Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 12, 2025

Simple Features

RRID:SCR_023393
Type: Tool

Proper Citation

Simple Features (RRID:SCR_023393)

Resource Information

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

Proper Citation: Simple Features (RRID:SCR_023393)

Description: Software R package as set of standards that specify common storage and access model of geographic features made of mostly two dimensional geometries used by geographic information systems. Standardized way to encode spatial vector data. Formalized by Open Geospatial Consortium and International Organization for Standardization.

Abbreviations: sf

Synonyms: Simple Feature Access, simple features

Resource Type: software toolkit, software resource

Keywords: common storage, access model, geographic features, two dimensional geometries, geographic information systems

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Simple Features

Resource ID: SCR_023393

Alternate URLs: Also https://r-spatial.github.io/sf/, https://github.com/r-spatial/sf/

Record Creation Time: 20230321T180026+0000

Record Last Update: 20250412T060541+0000

Ratings and Alerts

No rating or validation information has been found for Simple Features.

No alerts have been found for Simple Features.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 7 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Delalay G, et al. (2025) The use of scenario tree models in support of animal health surveillance: A scoping review. Preventive veterinary medicine, 234, 106371.

De Los Santos MB, et al. (2024) Sampling is decisive to determination of Leishmania (Viannia) species. PLoS neglected tropical diseases, 18(4), e0012113.

Li C, et al. (2024) The microgeo: an R package rapidly displays the biogeography of soil microbial community traits on maps. FEMS microbiology ecology, 100(7).

Kaur V, et al. (2024) Leveraging genetic resource diversity and identification of trait-enriched superior genotypes for accelerated improvement in linseed (Linum usitatissimum L.). Scientific reports, 14(1), 20266.

Popkin-Hall ZR, et al. (2024) High-throughput genotyping of Plasmodium vivax in the Peruvian Amazon via molecular inversion probes. Nature communications, 15(1), 10219.

Olkkonen E, et al. (2023) Analysis of population structure and genetic diversity in low-variance Saimaa ringed seals using low-coverage whole-genome sequence data. STAR protocols, 4(4), 102567.

van Eijs MJM, et al. (2023) Highly multiplexed spatial analysis identifies tissue-resident memory T cells as drivers of ulcerative and immune checkpoint inhibitor colitis. iScience, 26(10), 107891.