if (!require("tiledb", quietly = TRUE))

+ remotes::install\_github("TileDB-Inc/TileDB-R", force = TRUE)

>

> if (!require("tiledbsc", quietly = TRUE))

+ remotes::install\_github("tiledb-inc/tiledbsc", force = TRUE)

>

> library(tiledb)

> library(tiledbsc)

>

> tiledbURI <- "LiverDataRelease\_TileDBArray/"

>

> s3Region <- "us-west-2"

>

> config <- tiledb::tiledb\_config()

> config["vfs.s3.region"] <- s3Region

> ctx <- tiledb::tiledb\_ctx(config)

>

>

> tiledb\_scdataset <- tiledbsc::SOMACollection$new(uri = tiledbURI,

+ verbose = FALSE)

>

>

> names(tiledb\_scdataset$somas)

character(0)

> ## [1] "falsecode" "negprobes" "RNA" "RNA\_normalized"

> names(tiledb\_scdataset$somas$RNA$members)

NULL

> ## [1] "X" "varp" "obs" "varm" "obsp" "uns" "obsm" "var"

>

>

> counts <- tiledb\_scdataset$somas$RNA$X$members$counts$to\_matrix(batch\_mode = TRUE)

Error: attempt to apply non-function

> library(ggplot2)

> library(ggpubr)

> library(ggrepel)

> library(gridExtra)

> library(matrixStats)

> library(patchwork)

> library(pheatmap)

> library(Seurat)

> library(RColorBrewer)

> library(reshape2)

> if (!require("tiledb", quietly = TRUE))

+ remotes::install\_github("TileDB-Inc/TileDB-R", force = TRUE)

>

> if (!require("tiledbsc", quietly = TRUE))

+ remotes::install\_github("tiledb-inc/tiledbsc", force = TRUE)

>

> library(tiledb)

> library(tiledbsc)

>

> tiledbURI <- "LiverDataRelease\_TileDBArray/"

>

> s3Region <- "us-west-2"

>

> config <- tiledb::tiledb\_config()

> config["vfs.s3.region"] <- s3Region

> ctx <- tiledb::tiledb\_ctx(config)

>

>

> tiledb\_scdataset <- tiledbsc::SOMACollection$new(uri = tiledbURI,

+ verbose = FALSE)

> library(ggplot2)

> library(ggpubr)

> library(ggrepel)

> library(gridExtra)

> library(matrixStats)

> library(patchwork)

> library(pheatmap)

> library(Seurat)

> library(RColorBrewer)

> library(reshape2)

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> if (!require("tiledbsc", quietly = TRUE))

+ remotes::install\_github("tiledb-inc/tiledbsc", force = TRUE)

>

> library(tiledb)

> library(tiledbsc)

>

> tiledbURI <- "LiverDataRelease\_TileDBArray/"

>

> s3Region <- "us-west-2"

>

> config <- tiledb::tiledb\_config()

> config["vfs.s3.region"] <- s3Region

> ctx <- tiledb::tiledb\_ctx(config)

>

>

> tiledb\_scdataset <- tiledbsc::SOMACollection$new(uri = tiledbURI,

+ verbose = FALSE)

> library(ggplot2)

> library(ggpubr)

> library(ggrepel)

> library(gridExtra)

> library(matrixStats)

> library(patchwork)

> library(pheatmap)

> library(Seurat)

> library(RColorBrewer)

> library(reshape2)

> if (!require("tiledb", quietly = TRUE))

+ remotes::install\_github("TileDB-Inc/TileDB-R", force = TRUE)

>

> if (!require("tiledbsc", quietly = TRUE))

+ remotes::install\_github("tiledb-inc/tiledbsc", force = TRUE)

>

> library(tiledb)

> library(tiledbsc)

>

> tiledbURI <- "LiverDataRelease\_TileDBArray/"

>

> s3Region <- "us-west-2"

>

> config <- tiledb::tiledb\_config()

> config["vfs.s3.region"] <- s3Region

> ctx <- tiledb::tiledb\_ctx(config)

>

>

> tiledb\_scdataset <- tiledbsc::SOMACollection$new(uri = tiledbURI,

+ verbose = FALSE)

>

>

> names(tiledb\_scdataset$somas)

character(0)

