Release Notes: Omics Playground v3.5.0

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Table of contents

Overview			3				
1	Wha	at's new in OmicsPlayground v3.5.0	4				
	1.1	Full Proteomics Support	4				
	1.2	Extended species support	4				
	1.3	Automatic Reports	4				
	1.4	New modules/boards	4				
	1.5	Improved information on methods	4				
	1.6	Improved information on plot settings	4				
	1.7	Other new features	5				
2	Wha	at has been fixed in v3.5.0	7				
3	Exte	External Databases					
	3.1	Genomic annotation	Ĝ				
		3.1.1 Homo Sapiens (Human)	Ć				
		3.1.2 Mus Musculus (Mouse)	Ć				
		3.1.3 Rattus Norvegicus (Rat)	10				
		3.1.4 Other supported species	11				
4	Syst	tem and R Version	18				
	4.1	Operating System	18				
	4.2	R version	18				
	4.3	R packages	18				
	4.4	OmicsPlayground configuration (OPTIONS)	22				
	4.5	OmicsPlayground default settings (DEFAULTS)	22				

Overview

Scope

The purpose of this document is to provide a list of configurations for OmicsPlayground Enterprise and subsystems. The specification consists of baseline configurations required to be set up at site level as well as project level configurations to meet the requirements defined in User Requirement Specification (URS).

Scope of this Configuration Specification is not limited to the below:

- OmicsPlayground configuration,
- ShinyProxy configuration,
- Operating System (OS) configuration,
- AWS EC2 configuration

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Support

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1 What's new in OmicsPlayground v3.5.0

1.1 Full Proteomics Support

- Missing value imputation using SVDimpute
- New normalization methods: maxMedian and maxSum
- Text and labels are adapted for proteomics terminologies
- UNIPROT id's are detected and annotated automatically
- Reference links to UniProtKB and PhosphoSite databases

1.2 Extended species support

OmicsPlayground v3.5.0 now supports annotation of well over 200 different species.

- Automatic annotation from ENSEMBL, symbol, UNIPROT or accession number.
- Automatic annotation to human ortholog gene/protein.
- Automatic annotation of organism-specific Gene Ontology

1.3 Automatic Reports

Also new in v3.5 is the ability to create automatic visual reports in PDF format.

1.4 New modules/boards

• The Prize-Collection Steiner Tree (PCSF) module (previously in beta) is now standard included under "SystemBio" in the main menu.

1.5 Improved information on methods

We have much improved the information about the methods including references for each plot or table. Click on the 'i' button on the top right of each plot to see this. This information can be copy and pasted for your paper submission.

1.6 Improved information on plot settings

For improved reproducibility, when downloading plots, you have now the possibility to include the plot settings in the PDF. In this way, you can remember what settings you used to create the plot.

1.7 Other new features

- feat: use database for credentials + expiry (prototype) - feat: utils for database - feat: read options from database - feat: add modal wizard to the upload module - feat: upload new data button now works - feat: upload button now has bigomics styles - feat: disable upload tab and handle upload UI directly via modal calls - feat: upload module can now be triggered via load dataset module button - feat: modal upload can now be triggered by welcome board - feat: upload module is not triggered at startup - feat: Add legend and checklist to upload_table_preview_counts_ui via server rendering - feat: dynamically render UI based on input of counts - feat: counts are now passing directly from counts_ui to checked_counts - feat: wizard can now be locked based on state of input file - feat: restyle buttons and load example counts when clicking load_example button - feat: logic for counts when other input files are uploaded feat: handle deletion of samples when contrasts are already uploaded - feat: contrast builder is embedded into contrasts_ui - feat: dynamically render contrast builder - feat: wizard now sends message to compute and active step - feat: upload module now responds to wizard commands - feat: rename compute tab and add an additional tab for review, to avoid the locking issues - feat: contrasts step now (un)locks depending on modified_ct - feat: block new uploads if we already have a processx computation running - feat: shinyvalidate now works! - feat: countsstats is displays correctly and checkTables deprecated input removed - feat: manage to render the plots in correct size (with a lot of flickering) - feat: initial prototype of wizard reset - feat: wizard reset on new upload - feat: wizard works without conflicts with shinyvalidate and shinyalert (preventing re-initialization) - feat: pass wizard controls to fire updateSelectInput exactly when contrast builder is triggered feat: validate dataset name is not at upload_server level for better wizard control - feat: end of computation does not trigger new wizard upload - feat: reset conditions when user add contrast - feat: prevent updateTextInput newname observer to change upon reset of builder - feat: shinyvalidate does not need to to be triggered at page trigger - feat: improve ux by warning user that a locked button was clicked - feat: centralize all warnings to give real-time feedback to use (in alerts, embed in wizard...) - feat: add shinyalert with error message only

