README:

QUANTIFICATION OF MULTIPLE RECEPTOR DISTRIBUTIONS FOR SELECTED AREAS

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Currently (December 19, 2017), this dataset comprises quantification of receptor densities (fmol/mg protein) of 15 different receptor binding cites for 14 receptors using autoradiography with the following tritiated ligands:

receptors	binding sites	filename label	radioligands
AMPA	glutamate	AMPA	[³H] AMPA
kainate	glutamate	kainate	[³H] Kainate
NMDA	glutamate	NMDA	[³H] MK-801
mGluR2/3	glutamate	mGluR2_3	[³H] LY 341 495
$GABA_A$	GABA	GABAA	[³H] muscimol
	benzodiazepine (BZ)	BZ	[³H] CGP 54626
$GABA_B$	GABA	GABAB	[³H] flumazenil
M_1	acetylcholine	M1	[³H] pirenzepine
M_2	acetylcholine	M2	[³H] oxotremorine-M
M_3	acetylcholine	M3	[³H] 4-DAMP
$\alpha_4\beta_2$	acetylcholine	alpha4beta2	[³H] epibatidine
α_1	noradrenaline	alpha1	[³H] prazosin
α_2	noradrenaline	alpha2	[³H] UK-14,304
5-HT_{1A}	serotonin	5-HT1A	[³H] 8-OH-DPAT
5-HT_2	serotonin	5-HT2	[³H] ketanserin
D_1	dopamine	D1	[³H] SCH23390

So far, the dataset consists of measurements that were performed postmortem in one or both hemispheres of seven adult humans (3 female, 4 male, between the age of 61-79 years) in six different brain areas. Information on all subjects (brain ID, gender, age, cause of death) and corresponding samples (sample ID, hemisphere) can be found in the corresponding metadata spreadsheet (metadata_subjects-samples.xlsx). The list of investigated brain areas currently comprises the following six cortical areas:

(filename) label	full name	functional association
hOc1	human occipital area one	primary visual cortex
4p	dorsal part of posterior precentral gyrus	primary motor cortex
44d	dorsal part of pars opercularis of inferior frontal gyurs	Broca's area (speech)
45	pars triangularis of inferior frontal gyrus	Broca's area (speech)
47	orbital area 47	multimodal
PFm	parietal area PF magnocellularis	multimodal

The semantic relation between these cortical areas to the areas of the JuBrain parcellation atlas is summarized in a corresponding metadata spreadsheet (metadata_brain-areas.xlsx).

The dataset provides access to the receptor density measurements in three ways: (I) density fingerprints, (II) laminar density profiles, and (III) color-coded autoradiography heatmap plots.

(I) The density fingerprints provide the mean density and standard deviation of each receptor in each brain area as average across four samples. Which samples were used to generate the density fingerprints can be found in the corresponding metadata spreadsheet (metadata_brainids_fingerprints.xlsx). The density fingerprints are available as values in fmol/mg protein (fingerprints_*version-date*.xlsx), and as polar plots (*area-label*_fingerprint.tif) with corresponding figure captions (*area-label*_fingerprint_caption.txt).

(II) For each cortical area (*area-label*_example_data/), the laminar density profiles show the course of the

density from the pial surface to the border between layer VI and the white matter for each receptor binding site, exemplary in one sample. Which sample was used for which receptor binding site in each cortical area can be found in the corresponding metadata spreadsheet (metadata_sampleIDs_example_profiles.xlsx). The example laminar density profiles are available as values in fmol/mg protein (*area-label*_pr_*receptor-label*.xlsx), and as profile plots (*area-label*_pr_*receptor-label*.tif) with corresponding figure captions (*area-label*_pr_*receptor-label*_caption.txt).

(III) The color-coded autoradiography heatmap plots (*area-label*_bm_*receptor-label*.tif) with the corresponding figure captions (*area-label*_bm_*receptor-label*_caption.txt) were generated for each receptor binding site in each cortical area. These heatmap plots display the laminar distribution for each receptor in an example cross section of cortical layers in one sample. Which sample was used for which receptor binding site in each cortical area can be found in the corresponding metadata spreadsheet (metadata_sampleIDs_example-autoradiographies.xlsx).

The corresponding file structure of this dataset is composed in the following way:

> README.pdf
> **data/**
> > fingerprints_*version-date*.xlsx
> > *area-label*_fingerprint.tif
> > *area-label*_fingerprint_caption.txt
> > **area-label*_example_data/**
> > > **profile_examples/**
> > > > *area-label*_pr_*receptor-label*.xlsx
> > > > *area-label*_pr_*receptor-label*.tif
> > > > *area-label*_pr_*receptor-label*_caption.txt
> > > **autoradiography_examples/**
> > > > *area-label*_bm_*receptor-label*.tif
> > > > *area-label*_bm_*receptor-label*_caption.txt
> **metadata/**
> > metadata_subjects-samples.xlsx
> > metadata_brain-areas.xlsx
> > metadata_sampleIDs_fingerprints.xlsx
> > metadata_sampleIDs_example-profiles.xlsx
> > metadata_sampleIDs_example-autoradiographies.xlsx

Folders are marked in bold. A *version-date* in the filename indicates the latest date the corresponding file was updated. An *area-label* and/or a *receptor-label* in the filename indicate that the corresponding folder or file exists for each brain area and/or receptor binding site, respectively (cf. filename labels for receptors and areas above).

For further information on the methods about the provenance and processing of the data see:

Zilles, K.; Schleicher, A.; Palomero-Gallagher, N.; Amunts, K. (2002). **Quantitative analysis of cyto- and receptorarchitecture of the human brain**, chapter 21, pp. 573-602. In: Brain Mapping: The Methods, 2nd edition (A.W. Toga and J.C. Mazziotta, eds.). San Diego, Academic Press. ISBN: 0-12-693019-8

For further information on the provenance of the brains see:

Zilles, K.; Bacha-Trams, M.; Palomero-Gallagher, N.; Amunts, K.; Friederici, A.D. (2015) **Common molecular basis of the sentence comprehension network revealed by neurotransmitter receptor fingerprints.** Cortex, vol 63, pp. 79-89. https://doi.org/10.1016/j.cortex.2014.07.007