

Analysis for Kilimanjaro IPBES Workshop Paper

R code for analyzing inter-group differences for: Masao CA, Prescott GW, Snethlage MA, Urbach D, Torre-Marin Rando A, Molina-Venegas R, Mollel NP, Hemp C, Hemp A, Fischer M (2022). Stakeholder Perspectives on Nature, People, and Sustainability at Mount Kilimanjaro. People and Nature.

```
library(tidyverse)

## Warning: package 'tidyverse' was built under R version 4.0.2
## -- Attaching packages ----- tidyverse 1.3.1 --
## v ggplot2 3.3.5      v purrr  0.3.4
## v tibble  3.1.3      v dplyr  1.0.7
## v tidyr   1.1.3      v stringr 1.4.0
## v readr   2.0.0      v forcats 0.5.1

## Warning: package 'ggplot2' was built under R version 4.0.2
## Warning: package 'tibble' was built under R version 4.0.2
## Warning: package 'tidyr' was built under R version 4.0.2
## Warning: package 'readr' was built under R version 4.0.2
## Warning: package 'dplyr' was built under R version 4.0.2
## Warning: package 'forcats' was built under R version 4.0.2

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()
```

```
library(vegan)
```

```
## Loading required package: permute
## Loading required package: lattice
## This is vegan 2.5-6
```

For background on Permutational Analysis of Variance (PERMANOVA): Anderson 2014 Permutational Analysis of Variance (PERMANOVA). Wiley StatsRef: Statistical Reference Online <https://onlinelibrary.wiley.com/doi/epdf/10.1002/9781118445112.stat07841>

Structure of the analyses:

Three questions based on the Ecosystem Services Questionnaire:

1. Are there significant differences between groups in listed NCPs? (Response ~ Group)
2. Are there significant differences between groups and NCP categories in reported changes in access and provision between 2008-2018? (Response ~ Group * ESCODE)
3. Are there significant differences between groups and NCP categories in predictions of how NCP access and provision will change between 2018-2028? (Response ~ Group * ESCODE)

And four further questions based on the Habitat Questionnaire:

4. Are there significant differences between groups and habitats in the reported changes in habitat area between 2008-2018? (Response ~ Group * Biome2)
5. Are there significant differences between groups and habitats in the reported direct drivers of these changes? (Response ~ Group * Biome2)
6. Are there significant differences between groups and habitats in the reported indirect drivers of these changes? (Response ~ Group * Biome2)
7. Are there significant differences between groups and habitats in what Actions are suggested to ensure a sustainable future for people and nature in Mount Kilimanjaro? (Response ~ Group * Biome2)

Enter data. Data available from: <https://zenodo.org/record/5846443>

```
# habitat questionnaire
habitat.questionnaire.original <- read.csv(
  "./kilimanjaro_ipbes_workshop_habitat_questionnaire.csv")

# ecosystem services questionnaire
es.questionnaire.original <- read.csv(
  "./kilimanjaro_ipbes_workshop_ecosystem_services_questionnaire.csv", sep = ";")
```

1. Are there significant differences between groups in listed NCPs? (Response ~ Group)

```
es.wider <- es.questionnaire.original %>%
  mutate(ESCODE = str_replace_all(ESCODE, c("ES.HAB" = "Habitat",
                                             "ES.POL" = "Pollination&PestControl",
                                             "ES.PST" = "Pollination&PestControl",
                                             "ES.AIR" = "Air&Climate",
                                             "ES.CLI" = "Air&Climate",
                                             "ES.OCE" = "Water",
                                             "ES.WQN" = "Water",
                                             "ES.WQL" = "Water",
                                             "ES.SOL" = "Soil&Hazards",
                                             "ES.HAZ" = "Soil&Hazards",
                                             "ES.NRG" = "Energy&Materials",
                                             "ES.MAT" = "Energy&Materials",
                                             "ES.FOD" = "Food&Medicine",
                                             "ES.MED" = "Food&Medicine",
                                             "ES.LRN" = "Cultural",
                                             "ES.EXP" = "Cultural",
                                             "ES.IDE" = "Cultural",
                                             "ES.OPT" = "Cultural",
                                             "ES.LIV" = "Livelihoods",
                                             "ES.WEB" = "Livelihoods")) %>%

  select(Participant, Group, ESCODE) %>%
  group_by(Participant, Group, ESCODE) %>%
  summarise(Count = length(ESCODE)) %>%
  pivot_wider(names_from = ESCODE, values_from = Count, values_fill = list(Count=0))
```