 - feat: add default step layout to batch correction module
- feat: option to color or not (up/down reg) volcano plots
- feat: echo playbase branch
- feat: aux function to check if user in DB
- feat: if user in DB use it, otherwise use user folder OPTIONS
- feat: extra duration for clustering board
- feat: colo up/down MA plot
- feat: act matrix with plotly
- feat: disable legen on small plot
- feat: drugconnect actmatrix change color gradient

feat: pathway actmatrix change color rampfeat: pathway invert y axisnew: add detection of mobile and show warning

2 What has been fixed in v3.5.0

Bug fixes improve security and stability of our application. Our team is continuously resolving bugs and errors. If you find a bug, please contact us or report this as an Issue at our GitHub page.

- fix: cookie + database fixes
- fix: umap different
- fix: umap mismatch problem
- improve button spacing
- improve color style of navbar steps when steps succeed
- improve styles of margins
- improve button border color style
- improve styling of wizard buttons to match load board styles
- improve style of run comparison builder
- fix: unload sidebar correctly
- fix: clean sidebar when loading welcome board
- minor improvements
- feat: improve ux by warning user that a locked button was clicked
- improve styles
- improve UI; match color/style of contrast builder button across entire upload
- improve style of comparison upload widget text
- minor fix: replace contrast with comparison
- improvement in alert message when step is incomplete
- attempt to improve bs_alert layout
- improve styles of description step
- improve style of computation options
- improve spacing between computation options; reorder description inputs
- minor improvement in message
- minor improvements in message
- add option to leave BC; reset BC state when wizard resets; improve leave BC button
- fix: move specific packages after playbase installation
- temp fix: to be removed after deploying new base image
- fix: show info text when no geneset is selected
- fix: remove test -- workflow is now fixed
- fix: use pgx geneset genes
- fix: remove browser
- fix: remove unused values
- fix: remove unused wait
- fix: extra time + connectivity more duration
- fix: threshold
- fix: add plot options
- fix: robust file extension detection
- fix: detect colored columns after modifying `df`
- fix: change drugconnect color scale + order
- fix: do not check user on credentials on this auth metdho

- fix: use db when logged with cookie
- fix: if no labels matched return plain wikipath
- fix: use mail variable, not reactive
- fix: use dir variable, not reactive
- fix: use req with a logic condition
- fix: plot tissue csv
- fix: plot barplot csv
- fix: plot decisiontree csv
- fix: plot boxplot csv
- fix: plot heatmap csv
- fix: plot correlation csv
- fix: plot volcanomethods csv
- fix: Partial correlation network csv download
- fix: Mechanism of action csv download
- fix: Activation matrix csv download
- fix: Similarity scores csv download
- fix: upload files check
- fix: singlecell broken csv download (removed them)
- fix: Enrichment analysis csv download
- fix: Frequency in top gene sets csv download
- fix: Differential expression analysis csv download
- fix: Dataset abundance of major gene types csv download
- fix: Abundance of major gene types per group csv download
- fix: Contrast table csv download
- fix: Correlation scatter plots csv download
- fix: abort invite if no mail server
- fix: abort invite if no mail server
- fix: Expression of top differentially expressed genes csv download
- fix: Gene in comparisson csv download
- fix: QC tab not appearing
- fix: use custom genelist when selected
- fix: unresponsive close button in modal
- fix: sending invite
- fix: reactivity feature map plots
- fix: show all contrasts
- fix: react on contrasts missing in pgx

3 External Databases

3.1 Genomic annotation

For the major organism (Human, Mouse and Rat) we have manually included the most up-to-date annotation databases as provided by the latest org.Xx.eg.db packages in BioConductor.