> ## [1] "falsecode" "negprobes" "RNA" "RNA\_normalized"

> names(tiledb\_scdataset$somas$RNA$members)

NULL

> ## [1] "X" "varp" "obs" "varm" "obsp" "uns" "obsm" "var"

> library(ggplot2)

> library(ggpubr)

> library(ggrepel)

> library(gridExtra)

> library(matrixStats)

> library(patchwork)

> library(pheatmap)

> library(Seurat)

> library(RColorBrewer)

> library(reshape2)

> if (!require("tiledb", quietly = TRUE))

+ remotes::install\_github("TileDB-Inc/TileDB-R", force = TRUE)

>

> if (!require("tiledbsc", quietly = TRUE))

+ remotes::install\_github("tiledb-inc/tiledbsc", force = TRUE)

>

> library(tiledb)

> library(tiledbsc)

>

> tiledbURI <- "LiverDataRelease\_TileDBArray/"

>

> s3Region <- "us-west-2"

>

> config <- tiledb::tiledb\_config()

> config["vfs.s3.region"] <- s3Region

> ctx <- tiledb::tiledb\_ctx(config)

>

>

> tiledb\_scdataset <- tiledbsc::SOMACollection$new(uri = tiledbURI,

+ verbose = FALSE)

>

>

> names(tiledb\_scdataset$somas)

character(0)

> ## [1] "falsecode" "negprobes" "RNA" "RNA\_normalized"

> names(tiledb\_scdataset$somas$RNA$members)

NULL

> ## [1] "X" "varp" "obs" "varm" "obsp" "uns" "obsm" "var"

>

>

> counts <- tiledb\_scdataset$somas$RNA$X$members$counts$to\_matrix(batch\_mode = TRUE)

Error: attempt to apply non-function

> library(ggplot2)

> library(ggpubr)

> library(ggrepel)

> library(gridExtra)

> library(matrixStats)

> library(patchwork)

> library(pheatmap)

> library(Seurat)

> library(RColorBrewer)

> library(reshape2)

> if (!require("tiledb", quietly = TRUE))

+ remotes::install\_github("TileDB-Inc/TileDB-R", force = TRUE)

>

> if (!require("tiledbsc", quietly = TRUE))

+ remotes::install\_github("tiledb-inc/tiledbsc", force = TRUE)

>

> library(tiledb)

> library(tiledbsc)

>

> tiledbURI <- "LiverDataRelease\_TileDBArray/"

>

> s3Region <- "us-west-2"

>

> config <- tiledb::tiledb\_config()

> config["vfs.s3.region"] <- s3Region

> ctx <- tiledb::tiledb\_ctx(config)

>

>

> tiledb\_scdataset <- tiledbsc::SOMACollection$new(uri = tiledbURI,

+ verbose = FALSE)

>

>

> names(tiledb\_scdataset$somas)

character(0)

> ## [1] "falsecode" "negprobes" "RNA" "RNA\_normalized"

> names(tiledb\_scdataset$somas$RNA$members)

NULL

> ## [1] "X" "varp" "obs" "varm" "obsp" "uns" "obsm" "var"

>

>

>

>

> ## [1] 1000 793318

> counts[1:4,1:4]

Error: object 'counts' not found

> library(ggplot2)

> library(ggpubr)

> library(ggrepel)

> library(gridExtra)

> library(matrixStats)

> library(patchwork)

> library(pheatmap)

> library(Seurat)

> library(RColorBrewer)

> library(reshape2)

> if (!require("tiledb", quietly = TRUE))

+ remotes::install\_github("TileDB-Inc/TileDB-R", force = TRUE)

>

> if (!require("tiledbsc", quietly = TRUE))

+ remotes::install\_github("tiledb-inc/tiledbsc", force = TRUE)

>

> library(tiledb)

> library(tiledbsc)

>

> tiledbURI <- "LiverDataRelease\_TileDBArray/"

>

> s3Region <- "us-west-2"

>

> config <- tiledb::tiledb\_config()

> config["vfs.s3.region"] <- s3Region

> ctx <- tiledb::tiledb\_ctx(config)

>

>

> tiledb\_scdataset <- tiledbsc::SOMACollection$new(uri = tiledbURI,

+ verbose = FALSE)

