

Resource Summary Report

Generated by PRECISE-TBI on Sep 7, 2026

Hierarchical Unsupervised Generative Embedding toolbox

RRID:SCR_018754

Type: Tool

Proper Citation

Hierarchical Unsupervised Generative Embedding toolbox (RRID:SCR_018754)

Resource Information

URL: <https://github.com/translationalneuromodeling/tapas/tree/master/huge>

Proper Citation: Hierarchical Unsupervised Generative Embedding toolbox (RRID:SCR_018754)

Description: Software toolbox to implement hierarchical extension to dynamic causal models for analyzing task based fMRI data.

Abbreviations: HUGE

Synonyms: Hierarchical Unsupervised Generative Embedding, Hierarchical Unsupervised Generative Embedding Toolbox, Hierarchical Unsupervised Generative Embedding (HUGE) toolbox

Resource Type: data analysis software, data processing software, software application, software resource, software toolkit

Defining Citation: [PMID:29964187](https://pubmed.ncbi.nlm.nih.gov/29964187/)

Keywords: Hierarchical extension, dynamic casual model, fMRI, fMRI data, fMRI data analysis

Funding: Rene und Susanne Braginsky Foundation ;
Research Center Julich ;
Germany ;
University of Zurich

Availability: Open source

Resource Name: Hierarchical Unsupervised Generative Embedding toolbox

Resource ID: SCR_018754

License: GNU GPL

Record Creation Time: 20220129T080341+0000

Record Last Update: 20260905T132842+0000

Ratings and Alerts

No rating or validation information has been found for Hierarchical Unsupervised Generative Embedding toolbox.

No alerts have been found for Hierarchical Unsupervised Generative Embedding toolbox.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at [PRECISE-TBI](#) .

Souza EL, et al. (2024) Family Vulnerability Scale: validity evidence in primary health care. Revista de saude publica, 57Suppl 3(Suppl 3), 5s.

Feltman NR, et al. (2022) HUGE pipeline to measure temporal genetic variation in Drosophila suzukii populations for genetic biocontrol applications. Frontiers in insect science, 2, 981974.

Bogdanovic B, et al. (2021) Almost 10 years of PET/MR attenuation correction: the effect on lesion quantification with PSMA: clinical evaluation on 200 prostate cancer patients. European journal of nuclear medicine and molecular imaging, 48(2), 543.

Björkman A, et al. (2020) Human RTEL1 associates with Poldip3 to facilitate responses to replication stress and R-loop resolution. Genes & development, 34(15-16), 1065.