3.1.1 Homo Sapiens (Human)

name	value
DBSCHEMAVERSION Db type Supporting package DBSCHEMA ORGANISM	2.1 OrgDb AnnotationDbi HUMAN_DB Homo sapiens
SPECIES EGSOURCEDATE EGSOURCENAME EGSOURCEURL CENTRALID	Human 2024-Mar12 Entrez Gene ftp://ftp.ncbi.nlm.nih.gov/gene/DATA EG
TAXID GOSOURCENAME GOSOURCEURL GOSOURCEDATE GOEGSOURCEDATE	9606 Gene Ontology http://current.geneontology.org/ontology/go-basic.obo 2024-01-17 2024-Mar12
GOEGSOURCENAME GOEGSOURCEURL GPSOURCENAME GPSOURCEURL GPSOURCEDATE	Entrez Gene ftp://ftp.ncbi.nlm.nih.gov/gene/DATA UCSC Genome Bioinformatics (Homo sapiens) 2024-Feb29
ENSOURCEDATE ENSOURCENAME ENSOURCEURL UPSOURCENAME UPSOURCEURL	2023-Nov22 Ensembl ftp://ftp.ensembl.org/pub/current_fasta Uniprot http://www.UniProt.org/
UPSOURCEDATE	Thu Apr 18 21:39:39 2024

3.1.2 Mus Musculus (Mouse)

name	value
DBSCHEMAVERSION	2.1

Db type OrgDbAnnotationDbi Supporting package DBSCHEMA MOUSE_DB ORGANISM Mus musculus **SPECIES** Mouse EGSOURCEDATE 2024-Mar12**EGSOURCENAME** Entrez Gene EGSOURCEURL ftp://ftp.ncbi.nlm.nih.gov/gene/DATA EGCENTRALID TAXID 10090 GOSOURCENAME Gene Ontology GOSOURCEURL http://current.geneontology.org/ontology/go-basic.obo GOSOURCEDATE 2024-01-17 $2024\text{-}\mathrm{Mar}12$ GOEGSOURCEDATE GOEGSOURCENAME Entrez Gene ftp://ftp.ncbi.nlm.nih.gov/gene/DATA GOEGSOURCEURL UCSC Genome Bioinformatics (Mus musculus) GPSOURCENAME GPSOURCEURL GPSOURCEDATE $2024\text{-}\mathrm{Feb}29$ ENSOURCEDATE 2023-Nov22 ENSOURCENAME Ensembl ENSOURCEURL $ftp://ftp.ensembl.org/pub/current_fasta$ UPSOURCENAME Uniprot http://www.UniProt.org/ UPSOURCEURL UPSOURCEDATE Thu Apr 18 21:47:52 2024

3.1.3 Rattus Norvegicus (Rat)

name	value
DBSCHEMAVERSION Db type Supporting package DBSCHEMA ORGANISM	2.1 OrgDb AnnotationDbi RAT_DB Rattus norvegicus
SPECIES EGSOURCEDATE EGSOURCENAME EGSOURCEURL CENTRALID	Rat 2024-Mar12 Entrez Gene ftp://ftp.ncbi.nlm.nih.gov/gene/DATA EG
TAXID GOSOURCENAME GOSOURCEURL GOSOURCEDATE GOEGSOURCEDATE	10116 Gene Ontology http://current.geneontology.org/ontology/go-basic.obo 2024-01-17 2024-Mar12
GOEGSOURCENAME GOEGSOURCEURL GPSOURCEURL GPSOURCEURL GPSOURCEDATE	Entrez Gene ftp://ftp.ncbi.nlm.nih.gov/gene/DATA UCSC Genome Bioinformatics (Rattus norvegicus) 2021-Apr27

ENSOURCEDATE	2023-Nov22
ENSOURCENAME	Ensembl
ENSOURCEURL	ftp://ftp.ensembl.org/pub/current_fasta
UPSOURCENAME	Uniprot
UPSOURCEURL	$\rm http://www.UniProt.org/$
UPSOURCEDATE	Thu Apr 18 21:41:50 2024

3.1.4 Other supported species

OmicsPlayground v3.5.0 supports annotation of a total of 298 species. For these organisms, we use the AnnotationHub package with snapshot date 2023-10-23. For annotation to human ortholog we use orthogene package.

