

Aligned Rank Transform T. anastrephae & P. vindemmiae on Peach

Segundo Núñez Campero

2022-12-16

The analysis was performed using a Aligned Rang Transformation with the packages ‘ARTool’ (Wobbrock et al. 2011), a factorial model done in preparation for a nonparametric analysis of variance models with numeric or ordinal responses. This is done by first aligning and ranking the fixed effects using the model function, then conducting an analysis of variance on linear models built from the transformed data using the function ‘anova.art’. A *post hoc* pairwise comparisons was conducted to show differences between factor levels, with a Bonferroni–Holm adjust method, using the ‘art.con’ function (Elkin et al. 2021). And a the library ‘rcompanion’ was used for obtain the letters that show significant difference.

T. anastrephae analysis

Model, sums of aligned responses and ANOVAs on aligned responses not of interest (should all be ~0)

```
m <- art(tric_suc ~ hab + fly_sp + hab * fly_sp, data=dt)
summary(m)

## Aligned Rank Transform of Factorial Model
##
## Call:
## art(formula = tric_suc ~ hab + fly_sp + hab * fly_sp, data = dt)
##
## Column sums of aligned responses (should all be ~0):
##      hab      fly_sp hab:fly_sp
##      0          0          0
##
## F values of ANOVAs on aligned responses not of interest (should all be ~0):
##   Min. 1st Qu. Median  Mean 3rd Qu. Max.
##      0      0      0      0      0      0
anova(m, response="aligned")

## Analysis of Variance of Aligned Rank Transformed Data
##
## Table Type: Anova Table (Type III tests)
## Model: No Repeated Measures (lm)
## Response: aligned(tric_suc)
##
##           Aligned By Df Df.res F value Pr(>F)
## 1  fly_sp          hab  1    714      0      1
## 2  hab:fly_sp       hab  2    714      0      1
## 3  hab            fly_sp  2    714      0      1
## 4  hab:fly_sp       fly_sp  2    714      0      1
## 5  hab          hab:fly_sp  2    714      0      1
```

```

## 6 fly_sp      hab:fly_sp  1     714      0      1
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
anova(m)

## Analysis of Variance of Aligned Rank Transformed Data
##
## Table Type: Anova Table (Type III tests)
## Model: No Repeated Measures (lm)
## Response: art(tric_suc)
##
##          Df Df.res F value    Pr(>F)
## 1 hab      2     714  566.19 < 2.22e-16 ***
## 2 fly_sp   1     714  389.58 < 2.22e-16 ***
## 3 hab:fly_sp 2     714  204.23 < 2.22e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Contrasts

```

m1 <- art.con(m, "hab:fly_sp", adjust="holm") %>%
  summary() %>% # add significance stars to the output
  mutate(sig. = symnum(p.value, corr=FALSE, na=FALSE,
                       cutpoints = c(0, .001, .01, .05, .10, 1),
                       symbols = c("***", "**", "*", ".", "")))
m1

```

Interaction contrast

	contrast	estimate	SE	df	t.ratio	p.value
## 1	Inside,Dsp - Inside,Dsuz	200.791667	14.37258	714	13.9704716	1.750721e-38
## 2	Inside,Dsp - Outside,Dsp	174.225000	14.37258	714	12.1220440	4.844841e-30
## 3	Inside,Dsp - Outside,Dsuz	322.529167	14.37258	714	22.4405954	1.065005e-83
## 4	Inside,Dsp - Soil,Dsp	451.691667	14.37258	714	31.4273281	1.218685e-135
## 5	Inside,Dsp - Soil,Dsuz	453.787500	14.37258	714	31.5731498	1.906506e-136
## 6	Inside,Dsuz - Outside,Dsp	-26.566667	14.37258	714	-1.8484276	1.299076e-01
## 7	Inside,Dsuz - Outside,Dsuz	121.737500	14.37258	714	8.4701238	4.179134e-16
## 8	Inside,Dsuz - Soil,Dsp	250.900000	14.37258	714	17.4568565	3.812415e-56
## 9	Inside,Dsuz - Soil,Dsuz	252.995833	14.37258	714	17.6026782	7.052360e-57
## 10	Outside,Dsp - Outside,Dsuz	148.304167	14.37258	714	10.3185515	1.386529e-22
## 11	Outside,Dsp - Soil,Dsp	277.466667	14.37258	714	19.3052841	4.241522e-66
## 12	Outside,Dsp - Soil,Dsuz	279.562500	14.37258	714	19.4511058	7.226850e-67
## 13	Outside,Dsuz - Soil,Dsp	129.162500	14.37258	714	8.9867327	8.996048e-18
## 14	Outside,Dsuz - Soil,Dsuz	131.258333	14.37258	714	9.1325544	3.390520e-18
## 15	Soil,Dsp - Soil,Dsuz	2.095833	14.37258	714	0.1458217	8.841033e-01
##	sig.					
## 1	***					
## 2	***					
## 3	***					
## 4	***					
## 5	***					
## 6						
## 7	***					
## 8	***					

