

# Rigid body analysis

We use this term for the process of factoring out head movement from speech movement data (and mapping the data to a new coordinate system), because it essentially involves determining the six mechanical degrees of freedom of a rigid body, i.e in this case the head.<sup>1</sup>

See the wrapper script `do_rigidbodyana`. for more details on how to proceed, and see the help text of `rigidbodyana.m` for more background.

By far the most important decision to make before running `do_rigidbodyana` is to choose the reference sensors to use. In particular, refer back to statistics or figures made with `do_do_compos` that show the stability of the euclidean distance between pairs of reference sensors.

## Notes on output of `rigidbodyana`

The main output is in the mat files whose name is defined by input argument `outpath`. These files contains the movement data with head movement factored out, and expressed in the coordinate system defined by the reference object.

Important note: Sensor orientation is now expressed by the x/y/z coordinates of the unit vector, not as aximuth and elevation. In addition to sensor position and orientation the datasets also contain rms and a parameter now referred to as 'compdist'. The latter is the distance between the two solutions compared with `euclidist2pos` (usually the final tapad and kalman solution). The second dimension of the 'data' variable is accordingly arranged thus (these are the designations used in the 'descriptor' and 'dimension' variables):  
`posx, posy, posz, orix, oriy, oriz, rms, compdist`

Additional datasets (i.e one file per trial) are also created with (usually) 'headrig' appended to the main part of the file name. These contain the time series of the six rigid body parameters of head movement (3 translations, 3 rotations) plus the so-called 'average taxonomic distance' ('taxdist' for short). This gives the average amount of distortion (in mm) when mapping the positions of the reference sensors in the actual movement data to their positions in the reference object.

At the end of processing `rigidbodyana` shows 8 figures, summarizing the processing over the trials. The statistics on which these figures are based are also stored in a mat file (with '\_stats' as the last part of the filename) in the same subdirectory as the other output files. However, for documentation purposes it is probably easier just to store any figures showing interesting/unusual features in the session with matlab's 'saveas' or 'print' command.

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<sup>1</sup>The functions used here for the basic procedure of reference object definition plus rigid body analysis could be applied to other objects. For speech, this means in particular the jaw, i.e the six degrees of freedom of jaw movement could be extracted if sufficient sensors are located on the jaw.

## Basic information on each figure

### 1. Total missing data

This refers to the input data. Normally, one should already know where any missing data occurs. This is just as a cross-check

### 2. Average taxonomic distance per trial

This should be as small as possible (ideally below 1mm), or failing this as stable as possible over trials.

If the values appear overall very high, one could try rigidbodyana with a different selection of reference sensors (or even a different reference object, if available)

Unusually high values for single trials could indicate that the subject did something unusual (e.g large body movement). The speech movement data in such trials may be less reliable.

### 3. SD of average taxonomic distance

The standard deviation. Should also be as small as possible (below 0.5mm?). Again, check for individual trials with unusually high values.

### 4. Reference object registration. Total missing samples per trial

Registration (i.e determining the mapping of the reference sensors in the movement data to their position in the reference object) may fail in very unusual cases. In addition, registration is not possible if there is missing data in any of the chosen reference sensors. Since failure of the registration will result in turn in missing data for *all* sensors in the output, this is summarized here explicitly as a complement to figure 1.

### 5. Rigid body translation: Means per trial

This in effect gives the mean position of the head in each trial relative to the position of the head in the recording on which the reference object was based. There are no intrinsically bad values here, but if the translations are very large for the whole session (say more than a couple of centimetres) then it means that speaker had adopted a position of the head for the reference object recording that was untypical of the head position for the normal trials. This may in turn lead to relatively high values for the taxonomic distance. As always, it is also worth checking for isolated trials with unusual behaviour.

### 6. Rigid body translation: SDs per trial

High values here mean that the speaker is moving the head a lot during the trials. Again, the main point is to watch out for individual trials with unusual behaviour. Quite apart from technical difficulties in compensating accurately for large amounts of head movement, one can also ask whether a speaker necessarily articulates in the same way when sitting quietly versus when moving the head around a lot.

### 7. Rigid body rotation: Means per trial

Figures 7 and 8 are the rotational counterparts to the translations in figures 5 and 6.

Basically the same remarks apply.

The rotations are labelled 'rx', 'ry', and 'rz', standing for rotation about the x, y and z axis respectively.

Particularly for lab speech experiments where the speaker is reading prompts from a screen it would be unusual for the orientation of the head to differ by more than a couple of degrees

from that in the reference object recording, i.e 10deg for any of the angles is already quite a lot.

#### 8. Rigid body rotation: SDs per trial

As for translation, look out for high values of the standard deviation in individual trials.