

# SOM3 - 3D Mesh distance analysis

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## Content

This script reads, measures and analysis 3D mesh data comparison between experimental samples.

## Load required libraries

## Define directories and file paths

```
# data folders
raw_dir <- "analysis/data/raw_data" # .ply and .pp
out_csv  <- "analysis/data/derived_data" # stats and summarised data analysis
out_plots <- "analysis/plots/" # all plots and figures
snap_dir <- "analysis/plots/comparisons" # plot and figures for sample comparison
```

## Parse filename to extract info about samples

```
parse_filename <- function(path) {
  fname <- fs::path_file(path)

  tibble(
    path = path,
    file = fname,

    # ID is everything before the first `_cycle`
    id = str_extract(fname, "^[^_]+(?:=_cycle)") %||%
          str_extract(fname, "^[^_]+") %||%
          NA_character_,

    # Extract cycle number safely
    cycle = str_extract(fname, "cycle[0-9]+") %>%
              str_remove("cycle") %>%
              as.integer()
  )
}
```

## Define a new variable not in the filename: raw material

```
raw_material_lookup <- tribble(
  ~id, ~raw_material,
  "DWG1S1", "Basalt",
  "DWG1S2", "Basalt",
  "DWG1S3", "Basalt",
  "DWG3S1", "Scoria",
  "DWG3S2", "Scoria",
  "DWG3S3", "Scoria",
  "DWG4S1", "Pumiceous",
  "DWG4S2", "Pumiceous",
  "DWG4S3", "Pumiceous",
  "KWG1S1", "Glassy ignimbrite",
  "KWG1S2", "Glassy ignimbrite",
  "KWG1S3", "Glassy ignimbrite",
  "MW6G2S1", "Regular ignimbrite",
  "MW6G2S2", "Regular ignimbrite",
  "MW6G2S3", "Regular ignimbrite"
)
```

## 3D meshes and landmarks

### Function to read landmarks (.pp)

```
read_pp <- function(file) {
  txt <- readLines(file, warn = FALSE)

  point_lines <- grep("<point", txt, value = TRUE)
  if (length(point_lines) == 0)
    stop("No <point ...> lines found in ", file)

  coords <- stringr::str_match(
    point_lines,
    'x="([0-9eE+\\. -]+)".*y="([0-9eE+\\. -]+)".*z="([0-9eE+\\. -]+)" '
  )[, 2:4]

  coords <- apply(coords, 2, as.numeric)

  rownames(coords) <- as.character(seq_len(nrow(coords)) - 1L)
  colnames(coords) <- c("x", "y", "z")

  coords
}
```

### Load meshes and landmarks

```

# List files
mesh_files <- fs::dir_ls(raw_dir, glob = "*.ply")
landmark_files <- fs::dir_ls(raw_dir, glob = "*.pp")

# Parse filenames into metadata tables
mesh_info <- mesh_files %>% map_dfr(parse_filename)
land_info <- landmark_files %>% map_dfr(parse_filename)

# Ensure cycles exist for both meshes and landmarks
mesh_info <- mesh_info %>% filter(!is.na(cycle))
land_info <- land_info %>% filter(!is.na(cycle))

# Identify IDs with meshes and landmarks
common_ids <- intersect(mesh_info$id, land_info$id)

mesh_info <- mesh_info %>% filter(id %in% common_ids)
land_info <- land_info %>% filter(id %in% common_ids)

# Create unique names for lists: id_cycle, e.g., DWG4S3_cycle1
mesh_keys <- paste0(mesh_info$id, "_cycle", mesh_info$cycle)
land_keys <- paste0(land_info$id, "_cycle", land_info$cycle)

# Read meshes
meshes <- map(mesh_info$path, ~ {
  Rvcg::vcgPlyRead(.x, updateNormals = TRUE, clean = TRUE)
})

```

```

## Removed 2 duplicate 0 unreferenced vertices and 2 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 2 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 12 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 1 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 1 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 1 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 3 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 3 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 13 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 11 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 15 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 5 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 16 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 5 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 6 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 10 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 3 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 4 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 3 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 14 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 7 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 2 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 4 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 2 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 2 duplicate faces
## Removed 0 duplicate 0 unreferenced vertices and 3 duplicate faces

```

```
names(meshes) <- mesh_keys

# Read landmarks
lands <- map(land_info$path, read_pp)
names(lands) <- land_keys

head(mesh_info, 5)
```

```
## # A tibble: 5 x 4
##   path                                file                id    cycle
##   <fs::path>                        <chr>              <chr> <int>
## 1 analysis/data/raw_data/DWG1S1_cycle0.ply DWG1S1_cycle0.ply DWG1S1     0
## 2 analysis/data/raw_data/DWG1S1_cycle2.ply DWG1S1_cycle2.ply DWG1S1     2
## 3 analysis/data/raw_data/DWG1S2_cycle0.ply DWG1S2_cycle0.ply DWG1S2     0
## 4 analysis/data/raw_data/DWG1S2_cycle2.ply DWG1S2_cycle2.ply DWG1S2     2
## 5 analysis/data/raw_data/DWG1S3_cycle0.ply DWG1S3_cycle0.ply DWG1S3     0
```

```
head(land_info, 5)
```

```
## # A tibble: 5 x 4
##   path                                file                id    cycle
##   <fs::path>                        <chr>              <chr> <int>
## 1 analysis/data/raw_data/DWG1S1_cycle0.pp DWG1S1_cycle0.pp DWG1S1     0
## 2 analysis/data/raw_data/DWG1S1_cycle2.pp DWG1S1_cycle2.pp DWG1S1     2
## 3 analysis/data/raw_data/DWG1S2_cycle0.pp DWG1S2_cycle0.pp DWG1S2     0
## 4 analysis/data/raw_data/DWG1S2_cycle2.pp DWG1S2_cycle2.pp DWG1S2     2
## 5 analysis/data/raw_data/DWG1S3_cycle0.pp DWG1S3_cycle0.pp DWG1S3     0
```

## Landmark checking in a table (including z, x, y)

```
summarize_landmarks_id_coords <- function(id, land_info, lands) {

  # All cycles available for this ID
  cycles <- land_info |>
    dplyr::filter(id == !!id) |>
    arrange(cycle) |>
    pull(cycle)

  # Load all cycles' landmarks for this ID
  lms <- lapply(cycles, function(cyc) {
    key <- paste0(id, "_cycle", cyc)
    lm <- lands[[key]]

    if (is.null(lm)) {
      warning("Landmarks missing for: ", key)
      return(NULL)
    }

    list(cycle = cyc, lm = lm)
  })
}
```

```

# Remove NULL entries
lms <- lms[!sapply(lms, is.null)]

# If nothing left, skip
if (length(lms) == 0) return(NULL)

# Determine reference landmark IDs
if (0 %in% cycles) {
  ref_ids <- rownames(lands[[paste0(id, "_cycle0")]])
} else {
  ref_ids <- rownames(lms[[1]]$lm)
}

# Build long table
long_tbl <- dplyr::bind_rows(lapply(lms, function(entry) {
  cyc <- entry$cycle
  lm <- entry$lm

  tibble::tibble(
    id = id,
    cycle = cyc,
    landmark_id = as.integer(rownames(lm)),
    x = lm[,1],
    y = lm[,2],
    z = lm[,3],
    missing_vs_ref = paste(setdiff(ref_ids, rownames(lm)), collapse = ", ")
  )
}))

return(long_tbl)
}

# Run for all IDs
landmark_comparison_table_coords <- purrr::map_dfr(
  unique(land_info$id),
  summarize_landmarks_id_coords,
  land_info = land_info,
  lands = lands
)

readr::write_csv(
  landmark_comparison_table_coords,
  file.path(out_csv, "landmark_summary_all_samples.csv")
)

head(landmark_comparison_table_coords, 5)

```

```

## # A tibble: 5 x 7
##   id      cycle landmark_id    x    y    z missing_vs_ref
##   <chr> <int>      <int> <dbl> <dbl> <dbl> <chr>
## 1 DWG1S1     0          0  22.4  25.3  30.5 ""
## 2 DWG1S1     0          1  40.0  12.8  32.9 ""

```

```
## 3 DWG1S1      0          2  27.6 11.3  50.5 ""
## 4 DWG1S1      0          3  15.3 -5.90 53.1 ""
## 5 DWG1S1      0          4 -12.1  8.49 11.4 ""
```

## Compute vertex distance (VD)

### Compute and export VD data

```
compute_vertex_distances <- function(mesh_ref, mesh_other) {
  kd <- Rvcg::vcgClostKD(mesh_other, mesh_ref)
  d <- kd$quality
  d[!is.finite(d)] <- 0
  d[d < 0] <- 0
  return(d)
}

compute_distance_table_id <- function(id, mesh_info, meshes) {
  pair <- mesh_info |>
    dplyr::filter(id == !!id & cycle %in% c(0, 2))
  if (!all(c(0, 2) %in% pair$cycle)) {
    message("skipping ", id, ": missing cycle0 or cycle2.")
    return(NULL)
  }
  key0 <- paste0(id, "_cycle0")
  key2 <- paste0(id, "_cycle2")
  mesh0 <- meshes[[key0]]
  mesh2 <- meshes[[key2]]
  dists <- compute_vertex_distances(mesh_ref = mesh0, mesh_other = mesh2)
  tibble::tibble(
    id = id,
    cycle0_file = key0,
    cycle2_file = key2,
    vertex_id = seq_along(dists),
    distance = dists
  )
}

export_all_distances_one_csv <- function(mesh_info,
                                         meshes,
```

```

        outfile = "analysis/data/derived_data/all_vertex_distances_cyc

ids <- unique(mesh_info$id)

df_list <- lapply(ids, function(id) compute_distance_table_id(id, mesh_info, meshes))

df_list <- df_list[!sapply(df_list, is.null)]

df_all <- dplyr::bind_rows(df_list) %>%
  dplyr::left_join(raw_material_lookup, by = "id")
outdir <- dirname(outfile)
if (!dir.exists(outdir)) dir.create(outdir, recursive = TRUE)

readr::write_csv(df_all, outfile)

message("Exported all vertex distances with raw material → ", outfile)

return(df_all)
}

df_all <- export_all_distances_one_csv(mesh_info, meshes)

