Marm\_Tables\_2025-5-24\_SA

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# Setup and Datasets

global <- config::get(config = "default")  
  
here::i\_am("Marm\_Tables\_2025-5-24\_SA.Rmd")

## here() starts at C:/Users/shayda/Documents/work/marm\_bioinfo

source(here::here(global$setup))

## All required packages are already installed.

## Warning: package 'knitr' was built under R version 4.3.3

## Warning: package 'ape' was built under R version 4.3.3

## Warning: package 'bibtex' was built under R version 4.3.3

## Warning: package 'BiocManager' was built under R version 4.3.3

## Warning in file(con, "r"): URL 'https://bioconductor.org/config.yaml': status  
## was 'Couldn't resolve host name'

## Bioconductor version '3.17' is out-of-date; the current release version '3.21'  
## is available with R version '4.5'; see https://bioconductor.org/install

## Warning: package 'bookdown' was built under R version 4.3.3

## Warning: package 'bsicons' was built under R version 4.3.3

## Warning: package 'bslib' was built under R version 4.3.3

##   
## Attaching package: 'bslib'

## The following object is masked from 'package:utils':  
##   
## page

## Warning: package 'config' was built under R version 4.3.3

## Do not use `library(config)` to attach the config package.  
## Use `config::get()` directly.  
## Attaching the config package can lead to namespace conflicts.

##   
## Attaching package: 'config'

## The following objects are masked from 'package:base':  
##   
## get, merge

## Warning: package 'conflicted' was built under R version 4.3.3

## Warning: package 'crosstalk' was built under R version 4.3.3

## Warning: package 'data.table' was built under R version 4.3.3

## Warning: package 'devtools' was built under R version 4.3.3

## Loading required package: usethis

## Warning: package 'usethis' was built under R version 4.3.3

## Warning: package 'fontawesome' was built under R version 4.3.3

## Warning: package 'forcats' was built under R version 4.3.3

## Warning: package 'ggtext' was built under R version 4.3.3

## Warning: package 'gt' was built under R version 4.3.3

## Warning: package 'gtExtras' was built under R version 4.3.3

## Warning: package 'gtable' was built under R version 4.3.3

## Warning: package 'hms' was built under R version 4.3.3

## Warning: package 'htmltools' was built under R version 4.3.3

## Warning: package 'htmlwidgets' was built under R version 4.3.3

## Warning: package 'kableExtra' was built under R version 4.3.3

## Warning: package 'lmerTest' was built under R version 4.3.3

## Loading required package: lme4

## Loading required package: Matrix

## Warning: package 'lubridate' was built under R version 4.3.3

## Warning: package 'magrittr' was built under R version 4.3.3

## Warning: package 'paletteer' was built under R version 4.3.3

## Warning: package 'pander' was built under R version 4.3.3

## Warning: package 'pandoc' was built under R version 4.3.3

## Registered S3 methods overwritten by 'treeio':  
## method from   
## MRCA.phylo tidytree  
## MRCA.treedata tidytree  
## Nnode.treedata tidytree  
## Ntip.treedata tidytree  
## ancestor.phylo tidytree  
## ancestor.treedata tidytree  
## child.phylo tidytree  
## child.treedata tidytree  
## full\_join.phylo tidytree  
## full\_join.treedata tidytree  
## groupClade.phylo tidytree  
## groupClade.treedata tidytree  
## groupOTU.phylo tidytree  
## groupOTU.treedata tidytree  
## inner\_join.phylo tidytree  
## inner\_join.treedata tidytree  
## is.rooted.treedata tidytree  
## nodeid.phylo tidytree  
## nodeid.treedata tidytree  
## nodelab.phylo tidytree  
## nodelab.treedata tidytree  
## offspring.phylo tidytree  
## offspring.treedata tidytree  
## parent.phylo tidytree  
## parent.treedata tidytree  
## root.treedata tidytree  
## rootnode.phylo tidytree  
## sibling.phylo tidytree

