Lab 5: Spatial Statistics

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Section 5.4 Exercise

https://bookdown.org/hhwagner1/LandGenCourse_book/r-exercise-week-2.html

a. Load libraries

```r
library(LandGenCourse)
#library(EcoGenetics)
library(GeNetIt)
```

```
## Loading required package: nlme
```

```r
library(hierfstat)
library(adegenet)
```

```
## Loading required package: ade4
##
##    /// adegenet 2.1.10 is loaded ////////////
##
##    > overview: '?adegenet'
##    > tutorials/doc/questions: 'adegenetWeb()'
##    > bug reports/feature requests: adegenetIssues()
##
## Attaching package: 'adegenet'
## The following objects are masked from 'package:hierfstat':
##
##     Hs, read.fstat
```

```r
require(gstudio)
```

```
## Loading required package: gstudio
## Warning: replacing previous import 'dplyr::union' by 'raster::union' when
## loading 'gstudio'
## Warning: replacing previous import 'dplyr::intersect' by 'raster::intersect'
## when loading 'gstudio'
## Warning: replacing previous import 'dplyr::select' by 'raster::select' when
## loading 'gstudio'
##
## Attaching package: 'gstudio'
```

```
## The following objects are masked from 'package:adegenet':
##
##     alleles, ploidy

## The following object is masked from 'package:hierfstat':
##
##     Ho
```

```r
require(dplyr)
```

```
## Loading required package: dplyr

##
## Attaching package: 'dplyr'

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

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

```r
require(tibble)
```

```
## Loading required package: tibble
```

```r
require(sf)
```

```
## Loading required package: sf

## Linking to GEOS 3.10.2, GDAL 3.4.1, PROJ 8.2.1; sf_use_s2() is TRUE
```

```r
require(popgraph)
```

```
## Loading required package: popgraph
```

```r
require(RgoogleMaps)
```

```
## Loading required package: RgoogleMaps

##
## Thank you for using RgoogleMaps!

##
## To acknowledge our work, please cite the package:

##  Markus Loecher and Karl Ropkins (2015). RgoogleMaps and loa: Unleashing R
##   Graphics Power on Map Tiles. Journal of Statistical Software 63(4), 1-18.
```

```r
require(geosphere)
```

```
## Loading required package: geosphere
```

```r
require(proto)
```

```
## Loading required package: proto
```

```r
require(sampling)
```

```
## Loading required package: sampling

##
## Attaching package: 'sampling'

## The following object is masked from 'package:adegenet':
##
##      strata
```

```r
require(seqinr)
```

```
## Loading required package: seqinr

##
## Attaching package: 'seqinr'

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

## The following object is masked from 'package:nlme':
##
##      gls
```

```r
require(spacetime)
```

```
## Loading required package: spacetime
```

```r
require(spdep)
```

```
## Loading required package: spdep

## Loading required package: spData

## To access larger datasets in this package, install the spDataLarge
## package with: 'install.packages('spDataLarge',
## repos='https://nowosad.github.io/drat/', type='source')'

## Registered S3 method overwritten by 'spdep':
##   method    from
##   plot.mst ape

##
## Attaching package: 'spdep'

## The following object is masked from 'package:ade4':
##
##      mstree
```

```r
require(here)
```

```
## Loading required package: here

## here() starts at /uufs/chpc.utah.edu/common/home/u6036559/git/usu-biol4750
```

b. Import to adegenet object with gstudio

```r
library(gstudio)
library(adegenet)

# 1. CSV file "./downloads/pulsatilla_genotypes.csv" --> data frame
# with "gstudio" function read_population()
g.Flr <- read_population("./downloads/pulsatilla_genotypes.csv",
```

```r
                        type = "column",locus.columns = c(6:19))

# 2. Select only adults with base R indexing of data frame
# rows where OffID==0, all columns
g.Flr <- g.Flr[g.Flr$OffID==0,]

# 3. Nothing to do here

# 4. Create genind object with "adegenet" function df2genind()
# using NA.char = ""
g.Flr.genind <- df2genind(X=g.Flr[,c(6:12)], sep=":", ncode=NULL, ind.names=g.Flr$ID, loc.names=NULL, p

# 5. Check genind object
g.Flr.genind
```

```
## /// GENIND OBJECT /////////
##
##  // 221 individuals; 7 loci; 105 alleles; size: 129.8 Kb
##
##  // Basic content
##    @tab:  221 x 105 matrix of allele counts
##    @loc.n.all: number of alleles per locus (range: 8-25)
##    @loc.fac: locus factor for the 105 columns of @tab
##    @all.names: list of allele names for each locus
##    @ploidy: ploidy of each individual  (range: 2-2)
##    @type:  codom
##    @call: df2genind(X = g.Flr[, c(6:12)], sep = ":", ncode = NULL, ind.names = g.Flr$ID,
##     loc.names = NULL, pop = g.Flr$Population, NA.char = "", ploidy = 2,
##     type = "codom", strata = NULL, hierarchy = NULL)
##
##  // Optional content
##    @pop: population of each individual (group size range: 14-56)
```

```r
summary(g.Flr.genind)
```

```
##
## // Number of individuals: 221
## // Group sizes: 21 56 21 22 14 42 45
## // Number of alleles per locus: 18 8 25 8 19 14 13
## // Number of alleles per group: 63 68 54 50 51 73 53
## // Percentage of missing data: 0.9 %
## // Observed heterozygosity: 0.74 0.54 0.89 0.71 0.74 0.68 0.74
## // Expected heterozygosity: 0.83 0.57 0.89 0.74 0.81 0.76 0.83
```

Without G-Studio, Drop offspring Using adegenet and base R