```

```
## Exported all vertex distances with raw material → analysis/data/derived_data/all_vertex_distances_cyc
```

```
head(df_all, 5)
```

```
## # A tibble: 5 x 6
##   id      cycle0_file  cycle2_file  vertex_id distance raw_material
##   <chr> <chr>          <chr>        <int>    <dbl> <chr>
## 1 DWG1S1 DWG1S1_cycle0 DWG1S1_cycle2     1     0     Basalt
## 2 DWG1S1 DWG1S1_cycle0 DWG1S1_cycle2     2 0.00305 Basalt
## 3 DWG1S1 DWG1S1_cycle0 DWG1S1_cycle2     3     0     Basalt
## 4 DWG1S1 DWG1S1_cycle0 DWG1S1_cycle2     4     0     Basalt
## 5 DWG1S1 DWG1S1_cycle0 DWG1S1_cycle2     5     0     Basalt
```

## Plot VD data

```

# Use violin plot per raw material

df_plot <- df_all %>%
  filter(!is.na(raw_material)) %>%
  mutate(raw_material = as.factor(raw_material))

p_vertex_rm <- ggplot(df_plot, aes(x = raw_material, y = distance, fill = raw_material)) +
  geom_violin(trim = FALSE, alpha = 0.6) +
  scale_y_continuous(trans = "log10") +
  geom_boxplot(width = 0.15, alpha = 0.5, outlier.shape = NA) +
  labs(
    title = "Per-Vertex Distances by Raw Material",
    subtitle = "Cycle 0 vs Cycle 2 - point-to-surface distances (log scale)",

```

```

    x = "Raw material",
    y = "Distance (log10 scale)"
  ) +
  theme_minimal(base_size = 14) +
  theme(
    legend.position = "none",
    axis.text.x = element_text(angle = 45, hjust = 1)
  )

ggsave(
  filename = file.path(out_plots, "vertex_distance_violin_facet_rawmaterial.png"),
  plot = p_vertex_rm,
  width = 12,
  height = 10,
  dpi = 300
)

```

```

## Warning in scale_y_continuous(trans = "log10"): log-10 transformation introduced infinite values.
## log-10 transformation introduced infinite values.

```

```

## Warning: Removed 2750073 rows containing non-finite outside the scale range
## ('stat_ydensity()').

```

```

## Warning: Removed 2750073 rows containing non-finite outside the scale range
## ('stat_boxplot()').

```

```

# Violin plot faceted by sample ID

```

```

p_vertex_id <- ggplot(df_plot, aes(x = id, y = distance, fill = raw_material)) +
  geom_violin(trim = FALSE, alpha = 0.6) +
  geom_boxplot(width = 0.15, alpha = 0.5, outlier.shape = NA) +
  scale_y_continuous(trans = "log10") +
  labs(
    title = "Per-Vertex Distances by Raw Material",
    subtitle = "Faceted by Sample ID (Cycle 0 vs Cycle 2)",
    x = "Samples",
    y = "Distance (log10 scale)"
  ) +
  facet_wrap(~ raw_material, scales = "free_x") + # <- changed here
  theme_minimal(base_size = 14) +
  theme(
    legend.position = "none",
    strip.text = element_text(size = 10, face = "bold"),
    axis.text.x = element_text(angle = 45, hjust = 1)
  )

ggsave(
  filename = file.path(out_plots, "vertex_distance_violin_facet_id.png"),
  plot = p_vertex_id,
  width = 12,
  height = 10,
  dpi = 300
)

```

```
## Warning in scale_y_continuous(trans = "log10"): log-10 transformation
## introduced infinite values.

## Warning in scale_y_continuous(trans = "log10"): log-10 transformation
## introduced infinite values.

## Warning: Removed 2750073 rows containing non-finite outside the scale range
## ('stat_ydensity()').

## Warning: Removed 2750073 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

p\_vertex\_rm

```
## Warning in scale_y_continuous(trans = "log10"): log-10 transformation
## introduced infinite values.

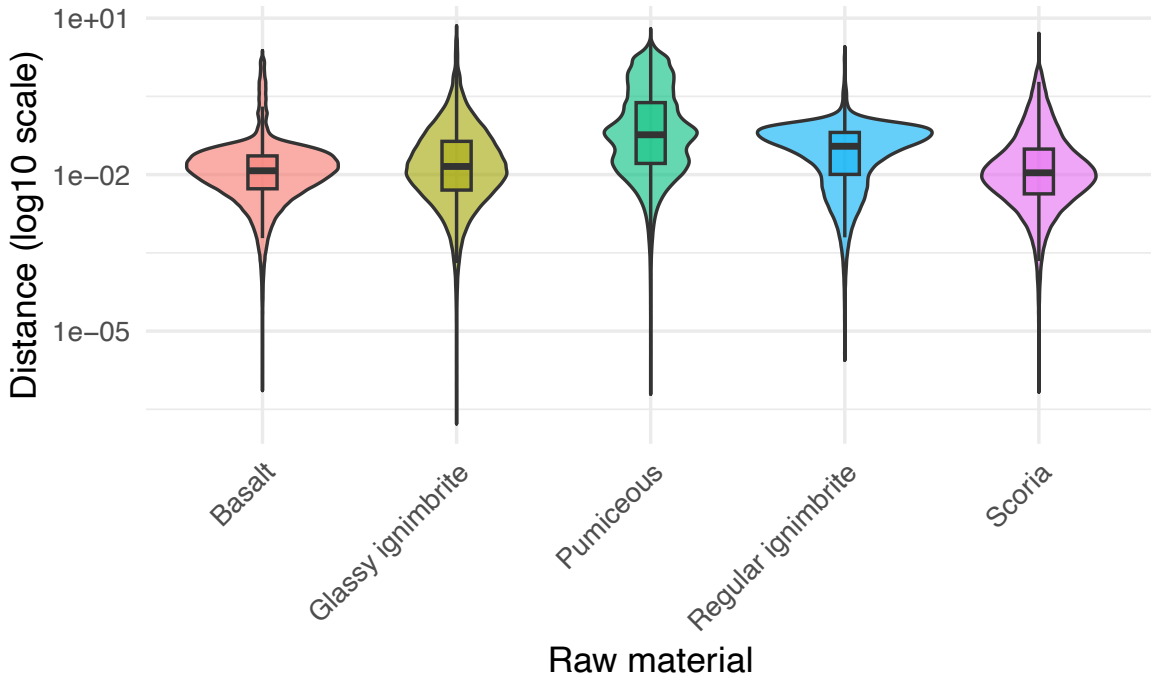
## Warning in scale_y_continuous(trans = "log10"): log-10 transformation
## introduced infinite values.

## Warning: Removed 2750073 rows containing non-finite outside the scale range
## ('stat_ydensity()').

## Warning: Removed 2750073 rows containing non-finite outside the scale range
## ('stat_boxplot()').
```

## Per-Vertex Distances by Raw Material

Cycle 0 vs Cycle 2 – point-to-surface distances (log scale)



```
p_vertex_id
```

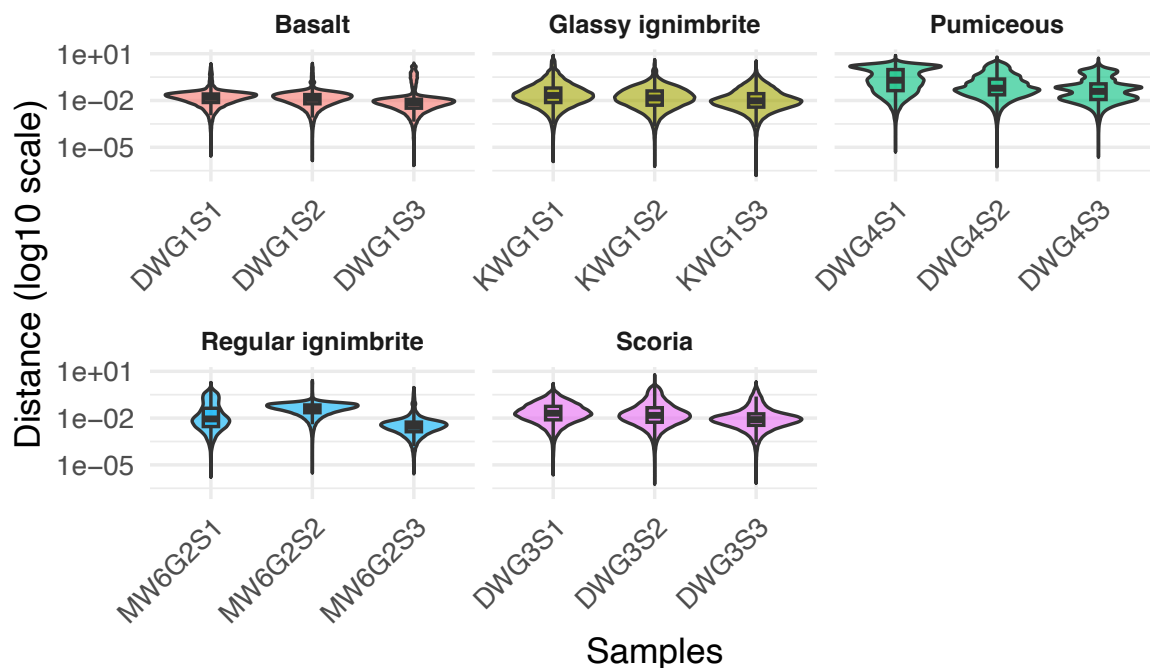
```
## Warning in scale_y_continuous(trans = "log10"): log-10 transformation  
## introduced infinite values.
```