## Warning: package 'rcompanion' was built under R version 4.3.3

## Warning: package 'reactable' was built under R version 4.3.3

## Warning: package 'rmarkdown' was built under R version 4.3.3

## Warning: package 'sass' was built under R version 4.3.3

## Warning: package 'scales' was built under R version 4.3.2

## Warning: package 'seqinr' was built under R version 4.3.3

## Warning: package 'shinydashboard' was built under R version 4.3.3

## Warning: package 'shinyjs' was built under R version 4.3.3

## Warning: package 'shinyMatrix' was built under R version 4.3.3

## Warning: package 'shinyTime' was built under R version 4.3.3

## Warning: package 'showtext' was built under R version 4.3.3

## Loading required package: sysfonts

## Warning: package 'sysfonts' was built under R version 4.3.3

## Loading required package: showtextdb

## Warning: package 'showtextdb' was built under R version 4.3.3

## Warning: package 'thematic' was built under R version 4.3.3

## Warning: package 'tidyverse' was built under R version 4.3.3

## Warning: package 'ggplot2' was built under R version 4.3.3

## Warning: package 'tidyr' was built under R version 4.3.3

## Warning: package 'readr' was built under R version 4.3.3

## Warning: package 'purrr' was built under R version 4.3.3

## Warning: package 'dplyr' was built under R version 4.3.3

## Warning: package 'stringr' was built under R version 4.3.3

## ── Attaching core tidyverse packages ──────────────────────── tidyverse 2.0.0 ──  
## ✔ dplyr 1.1.4 ✔ stringr 1.5.1  
## ✔ ggplot2 3.5.1 ✔ tibble 3.2.1  
## ✔ purrr 1.0.2 ✔ tidyr 1.3.1  
## ✔ readr 2.1.5

## Warning: package 'utf8' was built under R version 4.3.2

## Warning: package 'rmdformats' was built under R version 4.3.3

## Warning: package 'agricolae' was built under R version 4.3.3

## Warning: package 'aplot' was built under R version 4.3.3

## Warning: package 'Boruta' was built under R version 4.3.3

## Warning: package 'brms' was built under R version 4.3.3

## Loading required package: Rcpp

## Warning: package 'Rcpp' was built under R version 4.3.3

## Loading 'brms' package (version 2.21.0). Useful instructions  
## can be found by typing help('brms'). A more detailed introduction  
## to the package is available through vignette('brms\_overview').

## Warning: package 'caret' was built under R version 4.3.3

## Loading required package: lattice

## Warning: package 'lattice' was built under R version 4.3.3

## Loading required package: S4Vectors

## Loading required package: stats4

## Loading required package: BiocGenerics

##   
## Attaching package: 'BiocGenerics'

## The following objects are masked from 'package:dplyr':  
##   
## combine, intersect, setdiff, union

## The following objects are masked from 'package:lubridate':  
##   
## intersect, setdiff, union

## The following object is masked from 'package:config':  
##   
## get

## The following objects are masked from 'package:stats':  
##   
## IQR, mad, sd, var, xtabs

## The following objects are masked from 'package:base':  
##   
## anyDuplicated, aperm, append, as.data.frame, basename, cbind,  
## colnames, dirname, do.call, duplicated, eval, evalq, Filter, Find,  
## get, grep, grepl, intersect, is.unsorted, lapply, Map, mapply,  
## match, mget, order, paste, pmax, pmax.int, pmin, pmin.int,  
## Position, rank, rbind, Reduce, rownames, sapply, setdiff, sort,  
## table, tapply, union, unique, unsplit, which.max, which.min

