Resource Summary Report

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Semi-Manual Alignment to Reference Templates

RRID:SCR_019265
Type: Tool

Proper Citation

Semi-Manual Alignment to Reference Templates (RRID:SCR_019265)

Resource Information

URL: https://github.com/mjin1812/SMART

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Description: Software tool that extends WholeBrain framework in R for segmenting and registering experimental images to Allen Mouse Common Coordinate Framework (CCF). Streamlines processing of large volumetric LSFM datasets and solves issues with non-uniform morphing across anterior-posterior axis with interactive “choice game.” Accounts for duplicate cell counts in adjacent z images and presents new ways to easily parse apart and interactively visualize final mapped datasets.

Abbreviations: SMART

Resource Type: image analysis software, segmentation software, software resource, software application, data processing software

Defining Citation: DOI:10.1101/727529

Keywords: Segmenting experimental images, registering experimental images, Allen Mouse Common Coordinate Framework, data processing, experimental images

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Semi-Manual Alignment to Reference Templates

Resource ID: SCR_019265

Alternate URLs: https://mjin1812.github.io/SMART/installation.html

Record Creation Time: 20220129T080344+0000

Record Last Update: 20250522T061241+0000

Ratings and Alerts

No rating or validation information has been found for Semi-Manual Alignment to Reference Templates.

No alerts have been found for Semi-Manual Alignment to Reference Templates.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2818 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF.

Jafer M, et al. (2023) Using Intervention Mapping to Develop ISAC, a Comprehensive Intervention for Early Detection and Prevention of Oral Cancer in Saudi Arabia. Journal of cancer education : the official journal of the American Association for Cancer Education, 38(2), 505.

Park SH, et al. (2023) Glycogen Synthase Kinase-3 Isoform Variants and Their Inhibitory Phosphorylation in Human Testes and Spermatozoa. The world journal of men's health, 41(1), 215.

Wang S, et al. (2023) Host- and virus-induced gene silencing of HOG1-MAPK cascade genes in Rhizophagus irregularis inhibit arbuscule development and reduce resistance of plants to drought stress. Plant biotechnology journal, 21(4), 866.

Wang Y, et al. (2023) Identification of Alfalfa SPL gene family and expression analysis under biotic and abiotic stresses. Scientific reports, 13(1), 84.

Zou H, et al. (2023) Transcriptome profiling reveals the roles of pigment formation mechanisms in yellow Paeonia delavayi flowers. Molecular genetics and genomics : MGG, 298(2), 375.

Zhang Q, et al. (2023) TGF-?1 suppresses the T-cell response in teleost fish by initiating Smad3- and Foxp3-mediated transcriptional networks. The Journal of biological chemistry, 299(2), 102843.

Dundee JM, et al. (2023) P2Y6 receptor-dependent microglial phagocytosis of synapses mediates synaptic and memory loss in aging. Aging cell, 22(2), e13761.

Ma R, et al. (2023) KinasePhos 3.0: Redesign and Expansion of the Prediction on Kinase-specific Phosphorylation Sites. Genomics, proteomics & bioinformatics, 21(1), 228.

Qiu CW, et al. (2023) Genome resequencing and transcriptome profiling reveal molecular evidence of tolerance to water deficit in barley. Journal of advanced research, 49, 31.

Wolf C, et al. (2023) Motivation by reward jointly improves speed and accuracy, whereas task-relevance and meaningful images do not. Attention, perception & psychophysics, 85(3), 930.

Cheng K, et al. (2023) Genome-wide identification and characterization of polycomb repressive complex 2 core components in upland cotton (Gossypium hirsutum L.). BMC plant biology, 23(1), 66.

Olsen TR, et al. (2023) Scalable co-sequencing of RNA and DNA from individual nuclei. bioRxiv : the preprint server for biology.

Zhao H, et al. (2023) Genome-wide analysis of the CML gene family and its response to melatonin in common bean (Phaseolus vulgaris L.). Scientific reports, 13(1), 1196.

Zhang Y, et al. (2023) Genome-Wide Comparative Analysis of the Fasciclin-like Arabinogalactan Proteins (FLAs) in Salicacea and Identification of Secondary Tissue Development-Related Genes. International journal of molecular sciences, 24(2).

Cui H, et al. (2023) Genome-Wide Identification and Analysis of the Maize Serine Peptidase S8 Family Genes in Response to Drought at Seedling Stage. Plants (Basel, Switzerland), 12(2).

Mirhadi S, et al. (2023) Mitochondrial Aconitase ACO2 Links Iron Homeostasis with Tumorigenicity in Non-Small Cell Lung Cancer. Molecular cancer research : MCR, 21(1), 36.

Zhao Y, et al. (2023) Overexpression of chitinase PbChia1 from Plasmodiophora brassicae improves broad-spectrum disease resistance of Arabidopsis. Virulence, 14(1), 2233147.

Zhang R, et al. (2023) ADH Gene Cloning and Identification of Flooding-Responsive Genes in Taxodium distichum (L.) Rich. Plants (Basel, Switzerland), 12(3).

Stürzebecher PE, et al. (2023) [Treatment and LDL cholesterol adjustment in patients with high and very high cardiovascular risk in Germany compared with Europe - data from the SANTORINI registry]. Deutsche medizinische Wochenschrift (1946), 148(9), 55.

Saito-Takatsuji H, et al. (2023) Transthyretin Is Commonly Upregulated in the Hippocampus of Two Stress-Induced Depression Mouse Models. International journal of molecular sciences, 24(4).