```
## Warning in scale_y_continuous(trans = "log10"): log-10 transformation  
## introduced infinite values.
```

```
## Warning: Removed 2750073 rows containing non-finite outside the scale range  
## ('stat_ydensity()').
```

```
## Warning: Removed 2750073 rows containing non-finite outside the scale range  
## ('stat_boxplot()').
```

## Per-Vertex Distances by Raw Material Faceted by Sample ID (Cycle 0 vs Cycle 2)



Compute VD stats (difference between raw material)

```
df_test <- df_all %>%  
  filter(!is.na(raw_material)) %>%  
  mutate(raw_material = as.factor(raw_material))  
  
# Kruskal-Wallis  
kw_result <- kruskal_test(df_test, distance ~ raw_material)  
kw_result
```

```
## # A tibble: 1 x 6
##   .y.          n statistic   df    p method
## * <chr>      <int>      <dbl> <int> <dbl> <chr>
## 1 distance 3761250    37370.     4     0 Kruskal-Wallis
```

```
# EFFECT SIZE (Eta-squared)
kw_effect <- df_test %>%
  kruskal_effsize(distance ~ raw_material)
kw_effect
```

```
## # A tibble: 1 x 5
##   .y.          n effsize method magnitude
## * <chr>      <int>      <dbl> <chr>   <ord>
## 1 distance 3761250 0.00993 eta2[H] small
```

```
# work with means because dataset is massive
```

```
df_id_summary <- df_test %>%
  group_by(id, raw_material) %>%
  summarise(
    mean_dist = mean(distance, na.rm = TRUE),
    median_dist = median(distance, na.rm = TRUE),
    .groups = "drop"
  )
```

```
# POST-HOC TEST: Dunn test with BH correction
```

```
dunn_res <- df_id_summary %>%
  dunn_test(mean_dist ~ raw_material, p.adjust.method = "BH")
```

```
dunn_res
```

```
## # A tibble: 10 x 9
##   .y.      group1      group2    n1    n2 statistic     p  p.adj p.adj.signif
## * <chr>   <chr>      <chr>  <int> <int>   <dbl>  <dbl> <dbl> <chr>
## 1 mean_dist Basalt    Glass~     3     3    0.822  0.411  0.588 ns
## 2 mean_dist Basalt    Pumic~     3     3    2.10   0.0358 0.119 ns
## 3 mean_dist Basalt    Regul~     3     3   -0.365  0.715  0.871 ns
## 4 mean_dist Basalt    Scoria     3     3   -0.274  0.784  0.871 ns
## 5 mean_dist Glassy ign~ Pumic~     3     3    1.28   0.201  0.456 ns
## 6 mean_dist Glassy ign~ Regul~     3     3   -1.19   0.235  0.456 ns
## 7 mean_dist Glassy ign~ Scoria     3     3   -1.10   0.273  0.456 ns
## 8 mean_dist Pumiceous Regul~     3     3   -2.46   0.0137 0.0881 ns
## 9 mean_dist Pumiceous Scoria     3     3   -2.37   0.0176 0.0881 ns
## 10 mean_dist Regular ig~ Scoria     3     3    0.0913 0.927  0.927 ns
```

```
# Kolmogorov-Smirnov tests for every pair of raw materials
```

```
# Kolmogorov-Smirnov tests for every pair of raw materials
```

```
df_ks <- df_all %>%
  filter(!is.na(raw_material)) %>%
  mutate(raw_material = as.factor(raw_material))
```

```

materials <- unique(df_ks$raw_material)

ks_two_materials <- function(mat1, mat2, df) {
  d1 <- df %>% filter(raw_material == mat1) %>% pull(distance)
  d2 <- df %>% filter(raw_material == mat2) %>% pull(distance)

  ks <- ks.test(d1, d2)

  tibble(
    material1 = mat1,
    material2 = mat2,
    statistic = ks$statistic,
    p_value = ks$p.value
  )
}

# CREATE LIST OF ALL PAIRS
material_pairs <- combn(materials, 2, simplify = FALSE)

df_ks_results <- purrr::map_dfr(
  material_pairs,
  ~ ks_two_materials(.x[1], .x[2], df_ks)
)

```

```

## Warning in ks.test.default(d1, d2): p-value will be approximate in the presence
## of ties
## Warning in ks.test.default(d1, d2): p-value will be approximate in the presence
## of ties
## Warning in ks.test.default(d1, d2): p-value will be approximate in the presence
## of ties
## Warning in ks.test.default(d1, d2): p-value will be approximate in the presence
## of ties
## Warning in ks.test.default(d1, d2): p-value will be approximate in the presence
## of ties
## Warning in ks.test.default(d1, d2): p-value will be approximate in the presence
## of ties
## Warning in ks.test.default(d1, d2): p-value will be approximate in the presence
## of ties
## Warning in ks.test.default(d1, d2): p-value will be approximate in the presence
## of ties
## Warning in ks.test.default(d1, d2): p-value will be approximate in the presence
## of ties
## Warning in ks.test.default(d1, d2): p-value will be approximate in the presence
## of ties

```

```
df_ks_results
```

```

## # A tibble: 10 x 4
##   material1      material2      statistic p_value
##   <fct>          <fct>          <dbl>     <dbl>
## 1 Basalt        Scoria          0.0833     0
## 2 Basalt        Pumiceous       0.117     0

```

```
## 3 Basalt          Glassy ignimbrite    0.0511    0
## 4 Basalt          Regular ignimbrite   0.135     0
## 5 Scoria          Pumiceous             0.103     0
## 6 Scoria          Glassy ignimbrite    0.0776    0
## 7 Scoria          Regular ignimbrite   0.144     0
## 8 Pumiceous       Glassy ignimbrite   0.0666    0
## 9 Pumiceous       Regular ignimbrite  0.0858    0
## 10 Glassy ignimbrite Regular ignimbrite  0.0923    0
```

```
# Run KS for all pairs
```

```
ks_results <- map_dfr(material_pairs, ~ ks_two_materials(.x[1], .x[2], df_ks))
```

```
## Warning in ks.test.default(d1, d2): p-value will be approximate in the presence
## of ties
## Warning in ks.test.default(d1, d2): p-value will be approximate in the presence
## of ties
## Warning in ks.test.default(d1, d2): p-value will be approximate in the presence
## of ties
## Warning in ks.test.default(d1, d2): p-value will be approximate in the presence
## of ties
## Warning in ks.test.default(d1, d2): p-value will be approximate in the presence
## of ties
## Warning in ks.test.default(d1, d2): p-value will be approximate in the presence
## of ties
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## of ties
## Warning in ks.test.default(d1, d2): p-value will be approximate in the presence
## of ties
## Warning in ks.test.default(d1, d2): p-value will be approximate in the presence
## of ties
## Warning in ks.test.default(d1, d2): p-value will be approximate in the presence
## of ties
```

```
# Adjust p-values for multiple testing (BH recommended)
```

```
ks_results <- ks_results %>%
  mutate(p_adjusted = p.adjust(p_value, method = "BH"),
         signif = case_when(
           p_adjusted < 0.001 ~ "***",
           p_adjusted < 0.01  ~ "**",
           p_adjusted < 0.05  ~ "*",
           TRUE                ~ "ns"
         ))
```

```
ks_results
```

```
## # A tibble: 10 x 6
##   material1      material2      statistic p_value p_adjusted signif
##   <fct>         <fct>         <dbl>     <dbl>     <dbl> <chr>
## 1 Basalt        Scoria         0.0833     0         0 ***
## 2 Basalt        Pumiceous      0.117      0         0 ***
## 3 Basalt        Glassy ignimbrite 0.0511     0         0 ***
## 4 Basalt        Regular ignimbrite 0.135      0         0 ***
## 5 Scoria        Pumiceous      0.103      0         0 ***
```

```
## 6 Scoria          Glassy ignimbrite    0.0776    0    0 ***
## 7 Scoria          Regular ignimbrite   0.144     0    0 ***
## 8 Pumiceous       Glassy ignimbrite    0.0666    0    0 ***
## 9 Pumiceous       Regular ignimbrite   0.0858    0    0 ***
## 10 Glassy ignimbrite Regular ignimbrite  0.0923    0    0 ***
```

```
# Plot results of KS analysis

# Use the KS results from the previous chunk
df_heat <- ks_results %>%
  mutate(
    material1 = as.character(material1),
    material2 = as.character(material2)
  )

# Build a symmetric matrix for heat map
materials <- sort(unique(c(df_heat$material1, df_heat$material2)))

mat <- matrix(0, nrow = length(materials), ncol = length(materials),
              dimnames = list(materials, materials))

for (i in seq_len(nrow(df_heat))) {
  m1 <- df_heat$material1[i]
  m2 <- df_heat$material2[i]
  stat <- df_heat$statistic[i]

  mat[m1, m2] <- stat
  mat[m2, m1] <- stat
}

df_mat <- as_tibble(mat, rownames = "material1") %>%
  pivot_longer(-material1, names_to = "material2", values_to = "ks_statistic") %>%
  mutate(pair = paste(material1, material2)) # <-- ADD THIS

df_mat <- df_mat %>%
  left_join(
    ks_results %>%
      mutate(pair = paste(material1, material2)) %>% # ensure same format
      select(pair, signif),
    by = "pair"
  )