organism_id	species
80966	Acanthochromis polyacanthus
7029	Acyrthosiphon pisum
7159	Aedes aegypti
7160	Aedes albopictus
9646	Ailuropoda melanoleuca
13333	Amborella trichopoda
400682	Amphimedon queenslandica
80972	Amphiprion ocellaris
64144	Anabas testudineus
4615	Ananas comosus
8839	Anas platyrhynchos
28377	Anolis carolinensis
7173	Anopheles arabiensis
62324	Anopheles funestus
30066	Anopheles merus
30069	Anopheles stephensi
217634	Anophora glabripennis
37293	Aotus nancymaae
112090	Aphanomyces astaci
157072	Aphanomyces invadans
223781	Aquila chrysaetos chrysaetos
81972	Arabidopsis lyrata subsp. lyrata
3702	Arabidopsis thaliana
4686	Asparagus officinalis
8154	Astatotilapia calliptera
7994 9771 7038 3555 158456	Astyanax mexicanus Balaenoptera musculus Bemisia tabaci Beta vulgaris subsp. vulgaris Betta splendens
6526 43346 7091 30522 72004	Biomphalaria glabrata Bison bison bison Bombyx mori Bos indicus x Bos taurus Bos mutus
9913	Bos taurus

15368 3708 3711 6238	Brachypodium distachyon Brassica napus Brassica rapa Caenorhabditis briggsae
6239 31234 9483 7868 90675	Caenorhabditis elegans Caenorhabditis remanei Callithrix jacchus Callorhinchus milii Camelina sativa
9838 286419 9615 3483 9925	Camelus dromedarius Canis lupus dingo Canis lupus familiaris Cannabis sativa Capra hircus
4072 7957 1868482 10141 2715852	Capsicum annuum Carassius auratus Carlito syrichta Cavia porcellus Cebus imitator
9531 106734 63459 34839 3055	Cercocebus atys Chelonoidis abingdonii Chenopodium quinoa Chinchilla lanigera Chlamydomonas reinhardtii
60711 7719 85681 7950 13451	Chlorocebus sabaeus Ciona intestinalis Citrus clementina Clupea harengus Corylus avellana
56716 93934 29159 10029 8502	Cottoperca gobio Coturnix japonica Crassostrea gigas Cricetulus griseus Crocodylus porosus
3656 3659 7176 8103 244447	Cucumis melo Cucumis sativus Culex quinquefasciatus Cyclopterus lumpus Cynoglossus semilaevis
28743 7962 7955 35525 6669	Cyprinodon variegatus Cyprinus carpio Danio rerio Daphnia magna Daphnia pulex
9361 79200 9749 77166 299321	Dasypus novemcinctus Daucus carota subsp. sativus Delphinapterus leucas Dendroctonus ponderosae Denticeps clupeoides
13489 55577	Dicentrarchus labrax Dioscorea cayenensis subsp. rotundata

Dipodomys ordii

7217	Drosophila ananassae
7220	Drosophila erecta
7227 7230 7234 7238 7240	Drosophila melanogaster Drosophila mojavensis Drosophila persimilis Drosophila sechellia Drosophila simulans
7244	Drosophila virilis
7260	Drosophila willistoni
7245	Drosophila yakuba
9371	Echinops telfairi
8005	Electrophorus electricus
280463 9796 9365 27687 71139	Emiliania huxleyi CCMP1516 Equus caballus Erinaceus europaeus Erpetoichthys calabaricus Eucalyptus grandis
72664 9685 59894 158441 8078	Eutrema salsugineum Felis catus Ficedula albicollis Folsomia candida Fundulus heteroclitus
426428	Fusarium oxysporum f. sp. lycopersici 4287
660122	Fusarium vanettenii 77-13-4
334819	Fusarium verticillioides 7600
8049	Gadus morhua
644352	Gaeumannomyces tritici R3-111a-1
9031 69293 48883 3847 1825980	Gallus gallus Gasterosteus aculeatus Geospiza fortis Glycine max Gopherus evgoodei
9595	Gorilla gorilla gorilla
29730	Gossypium raimondii
905079	Guillardia theta CCMP2712
8153	Haplochromis burtoni
4232	Helianthus annuus
6412	Helobdella robusta
10181	Heterocephalus glaber
109280	Hippocampus comes
9606	Homo sapiens
112509	Hordeum vulgare subsp. vulgare
7998	Ictalurus punctatus
43179	Ictidomys tridecemlineatus
35885	Ipomoea triloba
6945	Ixodes scapularis
51337	Jaculus jaculus
51240	Juglans regia
37003	Kryptolebias marmoratus
56723	Labrus bergylta
4236	Lactuca sativa
215358	Larimichthys crocea