`summarise()` has grouped output by 'Participant', 'Group'. You can override using the `groups` argument

```
es.form.data.response <- es.wider[,c(1:2)]
es.form.data.predictor <- es.wider[,c(1:2)]

set.seed(42)
adonis(es.form.data.response ~ Group,
      data = es.form.data.predictor, permutations = 999)
```

```
##
## Call:
## adonis(formula = es.form.data.response ~ Group, data = es.form.data.predictor,      permutations = 9
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##           Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Group      4      3.9583 0.98957  3.8539 0.19659  0.001 ***
## Residuals 63     16.1764 0.25677      0.80341
## Total     67     20.1347      1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

2. Are there significant differences between groups and NCP categories in reported changes in access and provision between 2008-2018? (Response ~ Group * ESCODE)

```
ncp.access.wide.format <- es.questionnaire.original %>%
  select(Participant, Group, ESCODE, Provision, Access, Provision.will, Access.will)%>%
  mutate(Provision = str_replace_all(Provision, c("Decrease" = "decrease",
    "Increase" = "increase",
    "Not" = "not",
    "Deteriorate" = "decrease",
    "No answer" = "NA",
    "no answer" = "NA",
    "Mixed" = "NA",
    "decreased" = "decrease",
    "increased" = "increase",
    "not changed" = "Neutral",
    "not change" = "Neutral",
    "decrease" = "Negative",
    "deteriorate" = "Negative",
    "improve" = "Positive",
    "increase" = "Positive",
    "Improve" = "Positive")) %>%
  mutate(Provision.will = str_replace_all(Provision.will, c("Decrease" = "decrease",
    "Increase" = "increase",
    "Not" = "not",
    "Deteriorate" = "decrease",
    "No answer" = "NA",
    "no answer" = "NA",
    "Mixed" = "NA",
    "decreased" = "decrease",
    "increased" = "increase",
    "not changed" = "Neutral",
    "not change" = "Neutral",
    "decrease" = "Negative",
    "deteriorate" = "Negative",
    "improve" = "Positive",
    "increase" = "Positive",
    "Improve" = "Positive")) %>%
  mutate(Access = str_replace_all(Access, c("Decrease" = "decrease",
    "Increase" = "increase",
```

```

      "Not" = "not",
      "Deteriorate" = "decrease",
      "No answer" = "NA",
      "no answer" = "NA",
      "Mixed" = "NA",
      "decreased" = "decrease",
      "increased" = "increase",
      "not changed" = "Neutral",
      "not change" = "Neutral",
      "decrease" = "Negative",
      "deteriorate" = "Negative",
      "improve" = "Positive",
      "increase" = "Positive",
      "Improve" = "Positive")))) %>%
mutate(Access.will = str_replace_all(Access.will, c("Decrease" = "decrease",
      "Increase" = "increase",
      "Not" = "not",
      "Deteriorate" = "decrease",
      "No answer" = "NA",
      "no answer" = "NA",
      "Mixed" = "NA",
      "decreased" = "decrease",
      "increased" = "increase",
      "not changed" = "Neutral",
      "not change" = "Neutral",
      "decrease" = "Negative",
      "deteriorate" = "Negative",
      "improve" = "Positive",
      "increase" = "Positive",
      "Improve" = "Positive")))) %>%
mutate(ESCODE = str_replace_all(ESCODE, c("ES.HAB" = "Habitat",
      "ES.POL" = "Poll. & pest cont.",
      "ES.PST" = "Poll. & pest cont.",
      "ES.AIR" = "Air & Climate",
      "ES.CLI" = "Air & Climate",
      "ES.OCE" = "Water",
      "ES.WQN" = "Water",
      "ES.WQL" = "Water",
      "ES.SOL" = "Soil & hazards",
      "ES.HAZ" = "Soil & hazards",
      "ES.NRG" = "Energy & materials",
      "ES.MAT" = "Energy & materials",
      "ES.FOD" = "Food & medicine",
      "ES.MED" = "Food & medicine",
      "ES.LRN" = "Cultural",
      "ES.EXP" = "Cultural",
      "ES.IDE" = "Cultural",
      "ES.OPT" = "Cultural",
      "ES.LIV" = "Livelihoods",
      "ES.WEB" = "Livelihoods")))) %>%
mutate(Provision = as.numeric(str_replace_all(Provision, c("Positive" = "3",
      "Negative" = "1",
      "Neutral" = "2"))))) %>%

```