```r
library(adegenet)

# 1. CSV file "./downloads/pulsatilla_genotypes.csv" --> data frame
# with base R function read.csv()
Flr <- read.csv("./downloads/pulsatilla_genotypes.csv", header=TRUE)

# 2. Select only adults with base R indexing of data frame
# rows where OffID==0, all columns
Flr <- Flr[Flr$OffID==0,]
```

```
# 3. Combine columns with base R function paste()
Flr <- data.frame(Flr[,1:5],loc1 = paste(Flr[,6],  Flr[,7], sep=":"),
                            loc2 = paste(Flr[,8],  Flr[,9], sep=":"),
                            loc3 = paste(Flr[,10], Flr[,11], sep=":"),
                            loc4 = paste(Flr[,12], Flr[,13], sep=":"),
                            loc5 = paste(Flr[,14], Flr[,15], sep=":"),
                            loc6 = paste(Flr[,16], Flr[,17], sep=":"),
                            loc7 = paste(Flr[,18], Flr[,19], sep=":"))
# 4. Create genind object with "adegenet" function df2genind()
# using NA.char = "NA"
Flr.genind <- df2genind(X=Flr[,c(6:12)], sep=":", ncode=NULL, ind.names= Flr$ID, loc.names=names(Flr[,c

# 5. Check genind object
Flr.genind
```

```
## /// GENIND OBJECT /////////
##
##  // 221 individuals; 7 loci; 105 alleles; size: 130.8 Kb
##
##  // Basic content
##    @tab:  221 x 105 matrix of allele counts
##    @loc.n.all: number of alleles per locus (range: 8-25)
##    @loc.fac: locus factor for the 105 columns of @tab
##    @all.names: list of allele names for each locus
##    @ploidy: ploidy of each individual  (range: 2-2)
##    @type:  codom
##    @call: df2genind(X = Flr[, c(6:12)], sep = ":", ncode = NULL, ind.names = Flr$ID,
##     loc.names = names(Flr[, c(6:12)]), pop = Flr$Population,
##     NA.char = "NA", ploidy = 2, type = "codom", strata = NULL,
##     hierarchy = NULL)
##
##  // Optional content
##    @pop: population of each individual (group size range: 14-56)
```

```
Flr.genind@pop
```

```
##   [1] A21  A21  A21  A21  A21  A21  A21  A21  A21  A21  A21  A21  A21  A21  A21
##  [16] A25  A25  A25  A25  A25  A25  A25  A25  A25  A25  A25  A25  A25  A25  A25
##  [31] A25  A25  A25  A25  A25  A25  A25  A25  A25  A25  A25  A25  A25  A25  A25
##  [46] A25  A25  A25  A25  A25  A25  A25  A25  A25  A25  A25  A25  A25  A25  A25
##  [61] A25  A25  A25  A26  A26  A26  A26  A26  A26  A26  A26  A26  A26  A26  A26
##  [76] A26  A26  A45  A45  A45  A45  A45  A45  A45  A45  A45  A45  A45  A45  A45
##  [91] A45  A45  A45  A41  A41  A41  A41  A41  A03  A03  A03  A03  A03  A03  A03
## [106] A03  A03  A03  A03  A03  A03  A03  A03  A03  A03  A03  A03  A03  A03  A03
## [121] A03  A03  A03  A03  A03  A03  A03  A03  A03  A03  A03  A03  A03  A03  A03
## [136] G05a G05a G05a G05a G05a G05a G05a G05a G05a G05a G05a G05a G05a G05a G05a
## [151] G05a G05a G05a G05a G05a G05a G05a G05a G05a G05a G05a G05a G05a G05a G05a
## [166] G05a G05a G05a G05a G05a G05a G05a A25  A25  A25  A25  A25  A25  A25  A25
## [181] A26  A26  A26  A26  A26  A26  A26  A45  A45  A45  A45  A45  A45  A41  A41
## [196] A41  A41  A41  A41  A41  A41  A41  A21  A21  A21  A21  A21  A21  G05a G05a
## [211] G05a G05a G05a G05a G05a A03  A03  A03  A03  A03  G05a
## Levels: A21 A25 A26 A45 A41 A03 G05a
```

```
summary(Flr.genind)
```

```
##
## // Number of individuals: 221
## // Group sizes: 21 56 21 22 14 42 45
## // Number of alleles per locus: 18 8 25 8 19 14 13
## // Number of alleles per group: 63 68 54 50 51 73 53
## // Percentage of missing data: 0.9 %
## // Observed heterozygosity: 0.74 0.54 0.89 0.71 0.74 0.68 0.74
## // Expected heterozygosity: 0.83 0.57 0.89 0.74 0.81 0.76 0.83
```

c. PLot locations of individuals from site A25 From dataframe

```r
# Select data for Population "A25"
Sites <- Flr[Flr$Population == "A25", c("X", "Y")]

# Check if the data frame has valid coordinates
head(Sites)
```

```
##          X       Y
## 16 4422658 5425371
## 17 4422659 5425372
## 18 4422659 5425371
## 19 4422658 5425370
## 20 4422659 5425371
## 21 4422659 5425371
```

```r
# Convert to an 'sf' object
Pulsatilla <- st_as_sf(Sites, coords = c("X", "Y"), crs = 31468)

