### A Head-Related Transfer Function Database Consolidation Tool For High Variance Machine Learning Algorithms



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### Motivation

- Building a large HRTF database for binaural based machine learning applications can be time-consuming and tedious.
- An alternative method is to combine the data from different existing databases to create a large training dataset.
- Due to the large difference in measurement angles, filter size, normalisation schemes and sample rates inherent in different databases, this is a significant challenge.
- Training of some machine learning algorithms may require significant trial and error with different data and settings.

This paper presents a Matlab based tool that allows researchers to prepare and consolidate various HRTF datasets across different databases in a robust and fast manner.

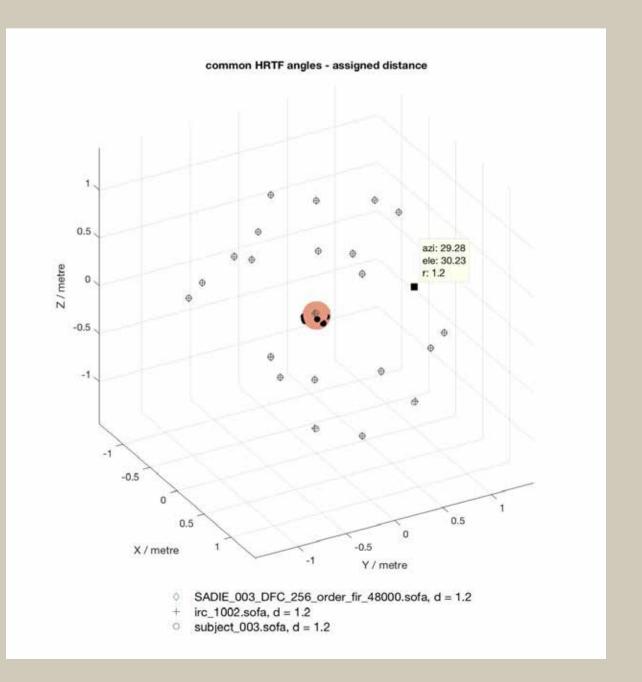
#### Pipeline preprocess\_SOFA group\_and\_fix\_SOFA - input\_files check\_hrtf - angle range **Group good SOFA files** - dist\_range **Check input SOFA files** into a new folder named - output\_dir and compare the files good\_SOFA and let user decide whether to keep from the same folder **Optional:** to find odd files. the bad ones or not. - plot\_trig (may need modification) - target length - target\_fs - target\_amplitude find\_represent\_SOFA common\_angle Group the files that have similar Find common angles between angular distribution and pick the represented SOFA files. one as representative. (remove file or adjust range if (To speed up the angle matching no match was found) process in the next step) Output normalise\_hrir find\_norm\_attributes **Processed SOFA files with Normalise and save HRTFs** summary includes: Find the maximum HRIR to a new folder with a log - bad folder length and minimum samthat details file names, - bad sofa pling frequency as default angles and conditions. - unique sofa\_table normalisation attributes. (any modification) - matching result - output\_file\_log

# Extra Tool: Plot Measurement Angles

Plot HRTF measurement points with maximum flexibility.

- Accepts different input types
- Plot different measurements on the same plot with different colours and markers

This helps comparing the differences between different angular distribution.



### **Function Highlights**

#### **Find and Fix Abnormal Files**

Find and fix abnormal files inside the folder or abnormal measurements in SOFA files before further processing.

#### Such as:

- Missing measurements
- Asymmetric angular distributions
- Singular measurements that are taken at a different distance due to measurement constraints

### Angle matching

The common angles between HRTF databases can be few and far between.

This function uses a hybrid method to find common measurement angles:

- Between multiple HRTF datasets
- Within a given orthodromic (global) distance
- In a relatively short amount of time

#### **Normalisation**

Other attributes may vary between different databases besides measurement angle, including sample rate, mean magnitude and HRIR length.

The built-in normalisation method handles the process in the frequency domain, to make sure the HRTF frequency response will not be affected by the normalisation.

## **Future Development**

- Graphical user interface,
- Visual-based HRTF/database selection control
- Options to readjust attributes during processing
- Anthropromorphic data selection
- HRIR interpolation schemes