8187 Lates calcarifer
7897 Latimeria chalumnae
72036 Lepeophtheirus salmonis
7918 Lepisosteus oculatus
7574 Lingula anatina
7209 Loa loa

225164 Lottia gigantea
9785 Loxodonta africana
7375 Lucilia cuprina
3871 Lupinus angustifolius

9541 Macaca fascicularis 9544 Macaca mulatta 9545 Macaca nemestrina 3750 Malus domestica 9568 Mandrillus leucophaeus

3983 Manihot esculenta 9994 Marmota marmota marmota 205130 Mastacembelus armatus

106582 Maylandia zebra 3880 Medicago truncatula

747676 Melampsora larici-populina 98AG31

9103 Meleagris gallopavo 113334 Melitaea cinxia 10036 Mesocricetus auratus 30608 Microcebus murinus 79684 Microtus ochrogaster

13616 Monodelphis domestica 40151 Monodon monoceros 10089 Mus caroli

10090 Mus musculus 10093 Mus pahari

9669 Mustela putorius furo 59463 Myotis lucifugus 586833 Myripristis murdjan 1026970 Nannospalax galili 7425 Nasonia vitripennis

7425 Nasonia vitripennis 51031 Necator americanus 45351 Nematostella vectensis

452646 Neogale vison

32507 Neolamprologus brichardi

49451 Nicotiana attenuata
61853 Nomascus leucogenys
8663 Notechis scutatus
105023 Nothobranchius furzeri
210225 Nymphaea colorata

9978 Ochotona princeps 10160 Octodon degus 37653 Octopus bimaculoides

158386 Olea europaea var. sylvestris

8019 Oncorhynchus kisutch 8022 Oncorhynchus mykiss 74940 Oncorhynchus tshawytscha 6198 Opisthorchis viverrini 8128 Oreochromis niloticus 9258 Ornithorhynchus anatinus 9986 Oryctolagus cuniculus 4533 Oryza brachyantha 4538 Oryza glaberrima 39947 Oryza sativa Japonica Group 8090 Oryzias latipes 30732 Oryzias melastigma 30611 Otolemur garnettii 9940 Ovis aries 9597 Pan paniscus 9598 Pan troglodytes 206008Panicum hallii 9689 Panthera leo 9691 Panthera pardus 3469Papaver somniferum 9555Papio anubis 5888 Paramecium tetraurelia 1676925Paramormyrops kingsleyae 321614 Parastagonospora nodorum SN15 9157Parus major 13735 Pelodiscus sinensis 230844 Peromyscus maniculatus bairdii Petromyzon marinus 7757 38626 Phascolarctos cinereus Phaseolus vulgaris 3885 42100 Phocoena sinus 3218 Physcomitrium patens 9755Physeter catodon 403677 Phytophthora infestans T30-4 67593Phytophthora sojae 55513 Pistacia vera 3888 Pisum sativum 64176 Podarcis muralis 48698 Poecilia formosa 48699 Poecilia latipinna 8081 Poecilia reticulata 9601 Pongo abelii 3694Populus trichocarpa 379532 Propithecus coquereli 42229 Prunus avium 3755 Prunus dulcis 3760 Prunus persica 8673 Pseudonaja textilis 132908 Pteropus vampyrus 418459 Puccinia graminis f. sp. tritici CRL 75-36-700-3 303518 Pundamilia nyererei 42514Pygocentrus nattereri

Rhinolophus ferrumequinum

Quercus lobata

Rattus norvegicus

97700

10116

59479

61621 Rhinopithecus bieti 61622 Rhinopithecus roxellana

74649 Rosa chinensis

559292 Saccharomyces cerevisiae S288C

8030 Salmo salar 8032 Salmo trutta 283035 Sander lucioperca 9305 Sarcophilus harrisii 113540 Scleropages formosus

665079 Sclerotinia sclerotiorum 1980 UF-70

52904 Scophthalmus maximus 88036 Selaginella moellendorffii

9135 Serinus canaria 41447 Seriola dumerili 1841481 Seriola lalandi dorsalis 4182 Sesamum indicum

4555 Setaria italica 4556 Setaria viridis

75366 Sinocyclocheilus grahami 4081 Solanum lycopersicum 4113 Solanum tuberosum 13686 Solenopsis invicta 42254 Sorex araneus 4558 Sorghum bicolor 8175 Sparus aurata 144197 Stegastes partitus 35570 Stomoxys calcitrans 2489341Strigops habroptila