# Confirm the CRS was set correctly
st_crs(Pulsatilla)
```

```
## Coordinate Reference System:
##   User input: EPSG:31468
##   wkt:
## PROJCRS["DHDN / 3-degree Gauss-Kruger zone 4",
##     BASEGEOGCRS["DHDN",
##         DATUM["Deutsches Hauptdreiecksnetz",
##             ELLIPSOID["Bessel 1841",6377397.155,299.1528128,
##                 LENGTHUNIT["metre",1]]],
##         PRIMEM["Greenwich",0,
##             ANGLEUNIT["degree",0.0174532925199433]],
##         ID["EPSG",4314]],
##     CONVERSION["3-degree Gauss-Kruger zone 4",
##         METHOD["Transverse Mercator",
##             ID["EPSG",9807]],
##         PARAMETER["Latitude of natural origin",0,
##             ANGLEUNIT["degree",0.0174532925199433],
##             ID["EPSG",8801]],
##         PARAMETER["Longitude of natural origin",12,
##             ANGLEUNIT["degree",0.0174532925199433],
##             ID["EPSG",8802]],
##         PARAMETER["Scale factor at natural origin",1,
##             SCALEUNIT["unity",1],
##             ID["EPSG",8805]],
```

```
##          PARAMETER["False easting",4500000,
##              LENGTHUNIT["metre",1],
##              ID["EPSG",8806]],
##          PARAMETER["False northing",0,
##              LENGTHUNIT["metre",1],
##              ID["EPSG",8807]]],
##      CS[Cartesian,2],
##          AXIS["northing (X)",north,
##              ORDER[1],
##              LENGTHUNIT["metre",1]],
##          AXIS["easting (Y)",east,
##              ORDER[2],
##              LENGTHUNIT["metre",1]],
##      USAGE[
##          SCOPE["Cadastre, engineering survey, topographic mapping."],
##          AREA["Germany - former West Germany onshore between 10°30'E and 13°30'E - states of Bayern, N
##          BBOX[47.39,10.5,54.59,13.51]],
##      ID["EPSG",31468]]

# Transform to WGS84 (lat/long, EPSG:4326)
Pulsatilla_latlon <- st_transform(Pulsatilla, crs = 4326)
```

d. Add geographic info to genind object

Genind object @other can hold a list such as spatial coordinates

```
# Convert data frame of xy coordinates from Flr into a matrix of xy coordinates
xy_matrix <- as.matrix(Flr[, c("X", "Y")])

# Add the matrix to the @other slot with the name "xy"
Flr.genind@other <- list(xy = xy_matrix)

# Check the class of the @other slot
class(Flr.genind@other)   # Should return "list"
```

```
## [1] "list"
```

```
# Inspect the genind object and its summary
print(Flr.genind)
```

```
## /// GENIND OBJECT /////////
##
##  // 221 individuals; 7 loci; 105 alleles; size: 148.9 Kb
##
##  // Basic content
##    @tab:  221 x 105 matrix of allele counts
##    @loc.n.all: number of alleles per locus (range: 8-25)
##    @loc.fac: locus factor for the 105 columns of @tab
##    @all.names: list of allele names for each locus
##    @ploidy: ploidy of each individual  (range: 2-2)
##    @type:  codom
##    @call: df2genind(X = Flr[, c(6:12)], sep = ":", ncode = NULL, ind.names = Flr$ID,
##     loc.names = names(Flr[, c(6:12)]), pop = Flr$Population,
##     NA.char = "NA", ploidy = 2, type = "codom", strata = NULL,
##     hierarchy = NULL)
```

```
##
##  // Optional content
##     @pop: population of each individual (group size range: 14-56)
##     @other: a list containing: xy
```

```r
summary(Flr.genind)
```

```
##
## // Number of individuals: 221
## // Group sizes: 21 56 21 22 14 42 45
## // Number of alleles per locus: 18 8 25 8 19 14 13
## // Number of alleles per group: 63 68 54 50 51 73 53
## // Percentage of missing data: 0.9 %
## // Observed heterozygosity: 0.74 0.54 0.89 0.71 0.74 0.68 0.74
## // Expected heterozygosity: 0.83 0.57 0.89 0.74 0.81 0.76 0.83
```

e. Calculate genetic and geographic euclidean distance (for Site A25)

Genetic with adegenet::propShared

```r
#Check genind object
Flr.genind
```

```
## /// GENIND OBJECT /////////
##
##  // 221 individuals; 7 loci; 105 alleles; size: 148.9 Kb
##
##  // Basic content
##     @tab:  221 x 105 matrix of allele counts
##     @loc.n.all: number of alleles per locus (range: 8-25)
##     @loc.fac: locus factor for the 105 columns of @tab
##     @all.names: list of allele names for each locus
##     @ploidy: ploidy of each individual  (range: 2-2)
##     @type:  codom
##     @call: df2genind(X = Flr[, c(6:12)], sep = ":", ncode = NULL, ind.names = Flr$ID,
##      loc.names = names(Flr[, c(6:12)]), pop = Flr$Population,
##      NA.char = "NA", ploidy = 2, type = "codom", strata = NULL,
##      hierarchy = NULL)
##
##  // Optional content
##     @pop: population of each individual (group size range: 14-56)
##     @other: a list containing: xy
```

