of experiments are compared. Use files2txt.m to generate this document but be aware that it sorts the input alphabetically. This causes problems for concatenated files with *all.grating* ending or files where the drug experiment preceded the baseline experiment.

If you want to analyze a particular list of experiments, give the filename as argument to either runExinfoAnalysis(…, 'fname', xx) or to initExinfo('fname', xx). Otherwise it will use

```
Z:\Corinna\filenames\SU110716_CL_all.txt
```

2. To create the target result structure exinfo.mat, call
   exinfo =runExinfoAnalysis('all')

   Output argument:

exinfo	the result structure. Each row in the structure represents a pair of a baseline and a drug experiment and contains the results of their spiking analyses and some non-analytical information such as identifiers and figure names.

   Input arguments:

'plot'	enables plotting functions
'save'	enables the saving of the output at the end of the function in the Data folder in the parent directory
'row_i_strt', val	starts the for-loop at the exinfo row val
'exinfo', resultstruct	uses the input result structure and skips initExinfo().
…	all arguments that are earmarked for sub-functions or functions called in the batch file, e.g. 'fname', name for initExinfo('fname', name).

   The target structure contains following fields

Field	**Origin**	**Comment**
exinfo.id	initExinfo	unit ID. Kaki is ID+0.5
exinfo.idi	initExinfo	experiment ID, self-initiated.
exinfo.monkey	initExinfo	Animal name, either 'mango' or 'kaki'
exinfo.fname / .fname_drug	initExinfo	Filenames of the baseline and drug experiment's ex files.
exinfo.data / .date_drug	initExinfo	Recording date stamp of the baseline and drug experiment.
Exinfo.ocul	initExinfo	Ocular experiment condition, one of {-1,0, 1}.
Exinfo.dose	initExinfo getDose	Applied drug dose in nA.

Exinfo.dosernd	initExinfo getDose	Binned drug dose.
Exinfo.volt	initExinfo getVolt	Recorded voltage.
Exinfo.resistance	initExinfo	Volt/dose
Exinfo.param1	initExinfo	The main stimulus type varied in the experiment (or, co, sz, sf)
Exinfo.param2	initExinfo	The second stimulus type varied in the experiment (mostly me or co)
Exinfo.ismango	initExinfo	Boolean value reflecting ´whether the experiment was performed with mango
Exinfo.ed	initExinfo	Electrode depth
Exinfo.expduration / .expduration_drug	initExinfo	Experiment duration
Exinfo.is5HT	initExinfo	Boolean value. True if 5HT was applied (compared to NaCl application).
exinfo.isadapt	initExinfo	Boolean value. True if it was an experiment with adaptation.
Exinfo.isRC	initExinfo	Boolean value. True if it was an experiment with flashed gratings.
Exinfo.isc2	initExinfo	Boolean value. True if the 2nd spike cluster was analyzed.
Exinfo.gridX /. gridY	initExinfo	Electrode position. The information is not yet correct bc the correct information is in the google spreadsheet and not in the ex files.
Exinfo.x0 / .y0	initExinfo	The stimulus position in 2D.
Exinfo.ecc	initExinfo	eccentricity
Exinfo.RFwx / . RFwy / .RFw / . RFw_corr	runExinfoAnalysis setReceptiveFieldWidth	Receptive field width estimated based on the XPos and YPos experiments. Raw (RFwx / . RFwy), average (.RFw) and eccentricity corrected (.RFw_corr)
Exinfo.tf	initExinfo	The temporal frequency of the stimulus.
Eixnfo.stimdur	initExinfo	Stimulus duration of

		flashed stimuli
Exinfo.cluster	initExinfo	The specific spike cluster
Figure names are set in initExinfo.mat		
Exinfo.fig_regl	runExinfoAnalysis evalBothEx type2reg	Figure for the type-II regression plot
Exinfo.fig_raster	runExinfoAnalysis rasterPlot	raster plot
Exinfo.fig_waveform	runExinfoAnalysis evalBothEx waveWidth	plot of the average spike waveform
Exinfo.fig_sdfs	runExinfoAnalysis rcPlot(exinfo);	figure showing the spike density function
Exinfo.fig_bri	runExinfoAnalysis getISI_All	filename for the bursting analysis
Exinfo.gslope / .yoff / .yoff_rel / .r2reg	runExinfoAnalysis evalBothExinfo type2reg	type-II regression slope, offset, normalized offset, and fit quality
Exinfo.nonparam_ratio	runExinfoAnalysis evalBothExinfo	mean firing rate in the drug experiment relative to the mean firing rate in the baseline experiment
Exinfo.lat Exinfo.lat_drug	runExinfoAnalysis evalSingleEx evalSingleDG HN_computeLatencyAndNetSpk CL_newLatency	ML estimate of the response latency
Exinfo.lat2Hmax exinfo.lat2Hmax_drug Exinfo.dur exinfo.dur_drug	runExinfoAnalysis evalSingleEx evalSingleDG HN_computeLatencyAndNetSpk CL_newLatency	Latency estimate as the time of half-maximal deviation across SDFs and response duration based on the same logic.
Exinfo.fitparam Exinfo.fitparam	runExinfoAnalysis evalSingleEx evalSingleDG/evalSingleRC	Results of the tuning fits including parameters of the best fit and the fitting quality
Exinfo.tcdiff / .tcdiff_drug	runExinfoAnalysis evalSingleEx evalSingleDG	Tuning height (max - min) / mean([max, min])
Exinfo.ff exinfo.ff_drug	runExinfoAnalysis evalSingleEx evalSingleDG/FF FanoFactors	Result structure for fano factor analysis

