Resource Summary Report

Generated by dkNET on May 8, 2025

maps

RRID:SCR_019296
Type: Tool

Proper Citation

maps (RRID:SCR_019296)

Resource Information

URL: https://CRAN.R-project.org/package=maps

Proper Citation: maps (RRID:SCR_019296)

Description: Software R package to draw geographical maps.

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

Keywords: Maps display, geographical maps drawing

Funding:

Availability: Free, Available for download, Freely available

Resource Name: maps

Resource ID: SCR_019296

License: GPL-2

Record Creation Time: 20220129T080344+0000

Record Last Update: 20250508T065926+0000

Ratings and Alerts

No rating or validation information has been found for maps.

No alerts have been found for maps.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Glemain B, et al. (2024) Estimating SARS-CoV-2 infection probabilities with serological data and a Bayesian mixture model. Scientific reports, 14(1), 9503.

Wright DJ, et al. (2024) An international estimate of the prevalence of differing visual imagery abilities. Frontiers in psychology, 15, 1454107.

Zhao D, et al. (2024) Members of the class Candidatus Ordosarchaeia imply an alternative evolutionary scenario from methanogens to haloarchaea. The ISME journal, 18(1).

Letcher B, et al. (2024) Role for gene conversion in the evolution of cell-surface antigens of the malaria parasite Plasmodium falciparum. PLoS biology, 22(3), e3002507.

Abhari N, et al. (2024) Measuring genetic diversity across populations. PLoS computational biology, 20(12), e1012651.

Saha I, et al. (2023) The AAA+ chaperone VCP disaggregates Tau fibrils and generates aggregate seeds in a cellular system. Nature communications, 14(1), 560.

Kusmec A, et al. (2023) A genetic tradeoff for tolerance to moderate and severe heat stress in US hybrid maize. PLoS genetics, 19(7), e1010799.

Tamaki I, et al. (2023) Phylogenetic, population structure, and population demographic analyses reveal that Vicia sepium in Japan is native and not introduced. Scientific reports, 13(1), 20746.

Chong F, et al. (2023) High concentrations of floating neustonic life in the plastic-rich North Pacific Garbage Patch. PLoS biology, 21(5), e3001646.

Wu D, et al. (2022) Dual genome-wide coding and lncRNA screens in neural induction of induced pluripotent stem cells. Cell genomics, 2(11).

Kreiling AK, et al. (2022) Invertebrate communities in springs across a gradient in thermal regimes. PloS one, 17(5), e0264501.

Lenton TM, et al. (2022) Resilience of countries to COVID-19 correlated with trust. Scientific reports, 12(1), 75.

Fukunaga K, et al. (2022) Recombinant inbred lines and next-generation sequencing enable

rapid identification of candidate genes involved in morphological and agronomic traits in foxtail millet. Scientific reports, 12(1), 218.

Parry R, et al. (2021) Uncovering the Worldwide Diversity and Evolution of the Virome of the Mosquitoes Aedes aegypti and Aedes albopictus. Microorganisms, 9(8).

, et al. (2021) From grassroots to global: A blueprint for building a reproducibility network. PLoS biology, 19(11), e3001461.

Wu H, et al. (2021) Identification of a novel interplay between intestinal bacteria and metabolites in Chinese patients with IgA nephropathy via integrated microbiome and metabolome approaches. Annals of translational medicine, 9(1), 32.

Spada A, et al. (2021) Structural equation modeling to shed light on the controversial role of climate on the spread of SARS-CoV-2. Scientific reports, 11(1), 8358.

Oorschot V, et al. (2021) TEM, SEM, and STEM-based immuno-CLEM workflows offer complementary advantages. Scientific reports, 11(1), 899.

Bi R, et al. (2021) Climate driven spatiotemporal variations in seabird bycatch hotspots and implications for seabird bycatch mitigation. Scientific reports, 11(1), 20704.

Ony M, et al. (2021) Genetic diversity in North American Cercis Canadensis reveals an ancient population bottleneck that originated after the last glacial maximum. Scientific reports, 11(1), 21803.