##   
## Attaching package: 'S4Vectors'

## The following objects are masked from 'package:dplyr':  
##   
## first, rename

## The following object is masked from 'package:tidyr':  
##   
## expand

## The following objects are masked from 'package:lubridate':  
##   
## second, second<-

## The following objects are masked from 'package:Matrix':  
##   
## expand, unname

## The following objects are masked from 'package:data.table':  
##   
## first, second

## The following object is masked from 'package:utils':  
##   
## findMatches

## The following objects are masked from 'package:base':  
##   
## expand.grid, I, unname

## Loading required package: IRanges

##   
## Attaching package: 'IRanges'

## The following objects are masked from 'package:dplyr':  
##   
## collapse, desc, slice

## The following object is masked from 'package:purrr':  
##   
## reduce

## The following object is masked from 'package:phyloseq':  
##   
## distance

## The following object is masked from 'package:lubridate':  
##   
## %within%

## The following object is masked from 'package:glue':  
##   
## trim

## The following object is masked from 'package:data.table':  
##   
## shift

## The following object is masked from 'package:grDevices':  
##   
## windows

## Loading required package: GenomicRanges

## Loading required package: GenomeInfoDb

##   
## Attaching package: 'GenomicRanges'

## The following object is masked from 'package:magrittr':  
##   
## subtract

## Loading required package: SummarizedExperiment

## Loading required package: MatrixGenerics

## Loading required package: matrixStats

## Warning: package 'matrixStats' was built under R version 4.3.3

##   
## Attaching package: 'matrixStats'

## The following object is masked from 'package:dplyr':  
##   
## count

## The following object is masked from 'package:seqinr':  
##   
## count

##   
## Attaching package: 'MatrixGenerics'

## The following objects are masked from 'package:matrixStats':  
##   
## colAlls, colAnyNAs, colAnys, colAvgsPerRowSet, colCollapse,  
## colCounts, colCummaxs, colCummins, colCumprods, colCumsums,  
## colDiffs, colIQRDiffs, colIQRs, colLogSumExps, colMadDiffs,  
## colMads, colMaxs, colMeans2, colMedians, colMins, colOrderStats,  
## colProds, colQuantiles, colRanges, colRanks, colSdDiffs, colSds,  
## colSums2, colTabulates, colVarDiffs, colVars, colWeightedMads,  
## colWeightedMeans, colWeightedMedians, colWeightedSds,  
## colWeightedVars, rowAlls, rowAnyNAs, rowAnys, rowAvgsPerColSet,  
## rowCollapse, rowCounts, rowCummaxs, rowCummins, rowCumprods,  
## rowCumsums, rowDiffs, rowIQRDiffs, rowIQRs, rowLogSumExps,  
## rowMadDiffs, rowMads, rowMaxs, rowMeans2, rowMedians, rowMins,  
## rowOrderStats, rowProds, rowQuantiles, rowRanges, rowRanks,  
## rowSdDiffs, rowSds, rowSums2, rowTabulates, rowVarDiffs, rowVars,  
## rowWeightedMads, rowWeightedMeans, rowWeightedMedians,  
## rowWeightedSds, rowWeightedVars

## Loading required package: Biobase

## Welcome to Bioconductor  
##   
## Vignettes contain introductory material; view with  
## 'browseVignettes()'. To cite Bioconductor, see  
## 'citation("Biobase")', and for packages 'citation("pkgname")'.

##   
## Attaching package: 'Biobase'

## The following object is masked from 'package:MatrixGenerics':  
##   
## rowMedians

## The following objects are masked from 'package:matrixStats':  
##   
## anyMissing, rowMedians

## The following object is masked from 'package:phyloseq':  
##   
## sampleNames

## Loading required package: limma

##   
## Attaching package: 'limma'

## The following object is masked from 'package:DESeq2':  
##   
## plotMA

## The following object is masked from 'package:BiocGenerics':  
##   
## plotMA

## The following object is masked from 'package:seqinr':  
##   
## zscore

## Warning: package 'file2meco' was built under R version 4.3.3

## Warning: package 'FSA' was built under R version 4.3.3

## ## FSA v0.9.5. See citation('FSA') if used in publication.  
## ## Run fishR() for related website and fishR('IFAR') for related book.

## Warning: package 'ggalluvial' was built under R version 4.3.3

## Warning: package 'GGally' was built under R version 4.3.3

## Registered S3 method overwritten by 'GGally':  
## method from   
## +.gg ggplot2

## Warning: package 'ggdendro' was built under R version 4.3.3

## Warning: package 'ggtern' was built under R version 4.3.3

## Registered S3 methods overwritten by 'ggtern':  
## method from   
## grid.draw.ggplot ggplot2  
## plot.ggplot ggplot2  
## print.ggplot ggplot2