```

mutate(Provision.will = as.numeric(str_replace_all(Provision.will, c("Positive" = "3",
                                                                    "Negative" = "1",
                                                                    "Neutral" = "2")))) %>%

mutate(Access = as.numeric(str_replace_all(Access, c("Positive" = "3",
                                                                    "Negative" = "1",
                                                                    "Neutral" = "2")))) %>%

mutate(Access.will = as.numeric(str_replace_all(Access.will, c("Positive" = "3",
                                                                    "Negative" = "1",
                                                                    "Neutral" = "2")))) %>%

filter(Access != "NA") %>%
filter(Access.will != "NA") %>%
filter(Provision != "NA") %>%
filter(Provision.will != "NA")

```

```
## Warning in mask$eval_all_mutate(quo): NAs introduced by coercion
```

```
## Warning in mask$eval_all_mutate(quo): NAs introduced by coercion
```

```
## Warning in mask$eval_all_mutate(quo): NAs introduced by coercion
```

```
## Warning in mask$eval_all_mutate(quo): NAs introduced by coercion
```

```

ncp.past.trends.data.response <- ncp.access.wide.format[,c(4:5)]
ncp.past.trends.data.predictor <- ncp.access.wide.format[,c(1:3)]

```

```

set.seed(42)
adonis(ncp.past.trends.data.response ~ Group * ESCODE,
       data = ncp.past.trends.data.predictor, permutations = 999, na.rm = TRUE)

```

```
##
```

```
## Call:
```

```
## adonis(formula = ncp.past.trends.data.response ~ Group * ESCODE, data = ncp.past.trends.data.pr
```

```
##
```

```
## Permutation: free
```

```
## Number of permutations: 999
```

```
##
```

```
## Terms added sequentially (first to last)
```

```
##
```

```

##              Df SumsOfSqs  MeanSqs F.Model      R2 Pr(>F)
## Group          4   0.7084 0.177108  5.4681 0.13413 0.002 **
## ESCODE          8   0.4362 0.054524  1.6834 0.08259 0.091 .
## Group:ESCODE   20   1.1572 0.057860  1.7864 0.21910 0.017 *
## Residuals      92   2.9798 0.032389           0.56418
## Total        124   5.2816           1.00000

```

```
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

3. Are there significant differences between groups and NCP categories in predictions of how NCP access and provision will change between 2018-2028? (Response ~ Group * ESCODE)

```

ncp.future.trends.data.response <- ncp.access.wide.format[,c(6:7)]
ncp.future.trends.data.predictor <- ncp.access.wide.format[,c(1:3)]

```

```

set.seed(42)
adonis(ncp.future.trends.data.response ~ Group * ESCODE,

```

```
data = ncp.future.trends.data.predictor, permutations = 999, na.rm = TRUE)
```

```
##
## Call:
## adonis(formula = ncp.future.trends.data.response ~ Group * ESCODE, data = ncp.future.trends.data,
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##              Df SumsOfSqs  MeanSqs F.Model    R2 Pr(>F)
## Group          4   0.05176 0.0129410 1.63506 0.05418 0.138
## ESCODE          8   0.03546 0.0044321 0.55998 0.03711 0.810
## Group:ESCODE   20   0.13997 0.0069985 0.88424 0.14651 0.497
## Residuals      92   0.72815 0.0079147          0.76219
## Total        124   0.95534          1.00000
```