```

## 9   ***
## 10  ***
## 11  ***
## 12  ***
## 13  ***
## 14  ***
## 15

Sum = as.data.frame(m1)

cldList(p.value ~ contrast, data=Sum)    ### alfa level = 0.05

##          Group Letter MonoLetter
## 1  Inside,Dsp      a      a
## 2  Inside,Dsuz     b      b
## 3  Outside,Dsp    b      b
## 4  Outside,Dsuz   c      c
## 5   Soil,Dsp       d      d
## 6   Soil,Dsuz      d      d

m2 <- art.con(m, "hab", adjust="holm") %>%
  summary() %>% # add significance stars to the output
  mutate(sig. = symnum(p.value, corr=FALSE, na=FALSE,
                       cutpoints = c(0, .001, .01, .05, .10, 1),
                       symbols = c("***", "**", "*", ".", "")))

```

Habitat Contrast

```

## NOTE: Results may be misleading due to involvement in interactions
m2

##          contrast estimate      SE df t.ratio      p.value sig.
## 1 Inside - Outside 161.3083 11.44667 714 14.09216 5.700952e-40 ***
## 2   Inside - Soil  383.5792 11.44667 714 33.51011 3.531643e-148 ***
## 3   Outside - Soil 222.2708 11.44667 714 19.41795 1.837929e-67 ***

Sum = as.data.frame(m2)

cldList(p.value ~ contrast, data=Sum)    ### alfa level = 0.05

```

```

##          Group Letter MonoLetter
## 1   Inside      a      a
## 2  Outside      b      b
## 3   Soil        c      c

```

Fly species contrast

```

m3 <- art.con(m, "fly_sp", adjust="holm") %>%
  summary() %>% # add significance stars to the output
  mutate(sig. = symnum(p.value, corr=FALSE, na=FALSE,
                       cutpoints = c(0, .001, .01, .05, .10, 1),
                       symbols = c("***", "**", "*", ".", "")))

```

NOTE: Results may be misleading due to involvement in interactions

```

m3

##      contrast estimate      SE df t.ratio     p.value sig.
## 1 Dsp - Dsuz 241.3111 12.22589 714 19.73771 1.547538e-69 ***

Sum = as.data.frame(m3)

library(rcompanion)

cldList(p.value ~ contrast, data=Sum)    ### alfa level = 0.05

##   Group Letter MonoLetter
## 1   Dsp      a      a
## 2   Dsuz     b      b

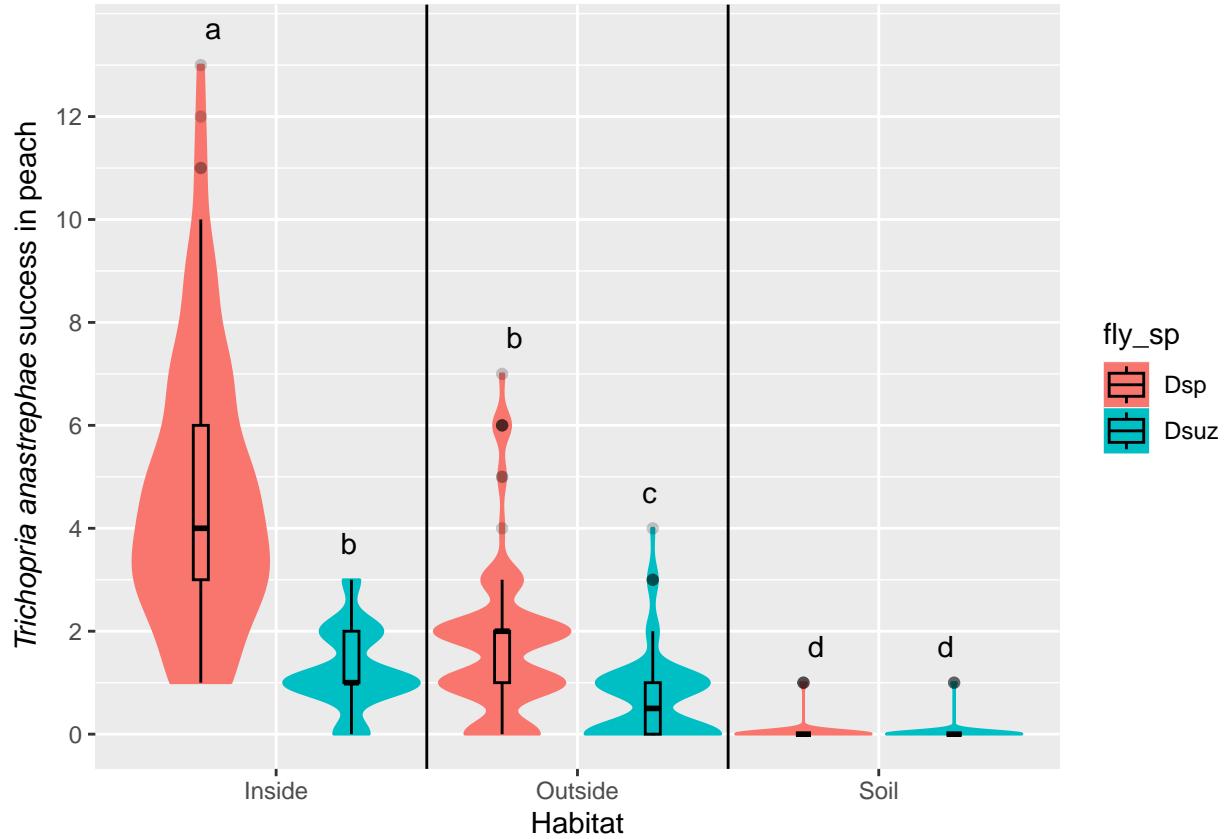
```

Graphic of *T. anastrephae* success with interactions.