## --  
## Remember to cite, run citation(package = 'ggtern') for further info.  
## --

## ggtree v3.8.2 For help: https://yulab-smu.top/treedata-book/  
##   
## If you use the ggtree package suite in published research, please cite  
## the appropriate paper(s):  
##   
## Guangchuang Yu, David Smith, Huachen Zhu, Yi Guan, Tommy Tsan-Yuk Lam.  
## ggtree: an R package for visualization and annotation of phylogenetic  
## trees with their covariates and other associated data. Methods in  
## Ecology and Evolution. 2017, 8(1):28-36. doi:10.1111/2041-210X.12628  
##   
## Guangchuang Yu, Tommy Tsan-Yuk Lam, Huachen Zhu, Yi Guan. Two methods  
## for mapping and visualizing associated data on phylogeny using ggtree.  
## Molecular Biology and Evolution. 2018, 35(12):3041-3043.  
## doi:10.1093/molbev/msy194  
##   
## LG Wang, TTY Lam, S Xu, Z Dai, L Zhou, T Feng, P Guo, CW Dunn, BR  
## Jones, T Bradley, H Zhu, Y Guan, Y Jiang, G Yu. treeio: an R package  
## for phylogenetic tree input and output with richly annotated and  
## associated data. Molecular Biology and Evolution. 2020, 37(2):599-603.  
## doi: 10.1093/molbev/msz240

## Warning: package 'glmmTMB' was built under R version 4.3.3

## Warning in checkMatrixPackageVersion(getOption("TMB.check.Matrix", TRUE)): Package version inconsistency detected.  
## TMB was built with Matrix ABI version 1  
## Current Matrix ABI version is 0  
## Please re-install 'TMB' from source using install.packages('TMB', type = 'source') or ask CRAN for a binary version of 'TMB' matching CRAN's 'Matrix' package

## Warning: package 'GUniFrac' was built under R version 4.3.3

## Registered S3 method overwritten by 'rmutil':  
## method from  
## print.response httr

## Warning: package 'igraph' was built under R version 4.3.3

## Warning: package 'job' was built under R version 4.3.3

## Warning: package 'mecoturn' was built under R version 4.3.3

## Registered S3 methods overwritten by 'car':  
## method from  
## hist.boot FSA   
## confint.boot FSA

## Loading required package: glmnet

## Warning: package 'glmnet' was built under R version 4.3.3

## Loaded glmnet 4.1-8

## Loading required package: RColorBrewer

## Registered S3 method overwritten by 'gplots':  
## method from   
## reorder.factor DescTools

## Warning: package 'MicrobiomeStat' was built under R version 4.3.3

## Warning: package 'multiROC' was built under R version 4.3.3

## Loading required package: SpiecEasi

## Registered S3 methods overwritten by 'huge':  
## method from  
## plot.roc pROC  
## plot.sim lava  
## print.roc pROC  
## print.sim lava