```r
summary(Flr.genind)
```

```
##
## // Number of individuals: 221
## // Group sizes: 21 56 21 22 14 42 45
## // Number of alleles per locus: 18 8 25 8 19 14 13
## // Number of alleles per group: 63 68 54 50 51 73 53
## // Percentage of missing data: 0.9 %
## // Observed heterozygosity: 0.74 0.54 0.89 0.71 0.74 0.68 0.74
## // Expected heterozygosity: 0.83 0.57 0.89 0.74 0.81 0.76 0.83
```

```
# Subset only site A25
Flr.A25 <- Flr.genind[Flr.genind@pop == "A25"]

# Calculate genetic distance
ind.dist <- adegenet::propShared(Flr.A25)
ind.dist <- as.dist(1-ind.dist)
class(ind.dist)
```

[1] "dist"

Geographic with dist()

```
# We have already changed coordinates and subset A25
# Extract coordinates from the sf object as a matrix
coords_wgs84 <- st_coordinates(Pulsatilla_latlon)

# Print the extracted WGS84 coordinates to verify
print(coords_wgs84)
```

```
##               X        Y
##  [1,] 10.94236 48.96085
##  [2,] 10.94239 48.96086
##  [3,] 10.94238 48.96086
##  [4,] 10.94237 48.96085
##  [5,] 10.94238 48.96086
##  [6,] 10.94239 48.96086
##  [7,] 10.94238 48.96086
##  [8,] 10.94237 48.96085
##  [9,] 10.94239 48.96087
## [10,] 10.94239 48.96084
## [11,] 10.94238 48.96084
## [12,] 10.94237 48.96083
## [13,] 10.94240 48.96082
## [14,] 10.94238 48.96080
## [15,] 10.94238 48.96081
## [16,] 10.94238 48.96081
## [17,] 10.94239 48.96080
## [18,] 10.94241 48.96079
## [19,] 10.94238 48.96081
## [20,] 10.94239 48.96079
## [21,] 10.94237 48.96080
## [22,] 10.94236 48.96080
## [23,] 10.94241 48.96077
## [24,] 10.94238 48.96079
## [25,] 10.94239 48.96079
## [26,] 10.94239 48.96078
## [27,] 10.94238 48.96077
## [28,] 10.94234 48.96076
## [29,] 10.94231 48.96075
## [30,] 10.94233 48.96075
## [31,] 10.94235 48.96076
## [32,] 10.94233 48.96077
## [33,] 10.94231 48.96070
## [34,] 10.94232 48.96070
## [35,] 10.94232 48.96061
```

```
## [36,]  10.94235 48.96063
## [37,]  10.94233 48.96062
## [38,]  10.94232 48.96062
## [39,]  10.94232 48.96064
## [40,]  10.94232 48.96064
## [41,]  10.94233 48.96063
## [42,]  10.94233 48.96063
## [43,]  10.94233 48.96063
## [44,]  10.94235 48.96064
## [45,]  10.94234 48.96064
## [46,]  10.94250 48.96070
## [47,]  10.94253 48.96072
## [48,]  10.94253 48.96072
## [49,]  10.94235 48.96086
## [50,]  10.94245 48.96080
## [51,]  10.94243 48.96080
## [52,]  10.94238 48.96085
## [53,]  10.94239 48.96085
## [54,]  10.94241 48.96083
## [55,]  10.94238 48.96078
## [56,]  10.94241 48.96085
```

```r
# Calculate the Euclidean distance using dist()
euclidean_distances <- dist(coords_wgs84, method = "euclidean")

# Print the Euclidean distance matrix
print(euclidean_distances)
```

```
##                 1            2            3            4            5
## 2   2.228977e-05
## 3   1.923686e-05 4.634166e-06
## 4   6.300033e-06 1.979748e-05 1.587047e-05
## 5   1.922449e-05 5.807367e-06 1.351288e-06 1.545900e-05
## 6   2.510122e-05 4.476402e-06 5.882784e-06 2.165374e-05 6.210366e-06
## 7   1.947767e-05 7.354475e-06 3.084638e-06 1.522315e-05 1.735537e-06
## 8   9.439574e-06 1.911386e-05 1.481852e-05 3.140692e-06 1.416699e-05
## 9   2.991668e-05 7.861282e-06 1.215316e-05 2.765858e-05 1.304162e-05
## 10  2.277153e-05 1.748207e-05 1.340338e-05 1.670609e-05 1.205229e-05
## 11  2.362780e-05 2.710495e-05 2.259257e-05 1.755577e-05 2.132125e-05
## 12  2.527583e-05 3.762699e-05 3.300297e-05 2.132719e-05 3.194465e-05
## 13  4.379720e-05 4.005196e-05 3.662231e-05 3.754365e-05 3.529671e-05
## 14  5.133393e-05 5.835646e-05 5.393444e-05 4.652001e-05 5.263378e-05
## 15  4.495374e-05 4.931212e-05 4.503152e-05 3.953313e-05 4.370153e-05
## 16  4.993929e-05 5.504723e-05 5.074683e-05 4.472129e-05 4.942026e-05
## 17  5.890550e-05 5.992038e-05 5.606701e-05 5.315132e-05 5.471612e-05
## 18  7.975462e-05 7.719937e-05 7.395145e-05 7.373090e-05 7.263601e-05
## 19  5.000466e-05 5.516987e-05 5.086564e-05 4.479810e-05 4.953968e-05
## 20  6.358186e-05 6.880090e-05 6.456305e-05 5.852670e-05 6.322866e-05
## 21  5.779112e-05 6.937987e-05 6.477550e-05 5.425869e-05 6.357374e-05
## 22  5.272705e-05 6.609410e-05 6.146043e-05 4.974139e-05 6.032889e-05
## 23  9.205171e-05 9.268110e-05 8.904030e-05 8.641622e-05 8.769526e-05
## 24  6.345088e-05 7.069919e-05 6.630927e-05 5.881536e-05 6.500099e-05
## 25  7.194949e-05 7.691207e-05 7.272897e-05 6.690757e-05 7.138914e-05
## 26  7.801185e-05 8.262707e-05 7.849629e-05 7.294185e-05 7.715241e-05
## 27  8.035659e-05 8.756099e-05 8.321945e-05 7.582839e-05 8.190145e-05
```