4. Are there significant differences between groups and habitats in the reported changes in habitat area between 2008-2018? (Response ~ Group * Biome2)

```
#Function to convert blank cells to NA, from Holger Brandl https://stackoverflow.com/questions/2417211
empty_as_na <- function(x){
  if("factor" %in% class(x)) x <- as.character(x)
  ifelse(as.character(x)!="", x, NA)
}
```

```
biome.trends.reduced <- habitat.questionnaire.original %>%
  select(Group,
    Participant,
    Biome2,
    Habitat.area) %>%
  mutate(Habitat.area = as.numeric(str_replace_all(Habitat.area, c("Increased" = "3",
    "Decreased" = "1",
    "Mixed" = "NA",
    "No answer" = "NA",
    "Not changed" = "2"))))# %>%
```

```
## Warning in mask$eval_all_mutate(quo): NAs introduced by coercion
```

```
biome.trends.reduced.na.omitted <- na.omit(biome.trends.reduced)
biome.trends.reduced.na.omitted.predictor <- biome.trends.reduced.na.omitted[,c(1:3)]
biome.trends.reduced.na.omitted.response <- biome.trends.reduced.na.omitted[,-(1:3)]

set.seed(42)
adonis(biome.trends.reduced.na.omitted.response ~ Group * Biome2,
  data = biome.trends.reduced.na.omitted.predictor, permutations = 999, na.rm = TRUE)
```

```
##
## Call:
## adonis(formula = biome.trends.reduced.na.omitted.response ~ Group * Biome2, data = biome.trends
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
```

```
##
##              Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Group         4   0.2433 0.060829  2.0169 0.05550  0.098 .
## Biome2        6   0.7112 0.118528  3.9301 0.16222  0.002 **
## Group:Biome2  16   0.2930 0.018309  0.6071 0.06682  0.862
## Residuals    104   3.1365 0.030159          0.71546
## Total        130   4.3840          1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

5. Are there significant differences between groups and habitats in the reported direct drivers of these changes? (Response ~ Group * Biome2)

```
habitat.questionnaire.dir <- habitat.questionnaire.original %>%
  select(Group,
    Participant,
    Biome2,
    DIR.ACT,
    DIR.CC,
    DIR.IAS,
    DIR.LUC,
    DIR.OVR,
    DIR.POL) %>%
  filter(DIR.ACT + DIR.CC + DIR.IAS + DIR.LUC + DIR.OVR + DIR.POL > 0)

habitat.questionnaire.dir.predictor <- habitat.questionnaire.dir[,c(1:3)]
habitat.questionnaire.dir.response <- habitat.questionnaire.dir[,c(1:3)] %>%
  mutate_if(is.numeric, ~1 * (. > 0))

set.seed(42)
adonis(habitat.questionnaire.dir.response ~ Group * Biome2,
  data = habitat.questionnaire.dir.predictor, permutations = 999)
```

```
##
## Call:
## adonis(formula = habitat.questionnaire.dir.response ~ Group *      Biome2, data = habitat.questionnaire.dir.predictor, permutations = 999)
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##              Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Group         4   0.8820 0.22050  1.0296 0.03247  0.418
## Biome2        6   2.7205 0.45342  2.1172 0.10016  0.019 *
## Group:Biome2  14   3.0013 0.21438  1.0010 0.11049  0.461
## Residuals     96  20.5591 0.21416          0.75688
## Total        120  27.1630          1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

