

## Analytical and other software on the Secure Research Environment

*The Research Environment runs with the operating system: Microsoft Windows Server 2022 DataCenter edition. The environment is based on the Microsoft Data Science virtual machine template and includes the following software:*

- 7-zip
- Acrobat Reader
- MiniConda, including:
  - Python 3.8, 3.9, and 3.10
  - PyTorch
  - TensorFlow
- Apache Spark 3.1
- cMakeGIT
- Git and Git Extensions UI
- JAGS, including rjags
- Julia 1.10.5
- Jupyter Notebook, with Kernels for R, Python, Julia, PySpark
- Microsoft Office 2016 Standard edition, including Word, Excel, PowerPoint, and OneNote (*Access not included*)
- Microsoft Photo Viewer
- Windows subsystem for Linux, with Ubuntu
- Nodejs
- OpenBUGS
- PLINK
- PowerBI Desktop
- PowerShell
- PyCharm 2024.2.1, and PyCharm Community Edition, 2024.1.1
- Python 3.14 and 3.12, including PySpark
- R Studio 2026.01.0+392
- R Version 4.5.2 (2025-10-31)
- Review Manager 5.4
- SQL Server Developer Edition (2019), including Management Studio and SQL Server Integration Services (SSIS)
- stan and rstan
- STATA 17
- Visual Studio Code 1.96.3
- Vowpal Wabbit
- xgboost

And in the Premium research environments:

- SAS 9.4, m4\*

\*Alternative pricing applies for industry users of SAS, email [support@vivli.org](mailto:support@vivli.org) for details.



Users also have the ability to bring in additional software if the software was specified in the data request, the software runs in the operating system described above, and the user can provide Vivli with any necessary licensing keys. Software licenses must be validated by the software only at installation or setup: software that validates the license on each invocation will not work. Users must attest that the license agreements they need for any of the software they want to bring in can be used in the Vivli research environment.

The following applications have been validated to work on the Vivli Research Environment when an appropriate license can be provided by the researcher – contact Vivli for details on license types:

- SAS Universal Viewer as an alternative to the full academic license for SAS.
- SPSS (Important: the usual academic site license will NOT work; Please contact Vivli for details on the correct license type)
- Mathlab
- MedCalc, from <https://medcalc.org>, but not the software available at <https://medcalc.com>
- Monlix or other applications from Lixoft.net)
- Comprehensive Meta Analysis

#### **How to add R packages from CRAN not pre-installed in the Vivli Research Environment:**

During the course of your analysis, if you find that you need to load R scripts from the CRAN repository, you can do that yourself using the following steps:

- To install a CRAN package in R, use the `install.packages()` function. This simple command downloads the package from a specified repository (by default, CRAN) and installs it on your machine (or);
- In RStudio go to Tools → Install Packages and in the Install from option select Repository (CRAN) and then specify the packages you want.

If you need any other R or Python scripts not pre-installed in the Vivli Research Environment, please reach out to Vivli via chat or [support@vivli.org](mailto:support@vivli.org) and let them know the names of the additional scripts that you require and they will add them to your research environment.

For the latest guide to working in the Vivli Research Environment, please see here <https://qa-api.vivli.dev/pages/display/ResearchEnvironmentGuide>

R Packages included in the Research Environment, associated with RStudio:

|                  |             |              |                   |
|------------------|-------------|--------------|-------------------|
| abind            | brglm       | corrplot     | ebal              |
| acepack          | brio        | covr         | editrules         |
| ada              | broom       | cowplot      | ellipse           |
| adabag           | BRugs       | cpp11        | ellipsis          |
| AnnotationDbi    | BSgenome    | crayon       | ensemldb          |
| AnnotationFilter | bslib       | credentials  | Epi               |
| arules           | C50         | crosstalk    | etm               |
| askpass          | cachem      | crpp         | evaluate          |
| assertthat       | cairoDevice | crrstep      | exactRankTests    |
| aweb             | callr       | Cubist       | fansi             |
| backports        | car         | curl         | farver            |
| bartMachine      | carData     | CVST         | fastICA           |
| bartMachineJARs  | caret       | data.table   | fastmap           |
| base             | caTools     | data.tree    | fastmatch         |
| base64enc        | CBPS        | datasets     | filelock          |
| BBmisc           | cellranger  | DBI          | forcats           |
| BH               | checkmate   | dbplyr       | foreach           |
| bibtex           | checkpoint  | ddalpha      | foreign           |
| bindr            | chron       | DelayedArray | forestplot        |
| bindrcpp         | class       | DEoptimR     | formatR           |
| Biobase          | classInt    | desc         | Formula           |
| BiocFileCache    | cli         | devtools     | formula.tools     |
| BiocGenerics     | clipr       | DiagrammeR   | fs                |
| BiocIO           | clisymbols  | dichromat    | futile.logger     |
| BiocManager      | cluster     | diffobj      | futile.options    |
| BiocParallel     | cmprsk      | digest       | future            |
| BiocVersion      | cobalt      | dimRed       | future.apply      |
| biomaRt          | coda        | doParallel   | gam               |
| Biostrings       | codetools   | downloader   | gargle            |
| biovizBase       | coin        | dplyr        | gbm               |
| bit              | colorspace  | drat         | gdata             |
| bit64            | combinat    | DRR          | geepack           |
| bitops           | commonmark  | DT           | generics          |
| blob             | compiler    | dtplyr       | GenomeInfoDb      |
| boot             | conquer     | e1071        | GenomeInfoDbData  |
| brew             | corpcor     | earth        | GenomicAlignments |