##   
## Attaching package: 'SpiecEasi'

## The following object is masked from 'package:igraph':  
##   
## make\_graph

## The following object is masked from 'package:seqinr':  
##   
## alr

## The following objects are masked from 'package:Matrix':  
##   
## tril, triu

## The following object is masked from 'package:MASS':  
##   
## fitdistr

##

## Registered S3 method overwritten by 'psych':  
## method from   
## plot.residuals rmutil

## Warning: package 'networkD3' was built under R version 4.3.3

## Warning: package 'NST' was built under R version 4.3.3

## Warning: package 'patchwork' was built under R version 4.3.3

## Warning: package 'performance' was built under R version 4.3.3

## Warning: package 'picante' was built under R version 4.3.3

## Loading required package: vegan

## Warning: package 'vegan' was built under R version 4.3.3

## Loading required package: permute

## Warning: package 'permute' was built under R version 4.3.3

##   
## Attaching package: 'permute'

## The following object is masked from 'package:igraph':  
##   
## permute

## The following object is masked from 'package:seqinr':  
##   
## getType

## The following object is masked from 'package:devtools':  
##   
## check

##   
## Attaching package: 'vegan'

## The following object is masked from 'package:igraph':  
##   
## diversity

## The following object is masked from 'package:caret':  
##   
## tolerance

## Loading required package: nlme

## Warning: package 'nlme' was built under R version 4.3.3

##   
## Attaching package: 'nlme'

## The following object is masked from 'package:ggtree':  
##   
## collapse

## The following object is masked from 'package:IRanges':  
##   
## collapse

## The following object is masked from 'package:dplyr':  
##   
## collapse

## The following object is masked from 'package:seqinr':  
##   
## gls

## The following object is masked from 'package:lme4':  
##   
## lmList

## Warning: package 'poweRlaw' was built under R version 4.3.3

## Warning: package 'randomForest' was built under R version 4.3.3

## randomForest 4.7-1.1

## Type rfNews() to see new features/changes/bug fixes.

## Warning: package 'rfPermute' was built under R version 4.3.3

## Welcome to rfPermute v2.5.2  
## See rfPermuteTutorial() for a guide to the package.

## Warning: package 'rgexf' was built under R version 4.3.3

## Warning: package 'rsample' was built under R version 4.3.3

## Warning: package 'SRS' was built under R version 4.3.3

## Loading required package: shiny

## Warning: package 'shiny' was built under R version 4.3.3

##   
## Attaching package: 'shiny'

## The following object is masked from 'package:shinyjs':  
##   
## runExample

## The following object is masked from 'package:seqinr':  
##   
## a

## The following object is masked from 'package:pander':  
##   
## p

## The following object is masked from 'package:crosstalk':  
##   
## getDefaultReactiveDomain

## Loading required package: DT

## Warning: package 'DT' was built under R version 4.3.3

##   
## Attaching package: 'DT'

## The following objects are masked from 'package:shiny':  
##   
## dataTableOutput, renderDataTable

## The following object is masked from 'package:networkD3':  
##   
## JS

## Loading required package: shinycssloaders

## Warning: package 'shinycssloaders' was built under R version 4.3.3

## Loading required package: shinybusy

## Warning: package 'shinybusy' was built under R version 4.3.3

## Warning: package 'TreeTools' was built under R version 4.3.3

## Registered S3 method overwritten by 'TreeTools':  
## method from   
## [.phyDat phangorn

## Warning: package 'WGCNA' was built under R version 4.3.3

## Loading required package: dynamicTreeCut

## Loading required package: fastcluster

## Warning: package 'fastcluster' was built under R version 4.3.2

##   
## Attaching package: 'fastcluster'

## The following object is masked from 'package:stats':  
##   
## hclust

## [conflicted] Will prefer dplyr::filter over any other package.  
## [conflicted] Will prefer dplyr::select over any other package.  
## [conflicted] Will prefer dplyr::left\_join over any other package.  
## [conflicted] Will prefer dplyr::inner\_join over any other package.  
## [conflicted] Will prefer dplyr::full\_join over any other package.  
## [conflicted] Will prefer dplyr::semi\_join over any other package.  
## [conflicted] Will prefer dplyr::rename over any other package.  
## [conflicted] Will prefer dplyr::setdiff over any other package.  
## [conflicted] Will prefer ggplot2::margin over any other package.  
## [conflicted] Will prefer ggplot2::theme\_classic over any other package.  
## [conflicted] Will prefer ggplot2::ggplot over any other package.  
## [conflicted] Will prefer ggplot2::theme\_minimal over any other package.  
## [conflicted] Will prefer ggplot2::aes over any other package.  
## [conflicted] Will prefer dplyr::lag over any other package.  
## [conflicted] Will prefer RefManageR::cite over any other package.  
## [conflicted] Will prefer shinydashboard::box over any other package.  
## [conflicted] Will prefer rlang::set\_names over any other package.  
## [conflicted] Will prefer purrr::flatten over any other package.  
## [conflicted] Will prefer purrr::discard\_at over any other package.  
## [conflicted] Will prefer base::which.max over any other package.  
## [conflicted] Will prefer lubridate::month over any other package.  
## [conflicted] Will prefer lubridate::year over any other package.  
## [conflicted] Will prefer lubridate::day over any other package.  
## [conflicted] Will prefer base::as.data.frame over any other package.  
## [conflicted] Will prefer htmltools::p over any other package.  
## [conflicted] Will prefer htmlwidgets::JS over any other package.  
## [conflicted] Will prefer dplyr::count over any other package.  
## [conflicted] Will prefer lubridate::mday over any other package.  
## [conflicted] Will prefer ggplot2::ggsave over any other package.