7668 Strongylocentrotus purpuratus 441894 Struthio camelus australis

9823 Sus scrofa

59729 Taeniopygia guttata 31033 Takifugu rubripes 139649 Teleopsis dalmanni

2587831 Terrapene carolina triunguis 312017 Tetrahymena thermophila SB210

Xenopus tropicalis

Theobroma cacao 3641 6334Trichinella spiralis 57577 Trifolium pratense 4565 Triticum aestivum 85692 Triticum dicoccoides 9739 Tursiops truncatus 9999 Urocitellus parryii 9643 Ursus americanus 29073Ursus maritimus 30538 Vicugna pacos 3914 Vigna angularis 29760 Vitis vinifera 29139 Vombatus ursinus 9627Vulpes vulpes

8364

8083	Xiphophorus maculatus
4577	Zea mays
136037	Zootermopsis nevadensis

4 System and R Version

4.1 Operating System

Description: Ubuntu 24.04 LTS

Release: 24.04 Codename: noble

4.2 R version

name	version
platform arch os system status	x86_64-pc-linux-gnu x86_64 linux-gnu x86_64, linux-gnu
major	4
minor	3.3
year	2024
month	02
day	29
svn rev	86002
language	R
version.string	R version 4.3.3 (2024-02-29)
nickname	Angel Food Cake
Bioconductor	3.18

4.3 R packages

Package	Version	License
AnnotationDbi	1.64.1	Artistic-2.0
AnnotationHub	3.10.1	Artistic-2.0
ape	5.8	GPL-2 GPL-3
aws.s3	0.3.21	GPL (>= 2)
Azimuth	0.5.0	GPL-3 file LICENSE
base	4.3.3	Part of R 4.3.3
base64enc	0.1 - 3	GPL-2 GPL-3
batchelor	1.18.1	GPL-3
beepr	2.0	GPL-3
beeswarm	0.4.0	Artistic-2.0

```
BiocParallel
                         1.36.0
                                     GPL-2 | GPL-3
blastula
                         0.3.5
                                     MIT + file LICENSE
Boruta
                         8.0.0
                                     GPL (>= 2)
bslib
                         0.8.0
                                     MIT + file LICENSE
bsutils
                         0.0.0.9000
                                     MIT + file LICENSE
caret
                         6.0 - 94
                                     GPL (>= 2)
                                     \mathrm{MIT} + file LICENSE
circlize
                         0.4.16
cluster
                         2.1.6
                                     GPL (>= 2)
                                     BSD_3_{clause} + file LICENSE
colorspace
                         2.1 - 1
ComICS
                         1.0.4
                                     GPL-2
                         2.18.0
                                     MIT + file LICENSE
ComplexHeatmap
cookies
                         0.2.3
                                     \mathrm{MIT} + file LICENSE
corpcor
                         1.6.10
                                     GPL (>= 3)
corpora
                         0.6
                                     GPL-3
corrplot
                         0.92
                                     \mathrm{MIT} + file LICENSE
                                     GPL-2
cowplot
                         1.1.3
data.table
                                     MPL-2.0 | file LICENSE
                         1.15.4
DBI
                         1.2.3
                                     LGPL (>= 2.1)
DeconRNASeq
                         1.44.0
                                     GPL-2
DESeq2
                         1.42.1
                                     LGPL (>= 3)
doParallel
                         1.0.17
                                     GPL-2
dplyr
                         1.1.4
                                     \mathrm{MIT} + file LICENSE
DT
                         0.33
                                     GPL-3 | file LICENSE
edgeR
                         4.0.16
                                     GPL (>=2)
EPIC
                         1.1.7
                                     file LICENSE
                                     FreeBSD | GPL-2 | file LICENSE
fastcluster
                         1.2.6
fgsea
                         1.29.1
                                     \mathrm{MIT} + file LICENCE
firebase
                         1.0.2
                                     AGPL-3
FNN
                         1.1.4
                                     GPL (>= 2)
forcats
                         1.0.0
                                     MIT + file LICENSE
foreach
                         1.5.2
                                     Apache License (==2.0)
future
                         1.34.0
                                     LGPL (>= 2.1)
GenomicRanges
                         1.54.1
                                     Artistic-2.0
                         2.70.0
GEOquery
                                     MIT
ggforce
                         0.4.2
                                     \mathrm{MIT} + file LICENSE
ggplot2
                         3.5.1
                                     MIT + file LICENSE
ggrepel
                         0.9.5
                                     GPL-3 \&#124; file LICENSE
ggtext
                         0.1.2
                                     GPL-2
{\rm ggVennDiagram}
                         1.5.2
                                     GPL-3
                                     GPL-2
glasso
                         1.11
glmnet
                         4.1-8
                                     GPL-2
glue
                         1.7.0
                                     MIT + file LICENSE
GO.db
                         3.18.0
                                     Artistic-2.0
gplots
                         3.1.3.1
                                     GPL-2
graphics
                         4.3.3
                                     Part of R 4.3.3
                         4.3.3
                                     Part of R 4.3.3
grDevices
                         4.3.3
                                     Part of R 4.3.3
grid
                                     GPL (>= 2)
gridExtra
                         2.3
GSVA
                                     GPL (>= 2)
                         1.50.5
                         1.2.0
                                     GPL-3
harmony
heatmaply
                         1.5.0
                                     GPL-2 | GPL-3
htmltools
                         0.5.8.9000
                                     GPL (>= 2)
```

