

Resource Summary Report

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Hierarchical Attribute Matching Mechanism for Elastic Registration

RRID:SCR_001960

Type: Tool

Proper Citation

Hierarchical Attribute Matching Mechanism for Elastic Registration (RRID:SCR_001960)

Resource Information

URL: <https://www.rad.upenn.edu/sbia/software/index.html#hammer>

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Description: Software package that performs high-dimensional warping of brain images. Standard voxel-based analysis can be applied to these tissue density maps, in order to examine regional volumetrics, effects of disease, or correlations with clinical measurements. In order to make HAMMER as robust as possible to different acquisition protocols and conditions, they provide a distribution that assumes that images have been skull-stripped and segmented into gray matter, white matter, and ventricular CSF. We have other software tools that can perform these steps, including skull stripping, reorientation and reslicing, and segmentation tools. Importantly, they use 250 for WM, 150 for GM, 50 for Ventricles and 10 for CSF in the tissue-segmented brain images. Current modules used for group analysis: Labeling subject brain using a manually-labeled brain Model; Generating RAVENS map for each tissue (WM, GM, VN); Normalizing subject brain images

Abbreviations: HAMMER

Synonyms: HAMMER: Deformable Registration

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

Defining Citation: [PMID:12575879](#), [PMID:12507441](#)

Keywords: magnetic resonance, software package, data processing, high dimensional warping

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Hierarchical Attribute Matching Mechanism for Elastic Registration

Resource ID: SCR_001960

Alternate IDs: nif-0000-00310

Alternate URLs: <http://www.nitrc.org/projects/hammerwml>

License: SBIA License

Record Creation Time: 20220129T080210+0000

Record Last Update: 20260808T190300+0000

Ratings and Alerts

No rating or validation information has been found for Hierarchical Attribute Matching Mechanism for Elastic Registration.

No alerts have been found for Hierarchical Attribute Matching Mechanism for Elastic Registration.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 50 mentions in open access literature.

Listed below are recent publications. The full list is available at [SPARC SAWG](#) .

Ye RZ, et al. (2025) A tombus-like virus in patients with lower respiratory tract infection: an observational study based on meta-transcriptomic sequencing. *Emerging microbes & infections*, 14(1), 2494704.

Yu M, et al. (2025) A systematic survey of type I secretion systems and their substrate proteins in *Salmonella*. *Virulence*, 16(1), 2533414.

Tang Y, et al. (2024) Multimodal diagnosis model of Alzheimer's disease based on improved Transformer. *Biomedical engineering online*, 23(1), 8.

Cheng T, et al. (2024) Genome-wide analysis of the common bean (*Phaseolus vulgaris*) laccase gene family and its functions in response to abiotic stress. *BMC plant biology*, 24(1), 688.

Sun J, et al. (2023) TMKit: a Python interface for computational analysis of transmembrane proteins. *Briefings in bioinformatics*, 24(5).

Shirasawa K, et al. (2023) Chromosome-scale genome assembly of *Eustoma grandiflorum*, the first complete genome sequence in the genus *Eustoma*. *G3 (Bethesda, Md.)*, 13(2).

Li Z, et al. (2023) Genome-wide analysis of the *Pleurotus eryngii* laccase gene (PeLac) family and functional identification of PeLac5. *AMB Express*, 13(1), 104.

Brouillet D, et al. (2023) The subjective feeling of a gap between conceptual and perceptual fluency is interpreted as a metacognitive signal of pastness. *Cognitive processing*, 24(1), 83.

Zhang LB, et al. (2023) Genome-wide study of *Cerrena unicolor* 87613 laccase gene family and their mode prediction in association with substrate oxidation. *BMC genomics*, 24(1), 504.

Henningsen-Schomers MR, et al. (2022) Modelling concrete and abstract concepts using brain-constrained deep neural networks. *Psychological research*, 86(8), 2533.

Shirasawa K, et al. (2022) De novo whole-genome assembly in an interspecific hybrid table grape, 'Shine Muscat'. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 29(6).

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Ryngaj??o M, et al. (2021) Complete genome sequence of lovastatin producer *Aspergillus terreus* ATCC 20542 and evaluation of genomic diversity among *A. terreus* strains. *Applied microbiology and biotechnology*, 105(4), 1615.

Shim YY, et al. (2021) Aquafaba from Korean Soybean I: A Functional Vegan Food Additive. *Foods (Basel, Switzerland)*, 10(10).

Nevárez-Rascón M, et al. (2020) Effectiveness of a microabrasion technique using 16% HCL with manual application on fluorotic teeth: A series of studies. *World journal of clinical cases*, 8(4), 743.

Zöllei L, et al. (2020) Infant FreeSurfer: An automated segmentation and surface extraction pipeline for T1-weighted neuroimaging data of infants 0-2 years. *NeuroImage*, 218, 116946.

McNorgan C, et al. (2020) Integrating functional connectivity and MVPA through a multiple constraint network analysis. *NeuroImage*, 208, 116412.

Ale Ebrahim S, et al. (2019) Publication Trends in Drug Delivery and Magnetic Nanoparticles. *Nanoscale research letters*, 14(1), 164.

He Y, et al. (2019) Chickpea Cultivar Selection to Produce Aquafaba with Superior Emulsion Properties. *Foods (Basel, Switzerland)*, 8(12).

Wang Q, et al. (2019) The Soybean Laccase Gene Family: Evolution and Possible Roles in Plant Defense and Stem Strength Selection. *Genes*, 10(9).