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|                 |             |                |                |
|-----------------|-------------|----------------|----------------|
| GenomicFeatures | hms         | lattice        | miniCRAN       |
| GenomicRanges   | htmlTable   | latticeExtra   | miniUI         |
| geometry        | htmltools   | lava           | minqa          |
| geosphere       | htmlwidgets | lazyeval       | misc3d         |
| gert            | httpuv      | libcoin        | missForest     |
| ggmap           | httr        | lifecycle      | mitml          |
| ggplot2         | huxtable    | linprog        | mitools        |
| ggpubr          | ids         | listenv        | mlbench        |
| ggraph          | igraph      | lme4           | mlr            |
| ggrepel         | incidence   | logistf        | mlr3           |
| ggsci           | influenceR  | loo            | mrmr           |
| ggsignif        | ini         | lpSolve        | mnormt         |
| ggtext          | inline      | lpSolveAPI     | ModelMetrics   |
| gh              | inum        | lubridate      | modelr         |
| git2r           | ipred       | magic          | modeltools     |
| gitcreds        | ipw         | magrittr       | multcomp       |
| glmnet          | IRanges     | mapproj        | munsell        |
| glmnetUtils     | IRdisplay   | maps           | mvtnorm        |
| globals         | IRkernel    | maptools       | nlme           |
| glue            | irlba       | markdown       | nloptr         |
| Gmisc           | isoband     | MASS           | NMF            |
| googledrive     | ISwR        | Matching       | nnet           |
| googlesheets4   | iterators   | MatchIt        | nnls           |
| gower           | itertools   | mathjaxr       | numDeriv       |
| gplots          | jomo        | Matrix         | openssl        |
| graphics        | jpeg        | MatrixGenerics | openxlsx       |
| grDevices       | jquerylib   | MatrixModels   | operator.tools |
| Greg            | jsonlite    | matrixStats    | ordinal        |
| grid            | KEGGREST    | maxstat        | packrat        |
| gridBase        | kernlab     | mboost         | pamr           |
| gridExtra       | KernSmooth  | mda            | pan            |
| gridtext        | klaR        | memoise        | pander         |
| gsubfn          | km.ci       | metafor        | parallel       |
| gtable          | KMsurv      | methods        | parallelly     |
| gtools          | knitr       | mets           | parallelMap    |
| Gviz            | labeling    | mfp            | ParamHelpers   |
| haven           | labelled    | mgcv           | party          |
| highr           | lambda.r    | mice           | partykit       |
| Hmisc           | later       | mime           | pastecs        |

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|              |                 |                |                      |
|--------------|-----------------|----------------|----------------------|
| pbapply      | psych           | rgexf          | SASxport             |
| pbdZMQ       | Publish         | RgoogleMaps    | scales               |
| pbkrtest     | purrr           | RGtk2          | selectr              |
| pdp          | quadprog        | Rhtslib        | servr                |
| pec          | quantreg        | rio            | sessioninfo          |
| penalized    | questionr       | riskRegression | sfsmisc              |
| pillar       | R.cache         | rJava          | shape                |
| pkgbuild     | R.methodsS3     | rjson          | shiny                |
| pkgcache     | R.oo            | RJSONIO        | snow                 |
| pkgconfig    | R.utils         | rlang          | sourcetools          |
| pkgdepends   | R2WinBUGS       | rmarkdown      | sp                   |
| pkgload      | R6              | rms            | SparseM              |
| pkgmaker     | randomForest    | rngtools       | spatial              |
| PKI          | randomForestSRC | robustbase     | splines              |
| plogr        | ranger          | ROCR           | spls                 |
| plot3D       | RANN            | RODBC          | sqldf                |
| plotmo       | rappdirs        | Rook           | SQUAREM              |
| plotrix      | rattle          | roxygen2       | stabs                |
| pls          | rcmdcheck       | rpart          | STAN                 |
| plyr         | RColorBrewer    | rpart.plot     | StanHeaders          |
| png          | Rcpp            | rprojroot      | statmod              |
| poilog       | RcppArmadillo   | Rsamtools      | stats                |
| polyspline   | RcppEigen       | rsconnect      | stats4               |
| polyclip     | RcppParallel    | Rsolnp         | stepp                |
| polynom      | RcppProgress    | SQLite         | stringi              |
| pracma       | RcppRoll        | rstan          | stringr              |
| praise       | RCurl           | rstatix        | strucchange          |
| prettyunits  | readr           | Rstudioapi     | styler               |
| pROC         | readxl          | Rtools         | subselect            |
| processx     | recipes         | rtracklayer    | SummarizedExperiment |
| prodlim      | registry        | RUnit          | superpc              |
| profileModel | rematch         | rversions      | survAUC              |
| progress     | rematch2        | rvest          | survey               |
| progressr    | remotes         | RWeka          | survival             |
| promises     | repr            | RWekajars      | survivalROC          |
| ProtGenerics | reprex          | S4Vectors      | survivalsvm          |
| proto        | reshape2        | sandwich       | survminer            |
| proxy        | restfulr        | sas7bdat       | survMisc             |
| ps           | rex             | saas           | sys                  |