>

>

> names(tiledb\_scdataset$somas)

character(0)

> ## [1] "falsecode" "negprobes" "RNA" "RNA\_normalized"

> names(tiledb\_scdataset$somas$RNA$members)

NULL

> ## [1] "X" "varp" "obs" "varm" "obsp" "uns" "obsm" "var"

>

>

> counts <- 0

> dim(counts)

NULL

>

> ## [1] 1000 793318

> counts[1:4,1:4]

Error in counts[1:4, 1:4] : incorrect number of dimensions

> library(ggplot2)

> library(ggpubr)

> library(ggrepel)

> library(gridExtra)

> library(matrixStats)

> library(patchwork)

> library(pheatmap)

> library(Seurat)

> library(RColorBrewer)

> library(reshape2)

> if (!require("tiledb", quietly = TRUE))

+ remotes::install\_github("TileDB-Inc/TileDB-R", force = TRUE)

>

> if (!require("tiledbsc", quietly = TRUE))

+ remotes::install\_github("tiledb-inc/tiledbsc", force = TRUE)

>

> library(tiledb)

> library(tiledbsc)

>

> tiledbURI <- "LiverDataRelease\_TileDBArray/"

>

> s3Region <- "us-west-2"

>

> config <- tiledb::tiledb\_config()

> config["vfs.s3.region"] <- s3Region

> ctx <- tiledb::tiledb\_ctx(config)

>

>

> tiledb\_scdataset <- tiledbsc::SOMACollection$new(uri = tiledbURI,

+ verbose = FALSE)

>

>

> names(tiledb\_scdataset$somas)

character(0)

> ## [1] "falsecode" "negprobes" "RNA" "RNA\_normalized"

> names(tiledb\_scdataset$somas$RNA$members)

NULL

> ## [1] "X" "varp" "obs" "varm" "obsp" "uns" "obsm" "var"

>

>

>

>

> ## [1] 1000 793318

>

> ## 4 x 4 sparse Matrix of class "dgTMatrix"

> ## c\_1\_100\_1000 c\_1\_100\_1017 c\_1\_100\_1028 c\_1\_100\_1043

> ## AATK 1 1 2 1

> ## ABL1 . . . .

> ## ABL2 . . . .

> ## ACACB . . . .

>

>

> norm <- tiledb\_scdataset$somas$RNA\_normalized$X$members$data$to\_matrix(batch\_mode = TRUE)

Error: attempt to apply non-function

> library(ggplot2)

> library(ggpubr)

> library(ggrepel)

> library(gridExtra)

> library(matrixStats)

> library(patchwork)

> library(pheatmap)

> library(Seurat)

> library(RColorBrewer)

> library(reshape2)

> if (!require("tiledb", quietly = TRUE))

+ remotes::install\_github("TileDB-Inc/TileDB-R", force = TRUE)

>

> if (!require("tiledbsc", quietly = TRUE))

+ remotes::install\_github("tiledb-inc/tiledbsc", force = TRUE)

>

> library(tiledb)

> library(tiledbsc)

>

> tiledbURI <- "LiverDataRelease\_TileDBArray/"

>

> s3Region <- "us-west-2"

>

> config <- tiledb::tiledb\_config()

> config["vfs.s3.region"] <- s3Region

> ctx <- tiledb::tiledb\_ctx(config)

>

>

> tiledb\_scdataset <- tiledbsc::SOMACollection$new(uri = tiledbURI,

+ verbose = FALSE)

>

>

> names(tiledb\_scdataset$somas)

character(0)

> ## [1] "falsecode" "negprobes" "RNA" "RNA\_normalized"

> names(tiledb\_scdataset$somas$RNA$members)

NULL

> ## [1] "X" "varp" "obs" "varm" "obsp" "uns" "obsm" "var"

>

>

>

>

> ## [1] 1000 793318

>

> ## 4 x 4 sparse Matrix of class "dgTMatrix"

> ## c\_1\_100\_1000 c\_1\_100\_1017 c\_1\_100\_1028 c\_1\_100\_1043

> ## AATK 1 1 2 1

> ## ABL1 . . . .

> ## ABL2 . . . .

> ## ACACB . . . .