Exinfo.pfi / .pfi_drug / .upfi / .upfi_drug	runExinfoAnalysis evalBothEx	Index of the preferred and unpreferred stimulus estimated by the average response
Exinfo.tf_f1f0	runExinfoAnalysis	Phase selectivity computed based on the TF experiments
Exinfo.phasesel / .phasesel_drug	runExinfoAnalysis phasePlot	Phase selectivity based on the baseline and drug experiment
Exinfo.p_anova Exinfo.p_anova_drug	runExinfoAnalysis evalSingleEx evalSingleDG	ANOVA p-value to test for significant tuning
Exinfo.electrodebroken	initExinfo	boolean value. true if the electrode was broken
Exinfo.electrodebroken_excl	initExinfo	boolean value. true if the electrode was broken and should be excluded from the analysis
Exinfo.electrodebroken_incl_underrest	initExinfo	boolean value. true if the electrode was broken but should be included to the analysis
Exinfo.psth Exinfo.psth_drug	TODO	cell containing the smoothed PSTH
Exinfo.wdt	runExinfoAnalysis evalBothEx waveWidth	Width of the averaged spike waveform
Exinfo.rsc Exinfo.rsc_drug Exinfo.prsc Exinfo.prsc_drug	runExinfoAnalysis evalSingleEx evalSingleDG	Pearson's correlation between single and multiunit activity and corresponding p-values
Exinfo.rsig Exinfo.rsig_drug Exinfo.prsig Exinfo.prsig_drug	runExinfoAnalysis evalSingleEx evalSingleDG	Pearson's correlation between single and multiunit tuning and corresponding p-values
Exinfo.rsc_2nd Exinfo.rsc_2nd_drug Exinfo.prsc_2nd Exinfo.prsc_2nd_drug	runExinfoAnalysis evalSingleEx evalSingleDG	Same but base on the 2nd half of the experiments only
Exinfo.rsig_2nd Exinfo.rsig_2nd_drug Exinfo.prsig_2nd Exinfo.prsig_2nd_drug	runExinfoAnalysis evalSingleEx evalSingleDG	Same but base on the 2nd half of the experiments only
Exinfo.c0rate Exinfo.c0rate_drug	runExinfoAnalysis evalSingleEx	Raw tuning of cluster 0

	evalSingleDG	
Exinfo.spkqual exinfo.spkqual_drug	runExinfoAnalysis addSortingValue(exinfo)	spike sorting quality, derived from the google spreadsheet
Exinfo.dn_id	runExinfoAnalysis addNumInExp	number of preceding drug experiments within the unit recording
Exinfo.dt_id		Absolute time since the first drug application while recording from this unit
Exinfo.dt_cum_id		cumulated time of drug application before this experiment within the unit recording
Exinfo.dn_session Exinfo.dt_cum_session		Same but within recording sessions
Exinfo.valid	runExinfoAnalysis getValidField	experiments with the best type-II regression fit within a stimulus dimension of a unit this was the first inclusion criteria for the population analysis, therefore it was given this name.
Exinfo.expstrt	initExinfo	time stamp of the first trial start
Exinfo.ret2base	TODO	Boolean value. true if this baseline experiment recovered from the effect of preceding drug application
Exinfo.ratemn Exinfo.ratemn_drug	runExinfoAnalysis evalSingelEx evalSingleDG/znormex evalSingleRC/RCsubspace/..	The average stimulus evoked spike rate, i.e. the raw tuning curve for the baseline and drug experiment
Exinfo.ratevars Exinfo.ratevars_drug Exinfo.ratesd Exinfo.ratesd_drug Exinfo.ratesme Exinfo.ratesme_drug		Variance, standard deviation and standard error of the mean.
Exinfo.ratepar Eixnfo.ratepar_drug		The corresponding stimulus parameter values.
Exinfo.nrep Exinfo.nrep_drug		The corresponding number of stimulus repeats
Exinfo.rawspkrates Exinfo.rawspkrates_drug		The raw spike rates grouped for stimulus
Exinfo.rate_resmpl		The resampled spike rates

Exinfo.rate_resmpl_drug		
Exinfo.reg_slope Exinfo.reg_off	TODO	result of the latency control analysis using subsampling. Slope and offset of the regression fit Latency ~ Noise (Baseline SD in SDFs)
Exinfo.noise Eixnfo.noise_drug		noise (SD) across SDFs, RC experiments only
Exinfo.lat_c Exinfo.lat_c_drug		noise corrected latency estimate, RC experiments only
Exinfo.predicted_lat_change		predicted latency change based on the change in baseline noise
Exinfo.fig_latjackknife		figure of the latency control analysis – subsampling baseline experiment to increase the variability and test for latency changes
Exinfo.isdominant	runExinfoAnalysis	Boolean value. If true, this is the result for data shown to the dominant eye.