```
## 28 9.360660e-05 1.092390e-04 1.046115e-04 9.173190e-05 1.035327e-04
## 29 1.178172e-04 1.358390e-04 1.312923e-04 1.170912e-04 1.303404e-04
## 30 1.042354e-04 1.200887e-04 1.154627e-04 1.024812e-04 1.143886e-04
## 31 9.608249e-05 1.100113e-04 1.053817e-04 9.355751e-05 1.042265e-04
## 32 9.353299e-05 1.106091e-04 1.060222e-04 9.229639e-05 1.050223e-04
## 33 1.633966e-04 1.794929e-04 1.748648e-04 1.618349e-04 1.737823e-04
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## 40 2.186471e-04 2.316381e-04 2.270492e-04 2.159890e-04 2.258310e-04
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##                 16              17              18              19              20
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##                26           27           28           29           30
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## 29 8.598275e-05 7.553484e-05 3.151074e-05
## 30 6.314619e-05 5.263760e-05 1.087130e-05 2.313738e-05
## 31 4.781174e-05 3.727701e-05 1.054880e-05 3.856310e-05 1.545524e-05
## 32 6.284344e-05 5.282385e-05 9.702391e-06 2.600380e-05 1.333687e-05
## 33 1.145827e-04 1.044652e-04 7.025446e-05 4.886901e-05 5.941584e-05
## 34 1.056721e-04 9.581876e-05 6.524382e-05 4.900871e-05 5.472362e-05
## 35 1.857959e-04 1.777255e-04 1.565832e-04 1.409896e-04 1.465886e-04
## 36 1.596064e-04 1.526179e-04 1.389310e-04 1.300286e-04 1.301085e-04
## 37 1.685867e-04 1.609540e-04 1.431131e-04 1.307261e-04 1.336206e-04
## 38 1.710992e-04 1.628988e-04 1.414507e-04 1.262657e-04 1.314815e-04
## 39 1.581675e-04 1.497913e-04 1.277371e-04 1.127870e-04 1.177613e-04
## 40 1.553576e-04 1.471198e-04 1.261023e-04 1.121099e-04 1.162718e-04
## 41 1.628257e-04 1.548424e-04 1.351053e-04 1.216290e-04 1.253937e-04
## 42 1.581496e-04 1.500987e-04 1.301479e-04 1.167837e-04 1.204373e-04
## 43 1.603916e-04 1.526228e-04 1.343216e-04 1.220459e-04 1.248178e-04
## 44 1.436523e-04 1.367815e-04 1.246500e-04 1.178952e-04 1.162276e-04
## 45 1.492589e-04 1.419125e-04 1.267149e-04 1.174012e-04 1.177505e-04
## 46 1.325409e-04 1.376321e-04 1.719215e-04 1.943993e-04 1.739760e-04
## 47 1.563553e-04 1.630259e-04 2.010010e-04 2.255972e-04 2.042231e-04
## 48 1.514998e-04 1.583410e-04 1.967926e-04 2.217754e-04 2.002268e-04
## 49 8.471825e-05 8.585285e-05 9.372305e-05 1.156160e-04 1.040198e-04
## 50 6.159186e-05 7.204300e-05 1.163789e-04 1.475691e-04 1.246660e-04
## 51 4.946387e-05 5.998716e-05 1.040924e-04 1.354002e-04 1.126098e-04
## 52 7.088495e-05 7.543279e-05 9.716287e-05 1.242761e-04 1.080265e-04
## 53 7.261882e-05 7.773523e-05 1.011154e-04 1.286026e-04 1.119862e-04
## 54 5.366132e-05 6.151640e-05 9.543348e-05 1.258677e-04 1.059485e-04
## 55 1.309496e-05 7.050823e-06 4.287671e-05 7.433327e-05 5.194926e-05
## 56 6.928254e-05 7.705594e-05 1.094407e-04 1.392888e-04 1.201085e-04
##                 31          32          33          34          35
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## 32 2.021296e-05
## 33 7.072521e-05 7.002567e-05
## 34 6.407416e-05 6.661846e-05 1.202272e-05
## 35 1.532920e-04 1.590427e-04 9.254050e-05 9.271449e-05
## 36 1.336291e-04 1.433049e-04 8.596072e-05 8.150220e-05 3.563845e-05
## 37 1.388570e-04 1.465112e-04 8.395053e-05 8.172367e-05 2.011302e-05
## 38 1.381524e-04 1.439785e-04 7.809467e-05 7.777119e-05 1.514517e-05
## 39 1.245101e-04 1.302681e-04 6.493299e-05 6.414436e-05 2.884647e-05
## 40 1.225677e-04 1.289228e-04 6.480534e-05 6.323159e-05 3.080896e-05
## 41 1.312906e-04 1.381351e-04 7.439371e-05 7.270272e-05 2.303317e-05
## 42 1.263523e-04 1.331846e-04 6.974101e-05 6.782974e-05 2.764647e-05
## 43 1.301199e-04 1.377085e-04 7.557633e-05 7.303721e-05 2.629335e-05
## 44 1.188724e-04 1.295193e-04 7.663338e-05 7.047202e-05 4.891232e-05
## 45 1.216700e-04 1.309072e-04 7.357113e-05 6.888879e-05 3.971744e-05
## 46 1.614511e-04 1.816238e-04 1.913432e-04 1.793346e-04 2.042852e-04
## 47 1.907559e-04 2.106463e-04 2.259536e-04 2.139310e-04 2.401633e-04
## 48 1.866019e-04 2.064154e-04 2.231705e-04 2.111524e-04 2.395611e-04
## 49 9.739917e-05 