# Diet Table

marm\_foods <- list(  
 "Zupreem^\u00AE Marmoset Diet" = list(  
 "Commercially formulated diet made up of wheat, soybean, egg, alfalfa, and various vitamins",  
 1,  
 "slice"  
 ),  
 "Mazuri^\u00AE Callitrichid Gel Diet" = list(  
 "Commercially formulated diet made up of soybean, corn, wheat, gelatin, and various vitamins",  
 1,  
 "slice"  
 ),  
 "Apple" = list(  
 "Cut into 1-cm^2 cubes",  
 4,  
 "pieces"  
 ),  
 "Sweet Potato" = list(  
 "Cut into 1-cm^2 cubes",  
 4,  
 "pieces"  
 ),  
 "Eggs" = list(  
 "Scrambled and microwave-cooked",  
 2,  
 "tsp"  
 )  
) %>%  
 enframe(name = "Food\_Item", value = "Details") %>%  
 unnest\_wider(Details, names\_sep = "\_") %>%  
 rename(Details = Details\_1, Amount = Details\_2, Unit = Details\_3) %>%  
 gt(rowname\_col = "Food\_Item") %>%  
 fmt\_units() %>%  
 cols\_merge(columns = c("Amount", "Unit"), pattern = "{1} {2}") %>%  
 tab\_stubhead("Food Item") %>%  
   
 cols\_width(  
 stub() ~ px(250),  
 Details ~ px(400),  
 Amount ~ px(100)  
 ) %>%  
   
 cols\_align("left") %>%  
   
 opt\_stylize(style = 3,  
 color = "blue") %>%  
   
 tab\_style(style = cell\_text(weight = "bold",  
 v\_align = "top"),  
 locations = cells\_stub()) %>%  
   
 tab\_style(style = cell\_text(v\_align = "top"),  
 locations = cells\_body()) %>%  
   
 tab\_header(title = "Table 2",  
 subtitle = "Standardized Diet per Marmoset Pair") %>%  
   
 tab\_style(style = cell\_text(align = "left",  
 style = "italic",  
 size = "18px"),  
 locations = cells\_title(groups = "subtitle")) %>%  
   
 tab\_style(style = cell\_text(align = "left",  
 weight = "bold",  
 size = "18px"),  
 locations = cells\_title(groups = "title"))  
marm\_foods

Table 1: Table 2

Standardized Diet per Marmoset Pair

| Food Item | Details | Amount |
| --- | --- | --- |
| **Zupreem<w:r><w:rPr><w:vertAlign w:val="superscript"></w:vertAlign></w:rPr><w:t xml:space="default">®</w:t></w:r> Marmoset Diet** | Commercially formulated diet made up of wheat, soybean, egg, alfalfa, and various vitamins | 1 slice |
| **Mazuri<w:r><w:rPr><w:vertAlign w:val="superscript"></w:vertAlign></w:rPr><w:t xml:space="default">®</w:t></w:r> Callitrichid Gel Diet** | Commercially formulated diet made up of soybean, corn, wheat, gelatin, and various vitamins | 1 slice |
| **Apple** | Cut into 1-cm<w:r><w:rPr><w:vertAlign w:val="superscript"></w:vertAlign></w:rPr><w:t xml:space="default">2</w:t></w:r> cubes | 4 pieces |
| **Sweet Potato** | Cut into 1-cm<w:r><w:rPr><w:vertAlign w:val="superscript"></w:vertAlign></w:rPr><w:t xml:space="default">2</w:t></w:r> cubes | 4 pieces |
| **Eggs** | Scrambled and microwave-cooked | 2 tsp |

marm\_diet\_trials <- list(  
 list(  
 "Days" = c(1, 14),  
 "Trials" = list(  
 "Group 1" = "Run-in",  
 "Group 2" = "Run-in"  
 )  
 ),  
 list(  
 "Days" = c(15, 28),  
 "Trials" = list(  
 "Group 1" = "Intervention",  
 "Group 2" = "Control"  
 )  
 ),  
 list(  
 "Days" = c(29, 42),  
 "Trials" = list(  
 "Group 1" = "Washout",  
 "Group 2" = "Washout"  
 )  
 ),  
 list(  
 "Days" = c(43, 56),  
 "Trials" = list(  
 "Group 1" = "Control",  
 "Group 2" = "Intervention"  
 )  
 ),  
 list(  
 "Days" = c(57, 70),  
 "Trials" = list(  
 "Group 1" = "Washout",  
 "Group 2" = "Washout"  
 )  
 )  
) %>%  
 enframe(name = NULL) %>%  
 unnest\_wider(value) %>%  
 unnest\_wider(Trials) %>%  
 pivot\_longer(c("Group 1", "Group 2"), names\_to = "Group") %>%  
 mutate(Days = str\_replace\_all(str\_remove\_all(as.character(Days), "[c()]"), ", ", " - ")) %>%  
 pivot\_wider(names\_from = "Days", values\_from = "value") %>%  
 gt(rowname\_col = "Group") %>%  
   