# Remove self-comparisons
df_mat$ks_statistic[df_mat$material1 == df_mat$material2] <- NA
df_mat$signif[df_mat$material1 == df_mat$material2] <- ""

df_mat
```

```
## # A tibble: 25 x 5
##   material1      material2      ks_statistic pair      signif
##   <chr>          <chr>          <dbl> <chr>      <chr>
## 1 Basalt        Basalt          NA     Basalt Basalt  ""
## 2 Basalt        Glassy ignimbrite 0.0511 Basalt Glassy ignim~ "***"
## 3 Basalt        Pumiceous       0.117  Basalt Pumiceous  "***"
```

```
## 4 Basalt          Regular ignimbrite      0.135 Basalt Regular igni~ "****"
## 5 Basalt          Scoria                  0.0833 Basalt Scoria      "****"
## 6 Glassy ignimbrite Basalt                0.0511 Glassy ignimbrite B~ <NA>
## 7 Glassy ignimbrite Glassy ignimbrite     NA      Glassy ignimbrite G~ ""
## 8 Glassy ignimbrite Pumiceous             0.0666 Glassy ignimbrite P~ <NA>
## 9 Glassy ignimbrite Regular ignimbrite    0.0923 Glassy ignimbrite R~ "****"
## 10 Glassy ignimbrite Scoria               0.0776 Glassy ignimbrite S~ <NA>
## # i 15 more rows
```

```
# Plot heat map
p_vd_heat <- ggplot(df_mat, aes(x = material1, y = material2, fill = ks_statistic)) +
  geom_tile(color = "white") +
  geom_text(aes(label = signif), size = 6, color = "black") +
  scale_fill_viridis_c(option = "plasma", na.value = "grey90") +
  labs(
    title = "Heatmap of KS Statistics Between Raw Materials",
    subtitle = "KS statistic (D) with significance annotations",
    x = "Material",
    y = "Material",
    fill = "KS Statistic (D)"
  ) +
  theme_minimal(base_size = 14) +
  theme(
    axis.text.x = element_text(angle = 45, hjust = 1),
    panel.grid = element_blank()
  )

ggsave(
  filename = file.path(out_plots, "KSanalysis_heat_rawmaterial.png"),
  plot = p_vd_heat,
  width = 12,
  height = 10,
  dpi = 300
)
```

```
## Warning: Removed 10 rows containing missing values or values outside the scale range
## ('geom_text()').
```

## Summarise VD data

```
# Compute summary stats for one ID
compute_distance_summary_id <- function(id, mesh_info, meshes) {

  pair <- mesh_info |>
  dplyr::filter(id == !!id & cycle %in% c(0,2))

  if (!all(c(0,2) %in% pair$cycle)) {
    message("Skipping ", id, ": missing cycle0 or cycle2.")
    return(NULL)
  }

  key0 <- paste0(id, "_cycle0")
```

```

key2 <- paste0(id, "_cycle2")

mesh0 <- meshes[[key0]]
mesh2 <- meshes[[key2]]

d <- compute_vertex_distances(mesh0, mesh2)

tibble::tibble(
  id = id,
  cycle0_file = key0,
  cycle2_file = key2,
  mean_dist = mean(d),
  median_dist = median(d),
  rms_dist = sqrt(mean(d^2)),
  min_dist = min(d),
  max_dist = max(d),
  n_vertices = length(d)
)
}

# Compute summary stats for ALL IDs and export to CSV
export_all_distance_summaries <- function(mesh_info,
                                          meshes,
                                          outfile = "analysis/data/derived_data/summary_vertex_distances_")

  ids <- unique(mesh_info$id)

  summaries <- lapply(ids, function(id) compute_distance_summary_id(id, mesh_info, meshes))

  summaries <- summaries[!sapply(summaries, is.null)]

  df_summary <- dplyr::bind_rows(summaries) %>%
    dplyr::left_join(raw_material_lookup, by = "id")

  outdir <- dirname(outfile)
  if (!dir.exists(outdir)) dir.create(outdir, recursive = TRUE)

  readr::write_csv(df_summary, outfile)

  message("Exported summary stats with raw material → ", outfile)

  return(df_summary)
}

df_summary <- export_all_distance_summaries(mesh_info, meshes)

## Exported summary stats with raw material → analysis/data/derived_data/summary_vertex_distances_cycle0

df_summary

## # A tibble: 15 x 10

```

```
##   id      cycle0_file  cycle2_file  mean_dist median_dist rms_dist min_dist
##   <chr>   <chr>         <chr>         <dbl>     <dbl>     <dbl>   <dbl>
##  1 DWG1S1 DWG1S1_cycle0 DWG1S1_cycle2  0.00853    0         0.0531    0
##  2 DWG1S2 DWG1S2_cycle0 DWG1S2_cycle2  0.00910    0         0.0559    0
##  3 DWG1S3 DWG1S3_cycle0 DWG1S3_cycle2  0.0155    0         0.108     0
##  4 DWG3S1 DWG3S1_cycle0 DWG3S1_cycle2  0.0106    0         0.0449    0
##  5 DWG3S2 DWG3S2_cycle0 DWG3S2_cycle2  0.00853    0         0.0623    0
##  6 DWG3S3 DWG3S3_cycle0 DWG3S3_cycle2  0.0116    0         0.0573    0
##  7 DWG4S1 DWG4S1_cycle0 DWG4S1_cycle2  0.0689    0         0.312     0
##  8 DWG4S2 DWG4S2_cycle0 DWG4S2_cycle2  0.0575    0         0.263     0
##  9 DWG4S3 DWG4S3_cycle0 DWG4S3_cycle2  0.0696    0         0.223     0
## 10 KWG1S1 KWG1S1_cycle0 KWG1S1_cycle2  0.0254    0         0.174     0
## 11 KWG1S2 KWG1S2_cycle0 KWG1S2_cycle2  0.0119    0         0.0689    0
## 12 KWG1S3 KWG1S3_cycle0 KWG1S3_cycle2  0.0138    0         0.0514    0
## 13 MW6G2S1 MW6G2S1_cycle0 MW6G2S1_cycle2  0.00268    0         0.0283    0
## 14 MW6G2S2 MW6G2S2_cycle0 MW6G2S2_cycle2  0.0307    0.0142    0.0667    0
## 15 MW6G2S3 MW6G2S3_cycle0 MW6G2S3_cycle2  0.00333    0         0.0206    0
## # i 3 more variables: max_dist <dbl>, n_vertices <int>, raw_material <chr>
```

## Compute Root Mean Square (RMS)

### Compute RMS distance using vcgClostKD

```
# Compute RMS for one sample ID
compute_rms_for_id <- function(id, mesh_info, meshes) {

  pair <- mesh_info |>
    filter(id == !!id & cycle %in% c(0,2))

  if (!all(c(0,2) %in% pair$cycle)) {
    message("Skipping ", id, ": missing cycle0 or cycle2.")
    return(NULL)
  }

  key0 <- paste0(id, "_cycle0")
  key2 <- paste0(id, "_cycle2")

  mesh0 <- meshes[[key0]]
  mesh2 <- meshes[[key2]]

  kd <- Rvcg::vcgClostKD(mesh2, mesh0)
  d <- kd$quality

  d[!is.finite(d)] <- 0
  d[d < 0] <- 0

  tibble(
    id = id,
    cycle0_file = key0,
    cycle2_file = key2,
    rms_dist = sqrt(mean(d^2)),
```

```

    mean_dist = mean(d),
    median_dist = median(d),
    min_dist = min(d),
    max_dist = max(d),
    n_vertices = length(d)
  )
}

# Compute vcgClostKD RMS for all IDs
compute_all_rms <- function(mesh_info, meshes) {

  ids <- unique(mesh_info$id)

  summaries <- lapply(ids, function(id) compute_rms_for_id(id, mesh_info, meshes))
  summaries <- summaries[!sapply(summaries, is.null)]

  df_rms <- bind_rows(summaries) %>%
    left_join(raw_material_lookup, by = "id")

  df_rms
}

# Run it
df_rms <- compute_all_rms(mesh_info, meshes)
df_rms

```

```

## # A tibble: 15 x 10
##   id      cycle0_file  cycle2_file  rms_dist mean_dist median_dist min_dist
##   <chr>  <chr>             <chr>         <dbl>    <dbl>    <dbl>    <dbl>
## 1 DWG1S1 DWG1S1_cycle0    DWG1S1_cycle2  0.0531  0.00853  0        0
## 2 DWG1S2 DWG1S2_cycle0    DWG1S2_cycle2  0.0559  0.00910  0        0
## 3 DWG1S3 DWG1S3_cycle0    DWG1S3_cycle2  0.108   0.0155   0        0
## 4 DWG3S1 DWG3S1_cycle0    DWG3S1_cycle2  0.0449  0.0106   0        0
## 5 DWG3S2 DWG3S2_cycle0    DWG3S2_cycle2  0.0623  0.00853  0        0
## 6 DWG3S3 DWG3S3_cycle0    DWG3S3_cycle2  0.0573  0.0116   0        0
## 7 DWG4S1 DWG4S1_cycle0    DWG4S1_cycle2  0.312   0.0689   0        0
## 8 DWG4S2 DWG4S2_cycle0    DWG4S2_cycle2  0.263   0.0575   0        0
## 9 DWG4S3 DWG4S3_cycle0    DWG4S3_cycle2  0.223   0.0696   0        0
## 10 KWG1S1 KWG1S1_cycle0    KWG1S1_cycle2  0.174   0.0254   0        0
## 11 KWG1S2 KWG1S2_cycle0    KWG1S2_cycle2  0.0689  0.0119   0        0
## 12 KWG1S3 KWG1S3_cycle0    KWG1S3_cycle2  0.0514  0.0138   0        0
## 13 MW6G2S1 MW6G2S1_cycle0  MW6G2S1_cycle2  0.0283  0.00268  0        0
## 14 MW6G2S2 MW6G2S2_cycle0  MW6G2S2_cycle2  0.0667  0.0307   0.0142   0
## 15 MW6G2S3 MW6G2S3_cycle0  MW6G2S3_cycle2  0.0206  0.00333  0        0
## # i 3 more variables: max_dist <dbl>, n_vertices <int>, raw_material <chr>

```