9.247363e-05 1.624794e-04 1.587266e-04 2.502448e-04
## 50 1.092606e-04 1.241126e-04 1.726675e-04 1.625682e-04 2.319604e-04
## 51 9.726376e-05 1.116626e-04 1.619675e-04 1.521665e-04 2.243826e-04
## 52 9.771789e-05 9.883818e-05 1.673967e-04 1.616771e-04 2.500639e-04
## 53 1.013359e-04 1.030532e-04 1.712913e-04 1.653731e-04 2.532614e-04
## 54 9.274239e-05 9.990903e-05 1.633261e-04 1.557899e-04 2.391916e-04
## 55 3.705608e-05 5.037359e-05 1.062922e-04 9.822029e-05 1.820662e-04
## 56 1.073800e-04 1.132859e-04 1.780869e-04 1.708173e-04 2.547663e-04
##                 36          37          38          39          40
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## 39 2.999735e-05 2.036643e-05 1.372027e-05
## 40 2.684346e-05 1.930171e-05 1.578935e-05 4.250077e-06
## 41 2.129860e-05 9.960698e-06 9.696689e-06 1.043131e-05 9.589668e-06
## 42 2.242452e-05 1.423792e-05 1.336222e-05 7.574934e-06 5.143147e-06
## 43 1.620413e-05 8.803431e-06 1.458546e-05 1.413387e-05 1.175683e-05
## 44 1.605107e-05 2.884932e-05 3.852217e-05 3.348111e-05 2.931508e-05
## 45 1.262998e-05 2.009710e-05 2.844174e-05 2.354098e-05 1.948400e-05
## 46 1.686487e-04 1.845002e-04 1.954945e-04 1.891085e-04 1.848706e-04
## 47 2.045449e-04 2.204592e-04 2.315877e-04 2.252996e-04 2.210606e-04
## 48 2.039236e-04 2.197618e-04 2.306828e-04 2.240910e-04 2.198613e-04
## 49 2.308219e-04 2.362362e-04 2.351035e-04 2.214010e-04 2.196631e-04
## 50 2.010438e-04 2.129529e-04 2.182895e-04 2.065842e-04 2.031586e-04
## 51 1.943878e-04 2.057091e-04 2.104268e-04 1.983940e-04 1.950958e-04
## 52 2.271523e-04 2.344231e-04 2.349915e-04 2.214906e-04 2.192551e-04
## 53 2.299059e-04 2.374235e-04 2.382135e-04 2.247538e-04 2.224581e-04
## 54 2.132526e-04 2.221883e-04 2.243967e-04 2.113075e-04 2.086225e-04
## 55 1.577588e-04 1.656533e-04 1.671470e-04 1.539025e-04 1.513576e-04
## 56 2.288683e-04 2.378018e-04 2.399539e-04 2.268367e-04 2.241756e-04
##                 41           42           43           44           45
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## 42 4.957952e-06
## 43 5.351593e-06 6.717515e-06
## 44 2.899368e-05 2.716907e-05 2.394229e-05
## 45 1.882819e-05 1.695988e-05 1.394434e-05 1.024375e-05
## 46 1.859904e-04 1.838054e-04 1.809101e-04 1.569986e-04 1.671820e-04
## 47 2.221080e-04 2.199670e-04 2.170068e-04 1.931143e-04 2.033112e-04
## 48 2.211544e-04 2.188981e-04 2.160973e-04 1.921709e-04 2.023351e-04
## 49 2.285350e-04 2.235849e-04 2.274861e-04 2.157788e-04 2.189911e-04
## 50 2.091348e-04 2.049356e-04 2.056973e-04 1.851906e-04 1.928692e-04
## 51 2.014367e-04 1.971114e-04 1.982101e-04 1.784168e-04 1.856923e-04
## 52 2.275772e-04 2.227045e-04 2.258646e-04 2.115069e-04 2.159953e-04
## 53 2.306988e-04 2.258423e-04 2.289010e-04 2.141964e-04 2.188583e-04
## 54 2.162721e-04 2.115530e-04 2.139436e-04 1.972837e-04 2.029128e-04
## 55 1.592815e-04 1.544895e-04 1.572320e-04 1.420157e-04 1.468382e-04
## 56 2.318581e-04 2.271315e-04 2.295488e-04 2.128958e-04 2.185340e-04
##                 46          47          48          49          50
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## 47 3.619665e-05
## 48 3.528001e-05 5.808305e-06
## 49 2.104417e-04 2.276017e-04 2.221091e-04
## 50 1.092464e-04 1.198159e-04 1.141370e-04 1.096104e-04
## 51 1.150312e-04 1.286136e-04 1.230434e-04 9.930329e-05 1.275986e-05
## 52 1.871065e-04 2.017943e-04 1.961918e-04 2.921575e-05 8.245215e-05
## 53 1.860276e-04 1.999081e-04 1.942718e-04 3.328443e-05 8.026575e-05
## 54 1.580704e-04 1.720115e-04 1.663996e-04 5.732146e-05 5.268679e-05
## 55 1.439634e-04 1.687369e-04 1.639654e-04 7.902166e-05 7.373897e-05
## 56 1.679219e-04 1.792460e-04 1.735320e-04 5.699968e-05 5.958053e-05
##                51            52            53            54            55
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## 52 7.323629e-05
## 53 7.158781e-05 4.929567e-06
## 54 4.355021e-05 2.980950e-05 2.805217e-05
## 55 6.131543e-05 6.964518e-05 7.219188e-05 5.782461e-05
## 56 5.300567e-05 2.781226e-05 2.385183e-05 1.562159e-05 7.316100e-05
```