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|               |                   |             |          |
|---------------|-------------------|-------------|----------|
| tcltk         | tools             | vctr        | xgboost  |
| TeachingDemos | translations      | VennDiagram | xlsx     |
| testthat      | truncnorm         | viridis     | xlsxjars |
| TH.data       | twang             | viridisLite | XML      |
| tibble        | tweenr            | visNetwork  | xml2     |
| tidyr         | tzdb              | visreg      | xopen    |
| tidyselect    | ucminf            | vroom       | xtable   |
| tidyverse     | usethis           | waldo       | XVector  |
| timeDate      | utf8              | WeightIt    | yaml     |
| timereg       | utils             | whisker     | zeallot  |
| timeROC       | uuid              | withr       | zip      |
| tinytex       | V8                | WriteXLS    | zlibbioc |
| tmvnsim       | VariantAnnotation | xfun        | zoo      |

## Python Packages included in the Research Environment, in the Python 3.14 environment

|                      |                          |                    |                         |
|----------------------|--------------------------|--------------------|-------------------------|
| absl-py              | ipython                  | nest-asyncio       | rfc3339-validator       |
| anyio                | ipython_pygments_lexers  | notebook           | rfc3986-validator       |
| argon2-cffi          | isoduration              | notebook_shim      | rfc3987-syntax          |
| argon2-cffi-bindings | jedi                     | numpy              | rich                    |
| arrow                | Jinja2                   | opt_einsum         | rpds-py                 |
| asttokens            | json5                    | optree             | scipy                   |
| astunparse           | jsonpointer              | overrides          | Send2Trash              |
| async-lru            | jsonschem                | packaging          | setuptools              |
| attrs                | jsonschem-specifications | pandas             | six                     |
| babel                | jupyter_client           | pandocfilters      | sniffio                 |
| beautifulsoup4       | jupyter_core             | parso              | soupsieve               |
| bleach               | jupyter-events           | pillow             | stack-data              |
| certifi              | jupyter-lsp              | pip                | tensorboard             |
| cffi                 | jupyter_server           | platformdirs       | tensorboard-data-server |
| charset-normalizer   | jupyter_server_terminals | prometheus_client  | termcolor               |
| colorama             | jupyterlab               | prompt_toolkit     | terminado               |
| comm                 | jupyterlab_pygments      | protobuf           | tinycss2                |
| debugpy              | jupyterlab_server        | psutil             | tornado                 |
| decorator            | keras                    | pure_eval          | traitlets               |
| defusedxml           | lark                     | py4j               | types-python-dateutil   |
| executing            | libclang                 | pycparser          | typing_extensions       |
| fastjsonschema       | Markdown                 | Pygments           | tzdata                  |
| flatbuffers          | markdown-it-py           | pyreadstat         | uri-template            |
| fqdn                 | MarkupSafe               | pyspark            | urllib3                 |
| gast                 | matplotlib-inline        | python-dateutil    | wcwidth                 |
| google-pasta         | mdurl                    | python-json-logger | webcolors               |
| grpcio               | mistune                  | pytz               | webencodings            |
| h11                  | ml_dtypes                | pywin32            | websocket-client        |
| h5py                 | namex                    | pywinpty           | Werkzeug                |
| httpcore             | narwhals                 | PyYAML             | wheel                   |
| httpx                | nbclient                 | pyzmq              | wrapt                   |
| idna                 | nbconvert                | referencing        | xgboost-cpu             |
| ipykernel            | nbformat                 | requests           |                         |

This document describes the software contained on Research Environments provisioned after 28 February 2026.