```

readr::write_csv(
  df_rms,
  file.path(out_csv, "ClostKD_cycle0_vs_cycle2.csv")
)

```

## Plots RMS vcgClotKD data

```
df_plot <- df_rms %>%
  filter(!is.na(raw_material)) %>%
  mutate(raw_material = as.factor(raw_material))

p_CKD_RMS <- ggplot(df_plot, aes(x = raw_material, y = rms_dist, fill = raw_material)) +
  geom_violin(trim = FALSE, alpha = 0.6) +
  geom_boxplot(width = 0.15, alpha = 0.5, outlier.shape = NA) +
  geom_jitter(width = 0.05, size = 2, alpha = 0.7) +
  labs(
    title = "RMS Distance (Cycle 0 vs Cycle 2) - Grouped by Raw material",
    x = "Raw material",
    y = "RMS distance"
  ) +
  theme_minimal(base_size = 14) +
  theme(
    legend.position = "none",
    axis.text.x = element_text(angle = 45, hjust = 1)
  )

ggsave(
  filename = file.path(out_plots, "vcgClotKD_rawmaterial.png"),
  plot = p_CKD_RMS,
  width = 12,
  height = 10,
  dpi = 300
)
```

## Plot RMS vcgClotKD data heatmap

```
mean_rms <- df_rms %>%
  filter(!is.na(raw_material)) %>%
  group_by(raw_material) %>%
  summarise(
    mean_RMS = mean(rms_dist),
    .groups = "drop"
  )

materials <- mean_rms$raw_material

diff_mat <- outer(
  mean_rms$mean_RMS,
  mean_rms$mean_RMS,
  FUN = function(a, b) abs(a - b)
)

colnames(diff_mat) <- materials
rownames(diff_mat) <- materials
```

```

df_diff <- as.data.frame(diff_mat) %>%
  mutate(material1 = rownames(.)) %>%
  pivot_longer(-material1, names_to = "material2", values_to = "diff_RMS")

# 3. Plot heat map
p_CKD_RMS_heat <- ggplot(df_diff, aes(x = material1, y = material2, fill = diff_RMS)) +
  geom_tile(color = "white") +
  geom_text(aes(label = sprintf("%.4f", diff_RMS)), color = "black", size = 4) +
  scale_fill_viridis_c(option = "plasma") +
  labs(
    title = "Heatmap of RMS differences between Raw materials",
    subtitle = "Absolute differences in mean RMS values (Cycle 0 vs Cycle 2)",
    x = "Raw Material",
    y = "Raw Material",
    fill = "RMS"
  ) +
  theme_minimal(base_size = 14) +
  theme(
    axis.text.x = element_text(angle = 45, hjust = 1),
    panel.grid = element_blank()
  )

ggsave(
  filename = file.path(out_plots, "vcgClostKD_heat_rawmaterial.png"),
  plot = p_CKD_RMS_heat,
  width = 12,
  height = 10,
  dpi = 300
)

```

## Run ANOVA for RMS vcgClostKD data

```

df_test <- df_rms %>%
  filter(!is.na(raw_material))

# 1. ANOVA (parametric)
anova_model <- aov(rms_dist ~ raw_material, data = df_test)
anova_summary <- summary(anova_model)
anova_summary

##              Df Sum Sq Mean Sq F value Pr(>F)
## raw_material  4 0.10198 0.025495  15.86 0.000249 ***
## Residuals    10 0.01607 0.001607
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# 2. ANOVA Assumptions

# Normality of residuals
shapiro_result <- shapiro_test(residuals(anova_model))
shapiro_result

```

```
## # A tibble: 1 x 3
##   variable      statistic p.value
##   <chr>          <dbl> <dbl>
## 1 residuals(anova_model) 0.942 0.413
```

```
# Homogeneity of variance (Levene test)
```

```
levene_result <- levene_test(rms_dist ~ raw_material, data = df_test)
```

```
## Warning in leveneTest.default(y = y, group = group, ...): group coerced to
## factor.
```

```
levene_result
```

```
## # A tibble: 1 x 4
##   df1 df2 statistic    p
##   <int> <int> <dbl> <dbl>
## 1     4    10 0.531 0.716
```

```
# Interpretation:
```

```
# - If residuals are NOT normal OR Levene test is significant (p < 0.05),
#   use Kruskal-Wallis instead of ANOVA.
```

```
# 3. Kruskal-Wallis (non-parametric alternative)
```

```
kw_result <- kruskal_test(rms_dist ~ raw_material, data = df_test)
```

```
kw_result
```

```
## # A tibble: 1 x 6
##   .y.      n statistic  df      p method
## * <chr> <int> <dbl> <int> <dbl> <chr>
## 1 rms_dist 15      8.53    4 0.0739 Kruskal-Wallis
```

```
# Effect size (Kruskal eta-squared)
```

```
kw_effect <- kruskal_effsize(rms_dist ~ raw_material, data = df_test)
```

```
kw_effect
```

```
## # A tibble: 1 x 5
##   .y.      n effsize method magnitude
## * <chr> <int> <dbl> <chr> <ord>
## 1 rms_dist 15 0.453 eta2[H] large
```

```
# 4. Post-hoc tests
```

```
# ANOVA post-hoc (Tukey HSD)
```

```
tukey_result <- TukeyHSD(anova_model)
```

```
tukey_result
```

```
## Tukey multiple comparisons of means
```

```
## 95% family-wise confidence level
```

```
##
```

```
## Fit: aov(formula = rms_dist ~ raw_material, data = df_test)
```

```
##
## $raw_material
##
##           diff           lwr           upr
## Glassy ignimbrite-Basalt      0.02563653 -0.08209489 0.13336795
## Pumiceous-Basalt              0.19366050 0.08592908 0.30139192
## Regular ignimbrite-Basalt    -0.03391706 -0.14164848 0.07381436
## Scoria-Basalt                -0.01761034 -0.12534176 0.09012108
## Pumiceous-Glassy ignimbrite  0.16802396 0.06029254 0.27575538
## Regular ignimbrite-Glassy ignimbrite -0.05955360 -0.16728502 0.04817782
## Scoria-Glassy ignimbrite    -0.04324687 -0.15097829 0.06448455
## Regular ignimbrite-Pumiceous -0.22757756 -0.33530898 -0.11984614
## Scoria-Pumiceous            -0.21127083 -0.31900225 -0.10353941
## Scoria-Regular ignimbrite    0.01630673 -0.09142469 0.12403815
##
##           p adj
## Glassy ignimbrite-Basalt      0.9298257
## Pumiceous-Basalt              0.0010797
## Regular ignimbrite-Basalt    0.8333841
## Scoria-Basalt                0.9810454
## Pumiceous-Glassy ignimbrite  0.0031428
## Regular ignimbrite-Glassy ignimbrite 0.4143498
## Scoria-Glassy ignimbrite     0.6855170
## Regular ignimbrite-Pumiceous 0.0002944
## Scoria-Pumiceous            0.0005412
## Scoria-Regular ignimbrite    0.9857048
```

```
# Kruskal-Wallis post-hoc (Dunn test with BH correction)
dunn_result <- df_test %>%
  dunn_test(rms_dist ~ raw_material, p.adjust.method = "BH")
dunn_result
```

```
## # A tibble: 10 x 9
##   .y.      group1      group2    n1    n2 statistic      p  p.adj p.adj.signif
## * <chr> <chr> <chr> <int> <int> <dbl> <dbl> <dbl> <chr>
## 1 rms_dist Basalt    Glass~     3     3  0.365 0.715 0.715 ns
## 2 rms_dist Basalt    Pumic~     3     3  1.83 0.0679 0.226 ns
## 3 rms_dist Basalt    Regul~     3     3 -0.913 0.361 0.602 ns
## 4 rms_dist Basalt    Scoria     3     3 -0.365 0.715 0.715 ns
## 5 rms_dist Glassy ign~ Pumic~     3     3  1.46 0.144 0.360 ns
## 6 rms_dist Glassy ign~ Regul~     3     3 -1.28 0.201 0.402 ns
## 7 rms_dist Glassy ign~ Scoria     3     3 -0.730 0.465 0.665 ns
## 8 rms_dist Pumiceous  Regul~     3     3 -2.74 0.00617 0.0617 ns
## 9 rms_dist Pumiceous  Scoria     3     3 -2.19 0.0285 0.142 ns
## 10 rms_dist Regular ign~ Scoria     3     3  0.548 0.584 0.715 ns
```

## Compute RMS using vcgMetro

```
compute_metro_pair <- function(mesh1, mesh2) {
  # mesh1, mesh2 are mesh objects from Rvcg
  # order: distances from mesh1 -> mesh2 (ForwardSampling),
  #         and mesh2 -> mesh1 (BackwardSampling)
```