```r
# Convert to a full matrix if needed
dist_matrix <- as.matrix(euclidean_distances)
print(dist_matrix)
```

```
##                    1             2             3             4             5
```

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## 1   0.000000e+00 2.228977e-05 1.923686e-05 6.300033e-06 1.922449e-05
## 2   2.228977e-05 0.000000e+00 4.634166e-06 1.979748e-05 5.807367e-06
## 3   1.923686e-05 4.634166e-06 0.000000e+00 1.587047e-05 1.351288e-06
## 4   6.300033e-06 1.979748e-05 1.587047e-05 0.000000e+00 1.545900e-05
## 5   1.922449e-05 5.807367e-06 1.351288e-06 1.545900e-05 0.000000e+00
## 6   2.510122e-05 4.476402e-06 5.882784e-06 2.165374e-05 6.210366e-06
## 7   1.947767e-05 7.354475e-06 3.084638e-06 1.522315e-05 1.735537e-06
## 8   9.439574e-06 1.911386e-05 1.481852e-05 3.140692e-06 1.416699e-05
## 9   2.991668e-05 7.861282e-06 1.215316e-05 2.765858e-05 1.304162e-05
## 10  2.277153e-05 1.748207e-05 1.340338e-05 1.670609e-05 1.205229e-05
## 11  2.362780e-05 2.710495e-05 2.259257e-05 1.755577e-05 2.132125e-05
## 12  2.527583e-05 3.762699e-05 3.300297e-05 2.132719e-05 3.194465e-05
## 13  4.379720e-05 4.005196e-05 3.662231e-05 3.754365e-05 3.529671e-05
## 14  5.133393e-05 5.835646e-05 5.393444e-05 4.652001e-05 5.263378e-05
## 15  4.495374e-05 4.931212e-05 4.503152e-05 3.953313e-05 4.370153e-05
## 16  4.993929e-05 5.504723e-05 5.074683e-05 4.472129e-05 4.942026e-05
## 17  5.890550e-05 5.992038e-05 5.606701e-05 5.315132e-05 5.471612e-05
## 18  7.975462e-05 7.719937e-05 7.395145e-05 7.373090e-05 7.263601e-05
## 19  5.000466e-05 5.516987e-05 5.086564e-05 4.479810e-05 4.953968e-05
## 20  6.358186e-05 6.880090e-05 6.456305e-05 5.852670e-05 6.322866e-05
## 21  5.779112e-05 6.937987e-05 6.477550e-05 5.425869e-05 6.357374e-05
## 22  5.272705e-05 6.609410e-05 6.146043e-05 4.974139e-05 6.032889e-05
## 23  9.205171e-05 9.268110e-05 8.904030e-05 8.641622e-05 8.769526e-05
## 24  6.345088e-05 7.069919e-05 6.630927e-05 5.881536e-05 6.500099e-05
## 25  7.194949e-05 7.691207e-05 7.272897e-05 6.690757e-05 7.138914e-05
## 26  7.801185e-05 8.262707e-05 7.849629e-05 7.294185e-05 7.715241e-05
## 27  8.035659e-05 8.756099e-05 8.321945e-05 7.582839e-05 8.190145e-05
## 28  9.360660e-05 1.092390e-04 1.046115e-04 9.173190e-05 1.035327e-04
## 29  1.178172e-04 1.358390e-04 1.312923e-04 1.170912e-04 1.303404e-04
## 30  1.042354e-04 1.200887e-04 1.154627e-04 1.024812e-04 1.143886e-04
## 31  9.608249e-05 1.100113e-04 1.053817e-04 9.355751e-05 1.042265e-04
## 32  9.353299e-05 1.106091e-04 1.060222e-04 9.229639e-05 1.050223e-04
## 33  1.633966e-04 1.794929e-04 1.748648e-04 1.618349e-04 1.737823e-04
## 34  1.588487e-04 1.739156e-04 1.692816e-04 1.568704e-04 1.681511e-04
## 35  2.493735e-04 2.624470e-04 2.578582e-04 2.467617e-04 2.566399e-04
## 36  2.285705e-04 2.394862e-04 2.349961e-04 2.252857e-04 2.337204e-04
## 37  2.347088e-04 2.468028e-04 2.422523e-04 2.317773e-04 2.410058e-04
## 38  2.342328e-04 2.473729e-04 2.427804e-04 2.316340e-04 2.415655e-04
## 39  2.205819e-04 2.338679e-04 2.292695e-04 2.180226e-04 2.280607e-04
## 40  2.186471e-04 2.316381e-04 2.270492e-04 2.159890e-04 2.258310e-04
## 41  2.273238e-04 2.399628e-04 2.353880e-04 2.245581e-04 2.341580e-04
## 42  2.223938e-04 2.350900e-04 2.305124e-04 2.196430e-04 2.292846e-04
## 43  2.260161e-04 2.382472e-04 2.336893e-04 2.231212e-04 2.324475e-04
## 44  2.132664e-04 2.238215e-04 2.193496e-04 2.098682e-04 2.180671e-04
## 45  2.169744e-04 2.283546e-04 2.238365e-04 2.138157e-04 2.225728e-04
## 46  2.009674e-04 1.949436e-04 1.925562e-04 1.948147e-04 1.913418e-04
## 47  2.172996e-04 2.079031e-04 2.062146e-04 