
Diffusion Profile Realignment

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This is the documentation detailing the internal of ‘Reducing variability in along-tract analysis with diffusion profile realignment’, which is available at <https://github.com/samuelstjean/dpr>.

It is most easily understood by looking at the code of each function since it contains comments about design choices and usage.

You can find the original paper and full details of the algorithm as presented in

Samuel St-Jean, Maxime Chamberland, Max A. Viergever, Alexander Leemans, Reducing variability in along-tract analysis with diffusion profile realignment, NeuroImage, Volume 199, 2019, Pages 663–679
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Which you can grab an open access copy from [Neuroimage](#).

The datasets are also available at [zenodo](#).

You can find below the documentation for each modules.

1.1 Submodules

1.1.1 dpr.register

Module Contents

Functions

```
align_bundles(bundles[, percent, padding, order, eps,  
...])
```

```
resample_bundles_to_same(bundles[, num_points])
```

apply_shift(bundles, shifts[, order, padding])

<code>flip_fibers(bundles, coordinates[, padding, template])</code>	bundle - 2D array of M bundles with each metrics of size N as a column
---	--

```
truncate(bundles[, mode, trimval, axis])
```

```
filter_pairs(allpairs, mode)
```

`get_shift_from_fft(x, y[, normalize])`

```
get_ffts(bundles[, whiten, remove_baseline])
```

`crosscorr(ffta, fftb[, normalize])`

`extrapolate(x, y[, return_value])`

```
dpr.register.align_bundles(bundles, percent=15, padding=0.0, order=1, eps=1e-05, mode='full_template',
                           remove_outliers=True, remove_baseline=True, whiten=True, normalize=False,
                           return_shifts_matrix=False, rematch_outliers=True)
```

```
dpr.register.resample_bundles_to_same(bundles, num_points=None)
```

```
dpr.register.apply_shift(bundles, shifts, order=1, padding=np.nan)
```

`dpr.register.flip_fibers(bundles, coordinates, padding=np.nan, template=None)`

bundle - 2D array of M bundles with each metrics of size N as a column
coordinates - list of points of size whatever x 3
template - Use this streamline to set the coordinate system.

If not set, we use the first one from coordinates.

`dpr.register.truncate(bundles, mode='shortest', trimval=np.nan, axis=0)`

`dpr.register.filter_pairs(allpairs, mode)`

`dpr.register.get_shift_from_fft(x, y, normalize=False)`

`dpr.register.get_ffts(bundles, whiten=True, remove_baseline=True)`

`dpr.register.crosscorr(ffia, ffib, normalize=False)`

`dpr.register.extrapolate(x, y, return_value=False)`

1.1.2 dpr.utils

Module Contents

Functions

`read_per_line(fname[, maxlines])`

`strip_first_col(fname[, delimiter])`

`strip_header(filename[, columns, delimiter])`

`colorbar(mappable)`

`draw_fancy_graph(pval, coords1, coords2, ...[, ...])`

Attributes

`blue`

`green`

`dpr.utils.read_per_line(fname, maxlines=50000)`

`dpr.utils.strip_first_col(fname, delimiter=None)`

`dpr.utils.strip_header(filename, columns=0, delimiter=None)`

`dpr.utils.blue`

`dpr.utils.green`


```
dpr.utils.colorbar(mappable)
```

```
dpr.utils.draw_fancy_graph(pval, coords1, coords2, truncated_coords1, truncated_coords2, average1,  
                           average2, coord1_label='X', coord2_label='Y', pval_threshold=1.0,  
                           pval_cmap=plt.cm.hot, mean_fiber_cmap=green, bundle_cmap=blue,  
                           shadow_cmap='gray', title=None, draw_colorbar=True)
```


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