```

md <- Rvcg::vcgMetro(mesh1, mesh2)

tibble(
  RMS_forward = md$ForwardSampling$RMSdist,
  RMS_backward = md$BackwardSampling$RMSdist,
  mean_forward = md$ForwardSampling$MeanDist,
  mean_backward = md$BackwardSampling$MeanDist,
  max_forward = md$ForwardSampling$MaxDist,
  max_backward = md$BackwardSampling$MaxDist
)
}

compute_metro_for_id <- function(id, mesh_info, meshes) {

  sub <- mesh_info %>%
    filter(id == !!id & cycle %in% c(0, 2))

  if (!all(c(0, 2) %in% sub$cycle)) {
    message("Skipping ", id, ": missing cycle0 or cycle2.")
    return(NULL)
  }

  key0 <- paste0(id, "_cycle0")
  key2 <- paste0(id, "_cycle2")

  mesh0 <- meshes[[key0]]
  mesh2 <- meshes[[key2]]

  metro_stats <- compute_metro_pair(mesh0, mesh2)

  tibble(
    id = id,
    cycle0_file = key0,
    cycle2_file = key2
  ) %>%
    bind_cols(metro_stats)
}

compute_all_metro <- function(mesh_info, meshes) {
  ids <- unique(mesh_info$id)

  res_list <- lapply(ids, function(id) compute_metro_for_id(id, mesh_info, meshes))
  res_list <- res_list[!sapply(res_list, is.null)]

  df_metro <- bind_rows(res_list) %>%
    left_join(raw_material_lookup, by = "id")

  df_metro
}

# run it
df_metro <- compute_all_metro(mesh_info, meshes)

```





```

readr::write_csv(
  df_metro,
  file.path(out_csv, "metro_cycle0_vs_cycle2.csv")
)

```

## # Plot RMS vcgMetro data

```

# forward
df_forward <- df_metro %>%
  filter(!is.na(raw_material)) %>%
  mutate(raw_material = factor(raw_material))

metro_fr <- ggplot(df_forward, aes(x = raw_material, y = RMS_forward, fill = raw_material)) +
  geom_boxplot(alpha = 0.7, outlier.shape = NA) +
  geom_jitter(width = 0.05, size = 2.5, alpha = 0.9) +
  labs(
    title = "Metro RMS (Forward: mesh0 → mesh2)",
    x = "Raw material",
    y = "RMS forward"
  ) +
  theme_minimal(base_size = 14) +
  theme(
    legend.position = "none",
    axis.text.x = element_text(angle = 45, hjust = 1)
  )

ggsave(
  filename = file.path(out_plots, "vector_fr.png"),
  plot = metro_fr,
  width = 12,
  height = 10,
  dpi = 300
)

# backwards
df_backward <- df_metro %>%
  filter(!is.na(raw_material)) %>%
  mutate(raw_material = factor(raw_material))

metro_br <- ggplot(df_backward, aes(x = raw_material, y = RMS_backward, fill = raw_material)) +
  geom_boxplot(alpha = 0.7, outlier.shape = NA) +
  geom_jitter(width = 0.05, size = 2.5, alpha = 0.9) +
  labs(
    title = "Metro RMS (Backward: mesh2 → mesh0)",
    x = "Raw material",
    y = "RMS backward"
  ) +
  theme_minimal(base_size = 14) +
  theme(
    legend.position = "none",
    axis.text.x = element_text(angle = 45, hjust = 1)
  )

```

```

)

ggsave(
  filename = file.path(out_plots, "vector_br.png"),
  plot = metro_br,
  width = 12,
  height = 10,
  dpi = 300
)

```

## Run ANOVA for RMS vcgMetro data

```

df_forward <- df_metro %>%
  filter(!is.na(raw_material)) %>%
  mutate(raw_material = factor(raw_material))

# ANOVA
anova_forward <- aov(RMS_forward ~ raw_material, data = df_forward)
anova_summary <- summary(anova_forward)
anova_summary

```

```

##              Df Sum Sq Mean Sq F value Pr(>F)
## raw_material  4 0.08104 0.020259   4.368 0.0267 *
## Residuals    10 0.04638 0.004638
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

# ANOVA ASSUMPTIONS
# 1. Normality of residuals
residuals_normality <- shapiro_test(residuals(anova_forward))
residuals_normality

```

```

## # A tibble: 1 x 3
##   variable          statistic p.value
##   <chr>              <dbl>   <dbl>
## 1 residuals(anova_forward)  0.911  0.142

```

```

# 2. Homogeneity of variance (Levene's test)
levene_test_forward <- leveneTest(RMS_forward ~ raw_material, data = df_forward)
levene_test_forward

```

```

## Levene's Test for Homogeneity of Variance (center = median)
##           Df F value Pr(>F)
## group    4  0.8658 0.5168
##           10

```

```

# Interpretation message
if (residuals_normality$p.value < 0.05) {
  message("Residuals are NOT normal: ANOVA assumptions violated. Use Kruskal-Wallis instead.")
}

```

```

}

if (levene_test_forward$`Pr(>F)`[1] < 0.05) {
  message("Variances are NOT equal: ANOVA assumptions violated. Use Kruskal-Wallis instead.")
}

# Tukey Post-hoc Test (Only valid if assumptions met)
tukey_forward <- TukeyHSD(anova_forward)
tukey_forward

```

```

## Tukey multiple comparisons of means
## 95% family-wise confidence level
##
## Fit: aov(formula = RMS_forward ~ raw_material, data = df_forward)
##
## $raw_material
##
##           diff           lwr           upr
## Glassy ignimbrite-Basalt -0.052056383 -0.23506621 0.13095344
## Pumiceous-Basalt         0.149728231 -0.03328160 0.33273806
## Regular ignimbrite-Basalt 0.025928992 -0.15708084 0.20893882
## Scoria-Basalt           -0.048397611 -0.23140744 0.13461222
## Pumiceous-Glassy ignimbrite 0.201784614 0.01877479 0.38479444
## Regular ignimbrite-Glassy ignimbrite 0.077985375 -0.10502445 0.26099520
## Scoria-Glassy ignimbrite 0.003658772 -0.17935106 0.18666860
## Regular ignimbrite-Pumiceous -0.123799239 -0.30680907 0.05921059
## Scoria-Pumiceous        -0.198125842 -0.38113567 -0.01511601
## Scoria-Regular ignimbrite -0.074326603 -0.25733643 0.10868322
##
##           p adj
## Glassy ignimbrite-Basalt 0.8764889
## Pumiceous-Basalt         0.1251602
## Regular ignimbrite-Basalt 0.9888146
## Scoria-Basalt           0.9014127
## Pumiceous-Glassy ignimbrite 0.0296049
## Regular ignimbrite-Glassy ignimbrite 0.6397588
## Scoria-Glassy ignimbrite 0.9999949
## Regular ignimbrite-Pumiceous 0.2454605
## Scoria-Pumiceous        0.0327841
## Scoria-Regular ignimbrite 0.6768545

```

## Plot Tukey test

```

tukey_tbl <- as.data.frame(tukey_forward$raw_material) %>%
  mutate(comparison = rownames(.)) %>%
  select(comparison, p_adj = `p adj`)

# Split "A-B" into two columns
tukey_tbl <- tukey_tbl %>%
  separate(comparison, into = c("mat1", "mat2"), sep = "-")

# Collect all raw materials (factor level order preserved)

```

```

materials <- levels(df_forward$raw_material)

# --- Build a full matrix of p-values ---
mat <- matrix(NA, nrow = length(materials), ncol = length(materials),
             dimnames = list(materials, materials))

for (i in seq_len(nrow(tukey_tbl))) {
  m1 <- tukey_tbl$mat1[i]
  m2 <- tukey_tbl$mat2[i]
  p <- tukey_tbl$p_adj[i]

  mat[m1, m2] <- p
  mat[m2, m1] <- p
}

diag(mat) <- NA # no self-comparisons

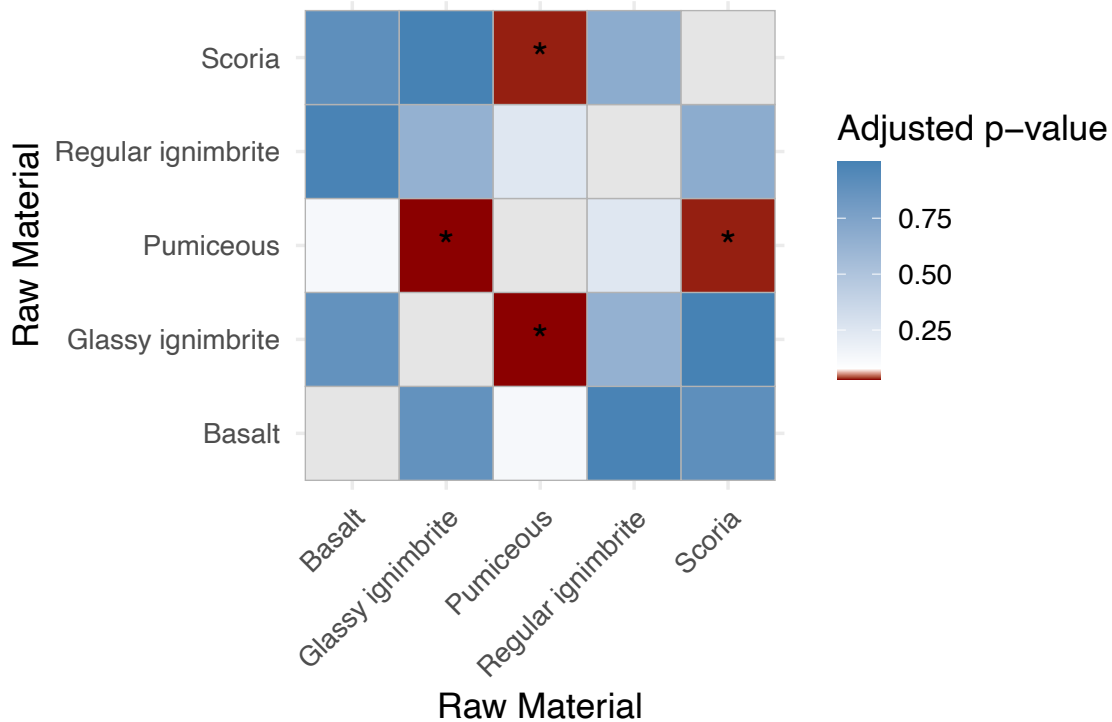
# --- Convert to long format for ggplot ---
df_heat <- as.data.frame(mat) %>%
  mutate(material1 = rownames(.)) %>%
  pivot_longer(-material1, names_to = "material2", values_to = "p_value")