htmlwidgets httr	1.6.4 $1.4.7$	MIT + file LICENSE MIT + file LICENSE
igraph	2.0.3	GPL (>= 2)
iheatmapr	0.7.1	MIT + file LICENSE
infercnv	1.21.0	BSD_3_clause + file LICENSE
inspectdf	0.0.12	GPL-2
irlba	2.3.5.1	GPL-3
isva	1.9	GPL-2
jpeg	0.1-10	GPL-2 GPL-3
jsonlite	1.8.8	MIT + file LICENSE
lazyeval	0.2.2	GPL-3
limma	3.58.1	GPL (>=2)
magrittr	2.0.3	MIT + file LICENSE
markdown	1.13	MIT + file LICENSE
Matrix	1.6-4	GPL (>= 2) file LICENCE
matrixStats	1.3.0	Artistic-2.0
matrixTests	0.2.3	GPL-2
methods	4.3.3	Part of R $4.3.3$
microbenchmark	1.4.10	BSD_2_clause + file LICENSE
miniUI	0.1.1.1	GPL-3
missForest	1.5	GPL (>= 2)
mixOmics	6.26.0	GPL (>= 2)
msa	1.34.0	GPL (>= 2)
msImpute MSnbase MultiAssayExperiment NNLM org.Hs.eg.db	1.12.0 2.28.1 1.28.0 0.4.4 3.19.1	GPL (>=2) Artistic-2.0 Artistic-2.0 BSD_2_clause + file LICENSE Artistic-2.0
org.Mm.eg.db	3.19.1	Artistic-2.0
org.Pf.plasmo.db	3.14.0	Artistic-2.0
org.Rn.eg.db	3.19.1	Artistic-2.0
orthogene	1.8.0	GPL-3
pairsD3	0.1.3	GPL (>= 3)
pamr parallel partykit patchwork pcaMethods	1.57 4.3.3 1.2-21 1.2.0 1.94.0	GPL-2 Part of R 4.3.3 GPL-2 GPL-3 MIT + file LICENSE GPL (>= 3)
PCSF plotly plsRcox png ppcor	0.99.1 4.10.4 1.7.7 0.1-8 1.1	MIT + file LICENSE MIT + file LICENSE GPL-3 GPL-2 GPL-3 GPL-2
processx	3.8.4	MIT + file LICENSE
promises	1.3.0	MIT + file LICENSE
psych	2.4.6.26	GPL (>= 2)
purrr	1.0.2	MIT + file LICENSE
qgraph	1.9.8	GPL-2
qlcMatrix	0.9.8	GPL-3
R6	2.5.1	MIT + file LICENSE
randomForest	4.7-1.1	GPL ($>= 2$)
randomForestSRC	3.3.1	GPL ($>= 3$)