6. Are there significant differences between groups and habitats in the reported indirect drivers of these changes? (Response ~ Group * Biome2)

```
habitat.questionnaire.ind <- habitat.questionnaire.original %>%
  select(Group,
```

```

      Biome2,
      Participant,
      IND.CLT,
      IND.DEM,
      IND.ECO,
      IND.GVN,
      IND.LUC,
      IND.S.T) %>%
filter(IND.CLT + IND.DEM + IND.ECO + IND.GVN + IND.LUC + IND.S.T > 0)

habitat.questionnaire.ind.predictor <- habitat.questionnaire.ind[,c(1:3)]
habitat.questionnaire.ind.response <- habitat.questionnaire.ind[,-c(1:3)] %>%
  mutate_if(is.numeric, ~1 * (. > 0))

set.seed(42)
adonis(habitat.questionnaire.ind.response ~ Group * Biome2,
      data = habitat.questionnaire.ind.predictor, permutations = 999)

##
## Call:
## adonis(formula = habitat.questionnaire.ind.response ~ Group *      Biome2, data = habitat.questionnaire.ind.predictor, permutations = 999)
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##              Df SumsOfSqs MeanSqs F.Model    R2 Pr(>F)
## Group          4    1.2688  0.31720  1.28011 0.09494  0.258
## Biome2          6    0.7152  0.11921  0.48108 0.05352  0.910
## Group:Biome2  11    2.2114  0.20104  0.81134 0.16548  0.700
## Residuals     37    9.1681  0.24779          0.68605
## Total         58   13.3636          1.00000

7. Are there significant differences between groups and habitats in what Actions are suggested to ensure a sustainable future for people and nature in Mount Kilimanjaro? (Response ~ Group * Biome2)

habitat.questionnaire.act <- habitat.questionnaire.original %>%
  select(Group,
    Participant,
    Biome2,
    ACT.LAND,
    ACT.SPEC,
    ACT.AWAR,
    ACT.ENFORC,
    ACT.ECON,
    ACT.PROTECT,
    ACT.LAWPOL,
    ACT.RSRCH,
    ACT.EDUC,
    ACT.INST) %>%
  filter(ACT.LAND + ACT.SPEC + ACT.AWAR + ACT.ENFORC + ACT.ECON + ACT.PROTECT + ACT.LAWPOL + ACT.RSRCH + ACT.EDUC + ACT.INST > 0)

habitat.questionnaire.act.predictor <- habitat.questionnaire.act[,c(1:3)]
habitat.questionnaire.act.response <- habitat.questionnaire.act[,-c(1:3)] %>%

```



```

mutate_if(is.numeric, ~1 * (. > 0))

set.seed(42)
adonis(habitat.questionnaire.act.response ~ Group * Biome2,
       data = habitat.questionnaire.act.predictor, permutations = 999)

##
## Call:
## adonis(formula = habitat.questionnaire.act.response ~ Group *      Biome2, data = habitat.questionnaire.act.predictor, permutations = 999)
##
## Permutation: free
## Number of permutations: 999
##
## Terms added sequentially (first to last)
##
##              Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## Group          4      1.907 0.47686 1.99275 0.05633 0.027 *
## Biome2          6      2.627 0.43782 1.82962 0.07758 0.020 *
## Group:Biome2    16      3.480 0.21753 0.90904 0.10279 0.626
## Residuals     108     25.844 0.23929          0.76329
## Total          134     33.859          1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Load table with unadjusted p-values
permanova.results.consolidated <- read.csv(
  "./p_values_raw_Kilimanjaro_IPBES_workshop_PERMANOVA_setseed42.csv")

Apply the Benjamini-Hochberg procedure to the p-values For further details, see: Benjamini and Hochberg
1995 Controlling the False Discovery Rate: A Practical and Powerful Approach to Multiple Testing. Journal of
the Royal Statistical Society: Series B (Methodological). https://doi.org/10.1111/j.2517-6161.1995.tb02031.x

p<- permanova.results.consolidated$p
round(p.adjust(p, "BH"), 3)

## [1] 0.207 0.013 0.910 0.013 0.013 0.207 0.063 0.262 0.905 0.674 0.662 0.063
## [13] 0.674 0.446 0.910 0.831 0.073 0.063 0.793

```