# Significance labels
df_heat <- df_heat %>%
  mutate(
    signif = case_when(
      is.na(p_value) ~ "",
      p_value < 0.001 ~ "****",
      p_value < 0.01 ~ "***",
      p_value < 0.05 ~ "**",
      TRUE ~ ""
    )
  )

# --- Plot heatmap ---
ggplot(df_heat, aes(x = material1, y = material2, fill = p_value)) +
  geom_tile(color = "grey70") +
  geom_text(aes(label = signif), size = 6, color = "black") +
  scale_fill_gradientn(
    colours = c("darkred", "white", "steelblue"),
    values = scales::rescale(c(0, 0.05, 1)),
    na.value = "grey90",
    name = "Adjusted p-value"
  ) +
  coord_fixed() +
  labs(
    title = "Tukey Post-Hoc Test - Adjusted p-value Heatmap",
    x = "Raw Material",
    y = "Raw Material"
  ) +
  theme_minimal(base_size = 14) +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))

```

## Tukey Post-Hoc Test – Adjusted p-value Heatmap



```
ggsave(
  file.path(out_plots, "tukey_heatmap_RMS_forward.png"),
  width = 10, height = 8, dpi = 300
)
```

## Hausdorff distance function

```
library(RANN)
```

```
## Warning: package 'RANN' was built under R version 4.3.3
```

```
hausdorff_mesh <- function(mesh1, mesh2) {
  # Extract vertex coordinates (remove homogeneous 4th row)
  v1 <- t(mesh1$vb[1:3, , drop = FALSE])
  v2 <- t(mesh2$vb[1:3, , drop = FALSE])

  # sanity check
  if (nrow(v1) < 3 | nrow(v2) < 3)
    stop("One of the meshes has fewer than 3 vertices.")

  # Directed distances
  nn12 <- nn2(data = v2, query = v1, k = 1)$nn.dists
  nn21 <- nn2(data = v1, query = v2, k = 1)$nn.dists
}
```

```

list(
  directed_1_to_2 = max(nn12),
  directed_2_to_1 = max(nn21),
  hausdorff      = max(max(nn12), max(nn21)),
  mean_1_to_2    = mean(nn12),
  mean_2_to_1    = mean(nn21),
  q12            = quantile(nn12, c(.5, .9, .95, .99)),
  q21            = quantile(nn21, c(.5, .9, .95, .99))
)
}

```

## Generate comparisons

```

# Build table of available IDs and cycles
mesh_pairs <- mesh_info %>%
  select(id, cycle) %>%
  distinct() %>%
  group_by(id) %>%
  filter(all(c(0, 2) %in% cycle)) %>% # ensure you have cycle0 and cycle2
  ungroup()

# Create pairs: id, mesh0_name, mesh2_name
comparison_table <- mesh_pairs %>%
  mutate(
    mesh0 = paste0(id, "_cycle0"),
    mesh2 = paste0(id, "_cycle2")
  ) %>%
  select(id, mesh0, mesh2) %>%
  left_join(raw_material_lookup, by = "id")

```

## Compute Hausdorff distances

```

hausdorff_results <- comparison_table %>%
  mutate(
    res = map2(mesh0, mesh2, ~ {
      m1 <- meshes[[.x]]
      m2 <- meshes[[.y]]
      hausdorff_mesh(m1, m2)
    })
  ) %>%
  mutate(
    H          = map_dbl(res, "hausdorff"),
    h_1_to_2   = map_dbl(res, "directed_1_to_2"),
    h_2_to_1   = map_dbl(res, "directed_2_to_1"),
    mean_12    = map_dbl(res, "mean_1_to_2"),
    mean_21    = map_dbl(res, "mean_2_to_1")
  ) %>%

```

```

select(id, raw_material, mesh0, mesh2,
       H, h_1_to_2, h_2_to_1, mean_12, mean_21)

write.csv(
  hausdorff_results,
  file.path(out_csv, "hausdorff_distances.csv"),
  row.names = FALSE
)

```

## Merge Hausdorff results into the per-vertex dataset

```

df_plot2 <- df_plot %>%
  left_join(
    hausdorff_results %>% select(id, H, h_1_to_2, h_2_to_1),
    by = "id"
  )

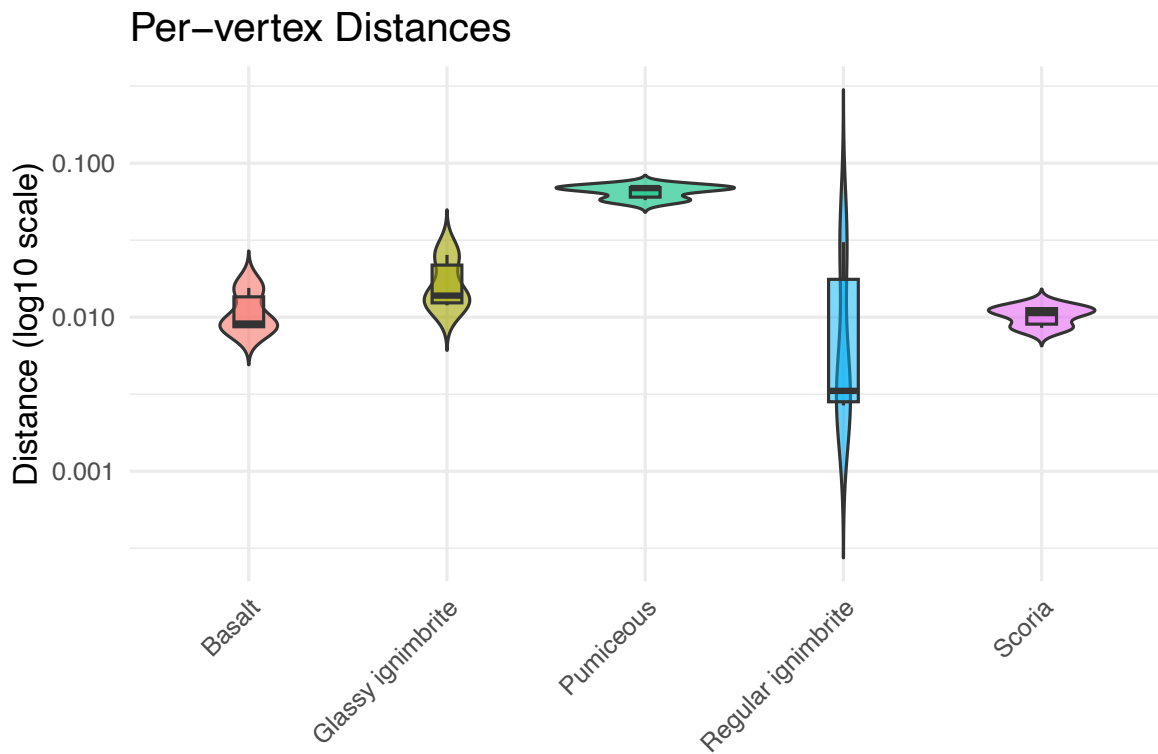
```

## Per-vertex individuals

```

pA <- ggplot(df_plot2, aes(x = raw_material, y = mean_dist, fill = raw_material)) +
  geom_violin(trim = FALSE, alpha = .6) +
  geom_boxplot(width = 0.15, alpha = .5, outlier.shape = NA) +
  scale_y_continuous(trans = "log10") +
  labs(
    title = "Per-vertex Distances",
    y = "Distance (log10 scale)",
    x = ""
  ) +
  theme_minimal(base_size = 13) +
  theme(
    axis.text.x = element_text(angle = 45, hjust = 1),
    legend.position = "none"
  )
pA

```

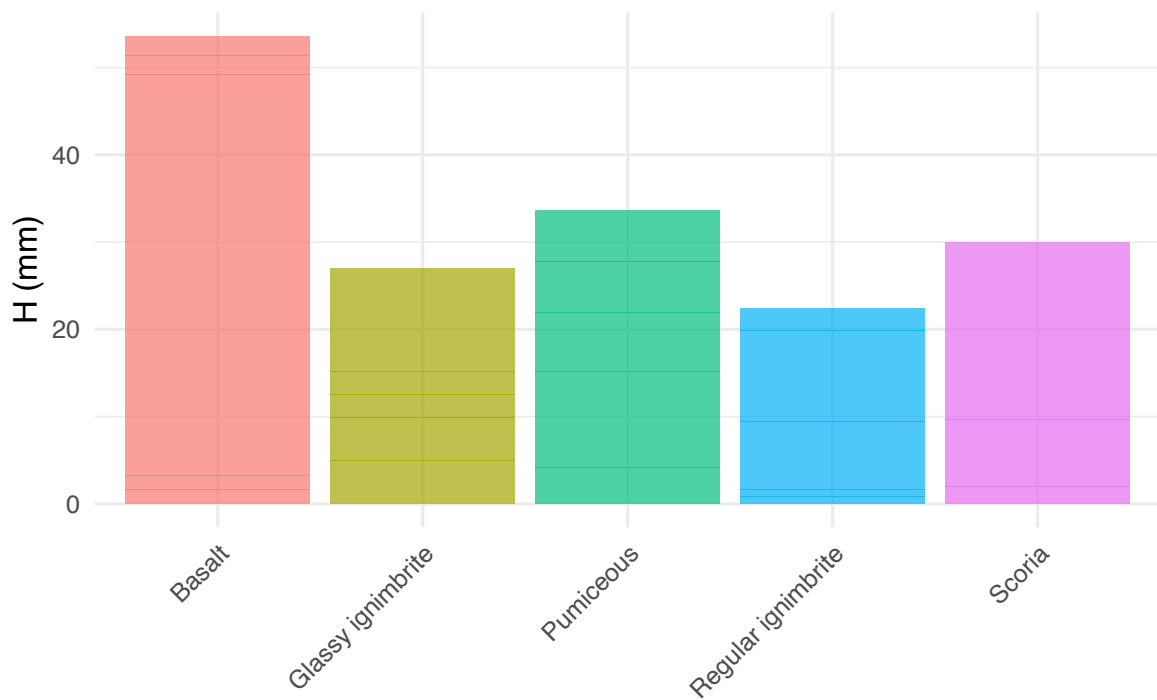


