

Resource Summary Report

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Simple Features

RRID:SCR_023393

Type: Tool

Proper Citation

Simple Features (RRID:SCR_023393)

Resource Information

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

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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 resource, software toolkit

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

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/>

License: GPLv2, MIT + file license

Record Creation Time: 20230321T180026+0000

Record Last Update: 20260821T194247+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 15 mentions in open access literature.

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

Lv H, et al. (2026) Shared historical refugia and genetic diversity hotspots of co-distributed species on the Qinghai Tibet plateau. *iScience*, 29(1), 114318.

Zambrano-Harvey AR, et al. (2026) Cancer incidence in the Pijao indigenous population of colombia using administrative health records, 1996-2022. *Scientific reports*, 16(1).

Tomasovic LM, et al. (2026) Mapping the Geographic Distribution of Lung Transplant Centers and Smoking-Associated Diseases Across the United States. *Transplantation proceedings*.

Veltman MA, et al. (2026) Molecular evidence reveals unsustainable harvest of wild orchids. *Current biology : CB*, 36(7), 1842.

Sanchez-Rendon JC, et al. (2025) Protocol for characterizing cell motility and extracellular signal-regulated kinase dynamics in epithelial monolayers using FRET imaging data. *STAR protocols*, 6(2), 103816.

Lin Y, et al. (2025) Global trends, health inequalities, and projections in the burden of neglected tropical diseases and malaria from 1990 to 2021. *Scientific reports*, 15(1), 20958.

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.

Ellis JR, et al. (2025) Sun-Exposed but Under-Treated: Mapping the Geospatial Imbalance of Dermatologists and Outdoor Laborers. *Photodermatology, photoimmunology & photomedicine*, 41(3), e70017.

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).

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

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.

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.

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_H17 cells as drivers of ulcerative and immune checkpoint inhibitor colitis. *iScience*, 26(10), 107891.

Andreeva TV, et al. (2022) Genomic analysis of a novel Neanderthal from Mezmaiskaya Cave provides insights into the genetic relationships of Middle Palaeolithic populations. *Scientific reports*, 12(1), 13016.