RColorBrewer	1.1-3	Apache License 2.0
recount reshape2 reticulate rgeolocate rhdf5	1.28.0 1.4.4 1.38.0 1.4.2 2.46.1	Artistic-2.0 MIT + file LICENSE Apache License 2.0 Apache License (== 2.0) Artistic-2.0
rliger rpart RSQLite Rtsne ruv	2.0.1 4.1.23 2.3.7 0.17 0.9.7.1	GPL-3 GPL-2 GPL-3 LGPL (>= 2.1) file LICENSE GPL
RUVSeq rworldmap SBGNview scales scatterD3	1.36.0 1.3-8 1.16.0 1.3.0 1.0.1	Artistic-2.0 GPL ($>= 2$) AGPL-3 MIT + file LICENSE GPL ($>= 3$)
scran Seurat sever shiny shiny.i18n	1.30.2 5.1.0 0.0.7 1.9.1 0.3.0	GPL-3 MIT + file LICENSE MIT + file LICENSE GPL-3 file LICENSE MIT + file LICENSE
shinyalert shinybrowser shinyBS shinybusy shinycssloaders	3.1.0 1.0.0 0.61.1 0.3.3 1.1.0	MIT + file LICENSE MIT + file LICENSE GPL-3 GPL-3 MIT + file LICENSE
shinydashboardPlus shinyjqui shinyjs shinyvalidate shinyWidgets	2.0.4 0.4.1 2.1.0 0.1.3 0.8.6	GPL (>= 2) file LICENSE MIT + file LICENSE MIT + file LICENSE MIT + file LICENSE GPL-3
SILGGM SingleR sodium sortable stats	1.0.0 2.4.1 1.3.1 0.5.0 4.3.3	GPL (>= 2) GPL-3 + file LICENSE MIT + file LICENSE MIT + file LICENSE Part of R 4.3.3
stringr SummarizedExperiment SuperCell survival sva	1.5.1 1.32.0 1.0 3.7-0 3.50.0	MIT + file LICENSE Artistic-2.0 file LICENSE LGPL (>= 2) Artistic-2.0
svgPanZoom tools umap utils uwot	0.3.4 4.3.3 0.2.10.0 4.3.3 0.2.2	MIT + file LICENSE Part of R 4.3.3 MIT + file LICENSE Part of R 4.3.3 GPL (>= 3)
vioplot viridis visNetwork waiter webshot2	0.5.0 0.6.5 2.1.3 0.2.5.9000 0.1.1	BSD_3_clause + file LICENSE MIT + file LICENSE MIT + file LICENSE MIT + file LICENSE GPL-2

WGCNA	1.72 - 5	GPL (>= 2)
withr	3.0.1	MIT + file LICENSE
wordcloud	2.6	LGPL-2.1
xfun	0.46	MIT + file LICENSE
xgboost	1.7.8.1	Apache License (== 2.0) file LICENSE
xml2	1.3.6	MIT + file LICENSE
yaml	2.3.10	$BSD_3_clause + file LICENSE$
zip	2.3.1	MIT + file LICENSE

4.4 OmicsPlayground configuration (OPTIONS)

```
TITLE
                     = 'Omics Playground'
AUTHENTICATION
ALLOW_NEW_USERS
                     = TRUE
ALLOW_PERSONAL_EMAIL = FALSE
USE_CREDENTIALS = FALSE
BLOCKED_DOMAIN = bigomics.com|massdynamics.com|pluto.bio|rosalind.bio
                    = TRUE
ENABLE_CHIRP
ENABLE_DELETE = TRUE
ENABLE_PGX_DOWNLOAD = TRUE
ENABLE_PUBLIC_SHARE = TRUE
{\tt ENABLE\_UPLOAD} = {\tt TRUE} \\ {\tt ENABLE\_USERDIR} = {\tt TRUE} \\
ENABLE_USER_SHARE = TRUE
ENABLE_USER_LOCK = TRUE
ENABLE_HEARTBEAT = TRUE
ENABLE_INACTIVITY = TRUE
                  = FALSE
ENABLE_ANNOT
MAX_DATASETS
MAX_SAMPLES
                    = 100
MAX_SAMPLES
MAX_COMPARISONS = 20
CENES = 20000
                    = 1000
MAX_GENESETS
                    = 5000
MAX_SHARED_QUEUE = 3
MAX SESSIONS
                    = 2
TIMEOUT
                     = 0
WATERMARK
                     = TRUE
APACHE_COOKIE_PATH = /app/omicsplayground/
DEVMODE
          = FALSE
```

4.5 OmicsPlayground default settings (DEFAULTS)

computation_options:

probe_filtering:

- remove.notexpressed
- remove.unknown
- only.proteincoding