```
ggsave(
  filename = file.path(out_plots, "per-vertex_id.png"),
  plot = pA,
  width = 12,
  height = 10,
  dpi = 300
)
```

### Global Hdf distance

```
pB <- ggplot(hausdorff_results, aes(x = raw_material, y = H, fill = raw_material)) +
  geom_col(alpha = 0.7) +
  labs(
    title = "Global Hausdorff Distance",
    x = "",
    y = "H (mm)"
  ) +
  theme_minimal(base_size = 13) +
  theme(
    axis.text.x = element_text(angle = 45, hjust = 1),
    legend.position = "none"
  )
pB
```

## Global Hausdorff Distance



```
ggsave(  
  filename = file.path(out_plots, "hdf_dist_global.png"),  
  plot = pB,  
  width = 12,  
  height = 10,  
  dpi = 300  
)  
  
# test  
  
p_haus_violin <- ggplot(hausdorff_results, aes(x = raw_material, y = mean_21, fill = raw_material)) +  
  geom_violin(alpha = 0.6, trim = FALSE) +  
  geom_jitter(width = 0.08, alpha = 0.8) +  
  labs(  
    title = "Distribution of Hausdorff distances per Raw material",  
    x = "Raw material",  
    y = "Hausdorff distance"  
  ) +  
  theme_minimal(base_size = 14) +  
  theme(  
    legend.position = "none",  
    axis.text.x = element_text(angle = 45, hjust = 1)  
  )  
  
ggsave(  
  filename = file.path(out_plots, "p_haus.png"),  
  plot = p_haus_violin,  
  width = 12,
```

```

    height = 10,
    dpi = 300
  )

# test2
# boxplots

p_haus_box <- ggplot(hausdorff_results, aes(x = raw_material, y = mean_21, fill = raw_material)) +
  geom_boxplot(alpha = 0.7, outlier.shape = NA) +
  geom_jitter(width = 0.05, size = 2.5, alpha = 0.8) +
  labs(
    title = "Hausdorff Distance by Raw Material",
    x = "Raw material",
    y = "Hausdorff distance"
  ) +
  theme_minimal(base_size = 14) +
  theme(
    legend.position = "none",
    axis.text.x = element_text(angle = 45, hjust = 1)
  )

ggsave(
  filename = file.path(out_plots, "haus_box.png"),
  plot = p_haus_box,
  width = 12,
  height = 10,
  dpi = 300
)

```

## direct distance

```

pC <- ggplot(hausdorff_results,
  aes(x = h_1_to_2, y = h_2_to_1, label = id, color = raw_material)) +
  geom_point(size = 3) +
  geom_abline(intercept = 0, slope = 1, linetype = 2) +
  geom_text(nudge_y = 0.003, size = 3) +
  labs(
    title = "Directed Hausdorff Distances",
    x = "h1-2 (mm)",
    y = "h2-1 (mm)"
  ) +
  theme_minimal(base_size = 13) +
  theme(
    legend.position = "none",
    axis.text.x = element_text(angle = 45, hjust = 1)
  )

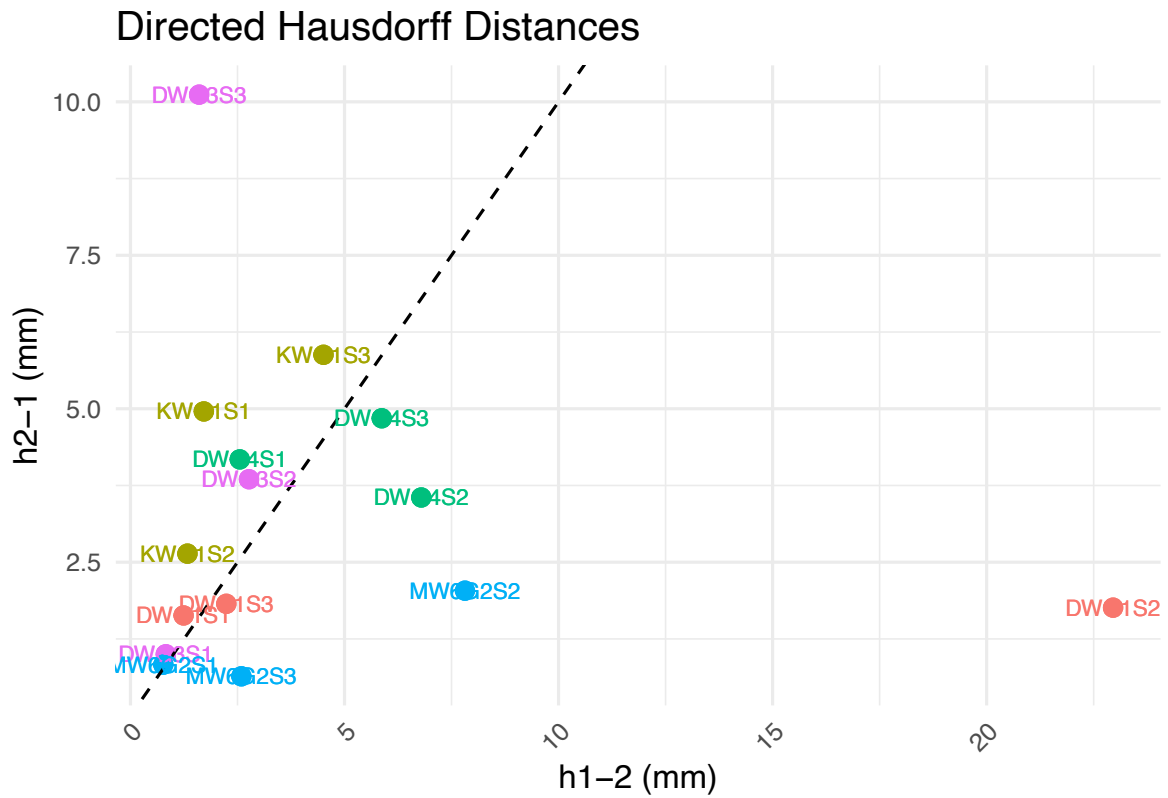
ggsave(
  filename = file.path(out_plots, "direct_dist_id.png"),
  plot = pC,
  width = 12,

```

```

height = 10,
dpi = 300
)
pC

```



combine 3 panels

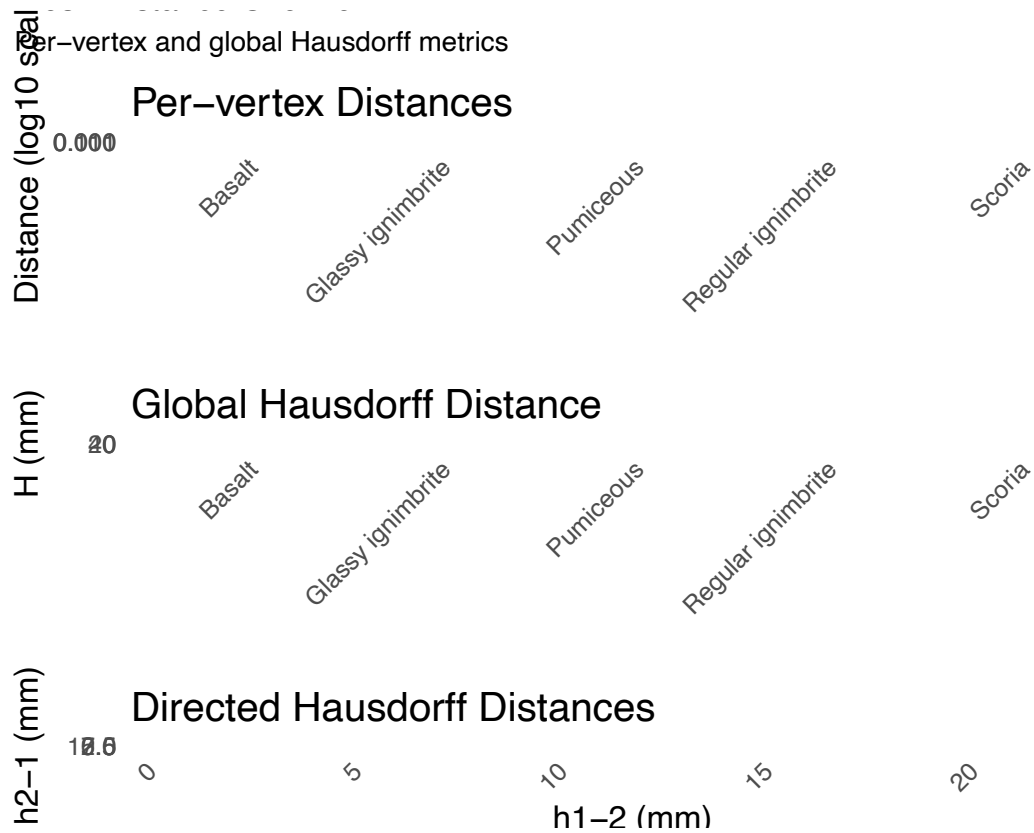
```

library(patchwork)

multi_panel <- pA / pB / pC +
  plot_annotation(title = "Mesh Distance Overview",
                 subtitle = "Per-vertex and global Hausdorff metrics")

multi_panel

```



```

ggsave(
  filename = file.path(out_plots, "multi_panel.png"),
  plot = multi_panel,
  width = 12,
  height = 10,
  dpi = 300
)

```

**End script**