>

>

>

>

>

> ## [1] 1000 793318

>

> ## 4 x 4 sparse Matrix of class "dgTMatrix"

> ## c\_1\_100\_1 c\_1\_100\_10 c\_1\_100\_100 c\_1\_100\_1000

> ## AATK -0.1429034 -0.06889529 -0.2645790 7.5780320

> ## ABL1 -0.1972264 -0.09509172 -0.3650734 -0.1790312

> ## ABL2 -0.1667603 -0.08039924 -0.3087212 -0.1513743

> ## ACACB -0.2951553 -0.14233400 -0.5460241 -0.2679370

>

>

>

> metadata <- tiledb\_scdataset$somas$RNA$obs$to\_dataframe()

Error: attempt to apply non-function

> library(ggplot2)

> library(ggpubr)

> library(ggrepel)

> library(gridExtra)

> library(matrixStats)

> library(patchwork)

> library(pheatmap)

> library(Seurat)

> library(RColorBrewer)

> library(reshape2)

> if (!require("tiledb", quietly = TRUE))

+ remotes::install\_github("TileDB-Inc/TileDB-R", force = TRUE)

>

> if (!require("tiledbsc", quietly = TRUE))

+ remotes::install\_github("tiledb-inc/tiledbsc", force = TRUE)

>

> library(tiledb)

> library(tiledbsc)

>

> tiledbURI <- "LiverDataRelease\_TileDBArray/"

>

> s3Region <- "us-west-2"

>

> config <- tiledb::tiledb\_config()

> config["vfs.s3.region"] <- s3Region

> ctx <- tiledb::tiledb\_ctx(config)

>

>

> tiledb\_scdataset <- tiledbsc::SOMACollection$new(uri = tiledbURI,

+ verbose = FALSE)

>

>

> names(tiledb\_scdataset$somas)

character(0)

> ## [1] "falsecode" "negprobes" "RNA" "RNA\_normalized"

> names(tiledb\_scdataset$somas$RNA$members)

NULL

> ## [1] "X" "varp" "obs" "varm" "obsp" "uns" "obsm" "var"

>

>

>

>

> ## [1] 1000 793318

>

> ## 4 x 4 sparse Matrix of class "dgTMatrix"

> ## c\_1\_100\_1000 c\_1\_100\_1017 c\_1\_100\_1028 c\_1\_100\_1043

> ## AATK 1 1 2 1

> ## ABL1 . . . .

> ## ABL2 . . . .

> ## ACACB . . . .

>

>

>

>

>

> ## [1] 1000 793318

>

> ## 4 x 4 sparse Matrix of class "dgTMatrix"

> ## c\_1\_100\_1 c\_1\_100\_10 c\_1\_100\_100 c\_1\_100\_1000

> ## AATK -0.1429034 -0.06889529 -0.2645790 7.5780320

> ## ABL1 -0.1972264 -0.09509172 -0.3650734 -0.1790312

> ## ABL2 -0.1667603 -0.08039924 -0.3087212 -0.1513743

> ## ACACB -0.2951553 -0.14233400 -0.5460241 -0.2679370

>

>

>

>

> ## [1] 793318 63

>

>

>

> ## RNA\_pca\_cluster\_default RNA\_pca\_cluster\_default.1 orig.ident nCount\_RNA nFeature\_RNA nCount\_negprobes

> ## c\_1\_100\_1 16 20 c 142 77 0

> ## c\_1\_100\_10 13 15 c 33 26 0

> ## c\_1\_100\_100 3 7 c 487 143 0

> ## c\_1\_100\_1000 13 16 c 117 69 0

> ## nFeature\_negprobes nCount\_falsecode nFeature\_falsecode fov

> ## c\_1\_100\_1 0 0 0 100

> ## c\_1\_100\_10 0 5 5 100

> ## c\_1\_100\_100 0 1 1 100

> ## c\_1\_100\_1000

>

> cellCoords <- tiledb\_scdataset$somas$RNA$obs$to\_dataframe(

+ attrs = c("x\_FOV\_px", "y\_FOV\_px", "x\_slide\_mm", "y\_slide\_mm",

+ "slide\_ID\_numeric", "Run\_Tissue\_name", "fov"))

Error: attempt to apply non-function

> library(ggplot2)

> library(ggpubr)