 cols\_align("center") %>%  
 tab\_stubhead("Days") %>%  
   
 tab\_header(title = "Table 1",  
 subtitle = "Timeline of Study") %>%  
   
 tab\_style(style = cell\_text(align = "left",  
 style = "italic",  
 size = "18px"),  
 locations = cells\_title(groups = "subtitle")) %>%  
   
 tab\_style(style = cell\_text(align = "left",  
 weight = "bold",  
 size = "18px"),  
 locations = cells\_title(groups = "title")) %>%  
   
 tab\_style(style = cell\_borders(sides = "top",  
 color = "lightgrey",  
 weight = px(2)),  
 locations = cells\_column\_labels()) %>%  
   
 tab\_style(style = cell\_borders(sides = "bottom",  
 color = "lightgrey",  
 weight = px(2)),  
 locations = cells\_column\_labels()) %>%  
   
 tab\_style(style = cell\_borders(sides = "bottom",  
 color = "lightgrey",  
 weight = px(2)),  
 locations = cells\_stubhead()) %>%  
   
 tab\_style(style = cell\_borders(sides = "right",  
 color = "lightgrey",  
 weight = px(2)),  
 locations = cells\_stub()) %>%  
   
 tab\_style(style = cell\_borders(sides = "bottom",  
 color = "lightgrey"),  
 locations = cells\_stub(rows = 1)) %>%  
   
 tab\_style(style = cell\_borders(sides = "bottom",  
 color = "lightgrey"),  
 locations = cells\_body(rows = 1)) %>%  
   
 tab\_style(style = cell\_borders(sides = "right",  
 color = "lightgrey",  
 weight = px(2)),  
 locations = cells\_stubhead()) %>%  
 tab\_style\_body(style = list(cell\_text(transform = "capitalize"),   
 cell\_fill("#F0C6A9")),  
 pattern = "Intervention") %>%  
   
 tab\_style\_body(style = list(cell\_text(transform = "capitalize"),   
 cell\_fill("#B6E9CB")),  
 pattern = "Control") %>%  
   
 tab\_style\_body(style = list(cell\_text(style = "normal"),   
 cell\_fill("#E0EAF2")),  
 pattern = "Washout") %>%  
   
 tab\_style\_body(style = list(cell\_text(style = "normal"),   
 cell\_fill("#F8F3EA")),  
 pattern = "Run-in") %>%  
   
 tab\_style(style = list(cell\_text(size = "small",  
 transform = "capitalize",  
 weight = "bold",  
 color = "#4D4D4D")),  
 locations = cells\_column\_labels()) %>%  
   
 tab\_style(style = list(cell\_text(size = "small",  
 transform = "capitalize",  
 weight = "bold",  
 color = "#4D4D4D")),  
 locations = cells\_stub()) %>%  
   
 tab\_style(style = list(cell\_text(size = "small",  
 transform = "capitalize",  
 weight = "bold",  
 color = "#4D4D4D")),  
 locations = cells\_stubhead()) %>%  
   
 tab\_style(style = list(cell\_text(align = "left"),  
 cell\_borders(sides = "bottom")),  
 locations = cells\_title(groups = "subtitle"))  
  
marm\_diet\_trials

Table 1: Table 1

Timeline of Study

| Days | 1 - 14 | 15 - 28 | 29 - 42 | 43 - 56 | 57 - 70 |
| --- | --- | --- | --- | --- | --- |
| **Group 1** | Run-in | Intervention | Washout | Control | Washout |
| **Group 2** | Run-in | Control | Washout | Intervention | Washout |