

Resource Summary Report

Generated by [NIF](#) on Sep 12, 2026

TeachingDemos

RRID:SCR_014689

Type: Tool

Proper Citation

TeachingDemos (RRID:SCR_014689)

Resource Information

URL: <https://imdevsoftware.wordpress.com/tutorials/>

Proper Citation: TeachingDemos (RRID:SCR_014689)

Description: A portal and resource for tutorials on a variety of data analysis techniques, the use of tools such as MetaMapR, workshops on data visualization, and R code manuals.

Resource Type: data or information resource, online course, portal, training resource

Availability: Freely available

Resource Name: TeachingDemos

Resource ID: SCR_014689

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260912T195820+0000

Ratings and Alerts

No rating or validation information has been found for TeachingDemos.

No alerts have been found for TeachingDemos.

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 [NIF](#) .

Tiezzi F, et al. (2025) Improvement of polygenic modeling of blood pressure traits using lifestyle information in the UK Biobank. *Genetics*, 230(3).

Wang W, et al. (2025) Identification of Potential Diagnostic Biomarkers and Drug Targets for Endometriosis from a Genetic Perspective: A Mendelian Randomization Study. *Gynecologic and obstetric investigation*, 90(5), 462.

Vajna F, et al. (2024) Contrasting Patterns of Plants, Bees, Hoverflies and Spiders in Different Habitats in a Central European Agricultural Landscape. *Ecology and evolution*, 14(12), e70711.

Peralvo-Vidal JM, et al. (2021) Association between gastric content fluidity and pars oesophageal ulcers in nursery pigs: a cross-sectional study of high-risk Danish herds using commercial feed. *Porcine health management*, 7(1), 19.

Innes BT, et al. (2018) scClustViz - Single-cell RNAseq cluster assessment and visualization. *F1000Research*, 7.

Rausch TK, et al. (2016) Comparison of pre-processing methods for multiplex bead-based immunoassays. *BMC genomics*, 17(1), 601.

Castro-Nallar E, et al. (2015) Concordance and discordance of sequence survey methods for molecular epidemiology. *PeerJ*, 3, e761.