> library(ggrepel)

> library(gridExtra)

> library(matrixStats)

> library(patchwork)

> library(pheatmap)

> library(Seurat)

> library(RColorBrewer)

> library(reshape2)

> if (!require("tiledb", quietly = TRUE))

+ remotes::install\_github("TileDB-Inc/TileDB-R", force = TRUE)

>

> if (!require("tiledbsc", quietly = TRUE))

+ remotes::install\_github("tiledb-inc/tiledbsc", force = TRUE)

>

> library(tiledb)

> library(tiledbsc)

>

> tiledbURI <- "LiverDataRelease\_TileDBArray/"

>

> s3Region <- "us-west-2"

>

> config <- tiledb::tiledb\_config()

> config["vfs.s3.region"] <- s3Region

> ctx <- tiledb::tiledb\_ctx(config)

>

>

> tiledb\_scdataset <- tiledbsc::SOMACollection$new(uri = tiledbURI,

+ verbose = FALSE)

>

>

> names(tiledb\_scdataset$somas)

character(0)

> ## [1] "falsecode" "negprobes" "RNA" "RNA\_normalized"

> names(tiledb\_scdataset$somas$RNA$members)

NULL

> ## [1] "X" "varp" "obs" "varm" "obsp" "uns" "obsm" "var"

>

>

>

>

> ## [1] 1000 793318

>

> ## 4 x 4 sparse Matrix of class "dgTMatrix"

> ## c\_1\_100\_1000 c\_1\_100\_1017 c\_1\_100\_1028 c\_1\_100\_1043

> ## AATK 1 1 2 1

> ## ABL1 . . . .

> ## ABL2 . . . .

> ## ACACB . . . .

>

>

>

>

>

> ## [1] 1000 793318

>

> ## 4 x 4 sparse Matrix of class "dgTMatrix"

> ## c\_1\_100\_1 c\_1\_100\_10 c\_1\_100\_100 c\_1\_100\_1000

> ## AATK -0.1429034 -0.06889529 -0.2645790 7.5780320

> ## ABL1 -0.1972264 -0.09509172 -0.3650734 -0.1790312

> ## ABL2 -0.1667603 -0.08039924 -0.3087212 -0.1513743

> ## ACACB -0.2951553 -0.14233400 -0.5460241 -0.2679370

>

>

>

>

> ## [1] 793318 63

>

>

>

> ## RNA\_pca\_cluster\_default RNA\_pca\_cluster\_default.1 orig.ident nCount\_RNA nFeature\_RNA nCount\_negprobes

> ## c\_1\_100\_1 16 20 c 142 77 0

> ## c\_1\_100\_10 13 15 c 33 26 0

> ## c\_1\_100\_100 3 7 c 487 143 0

> ## c\_1\_100\_1000 13 16 c 117 69 0

> ## nFeature\_negprobes nCount\_falsecode nFeature\_falsecode fov

> ## c\_1\_100\_1 0 0 0 100

> ## c\_1\_100\_10 0 5 5 100

> ## c\_1\_100\_100 0 1 1 100

> ## c\_1\_100\_1000

>

>

>

>

> ## x\_FOV\_px y\_FOV\_px x\_slide\_mm y\_slide\_mm slide\_ID\_numeric Run\_Tissue\_name fov

> ## c\_1\_100\_1 42 36 8.70804 9.73368 1 NormalLiver 100

> ## c\_1\_100\_10 2737 25 9.03144 9.73500 1 NormalLiver 100

> ## c\_1\_100\_100 2888 409 9.04956 9.68892 1 NormalLiver 100

> ## c\_1\_100\_1000 3457 3742 9.11784 9.28896 1 NormalLiver 100

> ## c\_1\_100\_1001 1298 3763 8.85876 9.28644 1 NormalLiver 100

> ## c\_1\_100\_1002 1001 3738 8.82312 9.28944 1 NormalLiver 100

> ggplot(cellCoords, aes(x=x\_slide\_mm, y=y\_slide\_mm))+

+ geom\_point(alpha = 0.05, size = 0.01)+

+ facet\_wrap(~Run\_Tissue\_name)+

+ coord\_equal()+

+ labs(title = "Cell coordinates in XY space")

Error: object 'cellCoords' not found