2.110107e-04 2.051170e-04
## 48  2.117678e-04 2.022267e-04 2.005655e-04 2.054760e-04 1.994732e-04
## 49  1.134716e-05 3.208976e-05 2.977788e-05 1.734842e-05 2.998493e-05
## 50  9.879039e-05 8.808968e-05 8.648808e-05 9.250326e-05 8.542075e-05
## 51  8.878308e-05 8.011840e-05 7.801800e-05 8.248478e-05 7.686154e-05
## 52  1.787987e-05 1.238559e-05 7.843749e-06 1.247902e-05 6.582884e-06
## 53  2.206941e-05 1.005754e-05 6.571021e-06 1.711843e-05 5.316563e-06
## 54  4.627957e-05 3.692360e-05 3.452570e-05 4.003693e-05 3.334339e-05
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## 55 7.379809e-05 8.188837e-05 7.747103e-05 6.943608e-05 7.617010e-05
## 56 4.568302e-05 2.935771e-05 2.888854e-05 4.015700e-05 2.813694e-05
##                6            7            8            9           10
## 1  2.510122e-05 1.947767e-05 9.439574e-06 2.991668e-05 2.277153e-05
## 2  4.476402e-06 7.354475e-06 1.911386e-05 7.861282e-06 1.748207e-05
## 3  5.882784e-06 3.084638e-06 1.481852e-05 1.215316e-05 1.340338e-05
## 4  2.165374e-05 1.522315e-05 3.140692e-06 2.765858e-05 1.670609e-05
## 5  6.210366e-06 1.735537e-06 1.416699e-05 1.304162e-05 1.205229e-05
## 6  0.000000e+00 6.889024e-06 2.035136e-05 7.731828e-06 1.542617e-05
## 7  6.889024e-06 0.000000e+00 1.360905e-05 1.419886e-05 1.032568e-05
## 8  2.035136e-05 1.360905e-05 0.000000e+00 2.691281e-05 1.372341e-05
## 9  7.731828e-06 1.419886e-05 2.691281e-05 0.000000e+00 2.313776e-05
## 10 1.542617e-05 1.032568e-05 1.372341e-05 2.313776e-05 0.000000e+00
## 11 2.579653e-05 1.975868e-05 1.464167e-05 3.352128e-05 1.072606e-05
## 12 3.742227e-05 3.070988e-05 1.991348e-05 4.490864e-05 2.367035e-05
## 13 3.675963e-05 3.357498e-05 3.444919e-05 4.363029e-05 2.366969e-05
## 14 5.651632e-05 5.100937e-05 4.433511e-05 6.419552e-05 4.110375e-05
## 15 4.715918e-05 4.202502e-05 3.699721e-05 5.476207e-05 3.186771e-05
## 16 5.291297e-05 4.774986e-05 4.229703e-05 6.051442e-05 3.761380e-05
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## 40 1.622996e-04 1.662563e-04 1.575900e-04 1.625198e-04 1.595648e-04
## 41 1.707004e-04 1.748170e-04 1.642657e-04 1.704878e-04 1.671908e-04
## 42 1.658108e-04 1.699016e-04 1.598246e-04 1.656867e-04 1.624733e-04
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## 47 1.854326e-04 1.922312e-04 1.366784e-04 1.712055e-04 1.608251e-04
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## 49 6.165251e-05 5.569815e-05 1.000397e-04 6.939011e-05 7.865265e-05
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## 52 5.701233e-05 5.386685e-05 8.197951e-05 5.849774e-05 6.507160e-05
## 53 6.043606e-05 5.767736e-05 8.268112e-05 6.096291e-05 6.693583e-05
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## 55 1.893226e-05 2.615066e-05 3.244110e-05 1.126371e-05 1.168276e-05
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## 3  7.849629e-05 8.321945e-05 1.046115e-04 1.312923e-04 1.154627e-04
## 4  7.294185e-05 7.582839e-05 9.173190e-05 1.170912e-04 1.024812e-04
## 5  7.715241e-05 8.190145e-05 1.035327e-04 1.303404e-04 1.143886e-04
## 6  8.009102e-05 8.544449e-05 1.088173e-04 1.360201e-04 1.196855e-04
## 7  7.544606e-05 8.024514e-05 1.022414e-04 1.292264e-04 1.131028e-04
## 8  7.055597e-05 7.374617e-05 9.104761e-05 1.169585e-04 1.018431e-04
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## 3  2.349961e-04 2.422523e-04 2.427804e-04 2.292695e-04 2.270492e-04
## 4  2.252857e-04 2.317773e-04 2.316340e-04 2.180226e-04 2.159890e-04
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## 3  2.353880e-04 2.305124e-04 2.336893e-04 2.193496e-04 2.238365e-04
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