

Resource Summary Report

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ipPCA

RRID:SCR_001262

Type: Tool

Proper Citation

ipPCA (RRID:SCR_001262)

Resource Information

URL: <https://cran.r-universe.dev/IPCAPS>

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Description: Software implementing a population structure analysis algorithm which assigns individuals to subpopulations and infers the total number of subpopulations present. Additional functions have been included that result in improved population assignment accuracy. # Universal genotype data encoding scheme which allows the population analysis of all types of genetic markers; Single Nucleotide Polymorphism (SNP), Short Tandem Repeat (STR) and RFLP. # New termination criterion called ?EigenDev? which is more robust to population sampling, thus provides the better estimation of number of assigned subpopulations (K) and higher accuracy for the analysis of large complex population datasets.

Abbreviations: ipPCA, i2pPCA

Synonyms: i2pPCA, Iterative pruning Principal Component Analysis

Resource Type: software resource

Defining Citation: [PMID:21699684](#), [PMID:19930644](#)

Keywords: principal component analysis, population, genetic marker, single nucleotide polymorphism, short tandem repeat, rflp

Availability: Free, Available for download, Freely available

Resource Name: ipPCA

Resource ID: SCR_001262

Alternate IDs: OMICS_02078

Alternate URLs: <http://www4a.biotech.or.th/GI/tools/ippca>

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260808T185739+0000

Ratings and Alerts

No rating or validation information has been found for ipPCA.

No alerts have been found for ipPCA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Songsungthong W, et al. (2017) The Plasmodium berghei RC strain is highly diverged and harbors putatively novel drug resistance variants. PeerJ, 5, e3766.