```

ggplot(dt, aes(x = factor(hab), y = tric_suc, fill = fly_sp, colour = fly_sp)) +
  geom_violin(trim = T, position=position_dodge(1), scale = "width") +
  scale_y_continuous(breaks=seq(0, 13, 2)) +
  labs(x = "Habitat",
       y = italic('Trichopria anastrephae')~ "success in peach") +
  annotate('text', label='a',
           x=0.77, y= 13.5, hjust=0.1, vjust=0, size=4, color='black') +
  annotate('text', label='b',
           x=1.22, y= 3.5, hjust=0.1, vjust=0, size=4, color='black') +
  annotate('text', label='b',
           x=1.77, y= 7.5, hjust=0.1, vjust=0, size=4, color='black') +
  annotate('text', label='c',
           x=2.22, y= 4.5, hjust=0.1, vjust=0, size=4, color='black') +
  annotate('text', label='d',
           x=2.77, y= 1.5, hjust=0.1, vjust=0, size=4, color='black') +
  annotate('text', label='d',
           x=3.20, y= 1.5, hjust=0.1, vjust=0, size=4, color='black') +
  geom_boxplot(width=0.1, color="black", alpha=0.2, position=position_dodge(1)) +
  geom_vline(xintercept = 1.5) +
  geom_vline(xintercept = 2.5)

```



P. vindeiae analysis

Model, sums of aligned responses and ANOVAs on aligned responses not of interest (should all be ~0)

```
m4 <- art(pach_suc ~ hab + fly_sp + hab * fly_sp, data=dt)
summary(m4)

## Aligned Rank Transform of Factorial Model
##
## Call:
## art(formula = pach_suc ~ hab + fly_sp + hab * fly_sp, data = dt)
##
## Column sums of aligned responses (should all be ~0):
##      hab     fly_sp hab:fly_sp
##      0         0         0
##
## F values of ANOVAs on aligned responses not of interest (should all be ~0):
##      Min. 1st Qu. Median   Mean 3rd Qu.   Max.
##      0       0       0       0       0       0
anova(m4, response="aligned")

## Analysis of Variance of Aligned Rank Transformed Data
##
```

```

## Table Type: Anova Table (Type III tests)
## Model: No Repeated Measures (lm)
## Response: aligned(pach_suc)
##
##          Aligned By Df Df.res F value Pr(>F)
## 1 fly_sp           hab  1    714      0      1
## 2 hab:fly_sp       hab  2    714      0      1
## 3 hab             fly_sp 2    714      0      1
## 4 hab:fly_sp       fly_sp 2    714      0      1
## 5 hab             hab:fly_sp 2    714      0      1
## 6 fly_sp          hab:fly_sp 1    714      0      1
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
anova(m4)

```

```

## Analysis of Variance of Aligned Rank Transformed Data
##
## Table Type: Anova Table (Type III tests)
## Model: No Repeated Measures (lm)
## Response: art(pach_suc)
##
##          Df Df.res F value     Pr(>F)
## 1 hab      2    714  85.728 < 2.22e-16 ***
## 2 fly_sp   1    714  84.386 < 2.22e-16 ***
## 3 hab:fly_sp 2    714 113.087 < 2.22e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Contrasts

```

m5 <- art.con(m4, "hab:fly_sp", adjust="holm") %>%
  summary() %>% # add significance stars to the output
  mutate(sig. = symnum(p.value, corr=FALSE, na=FALSE,
                       cutpoints = c(0, .001, .01, .05, .10, 1),
                       symbols = c("***", "**", "*", ".", "")))
m5

```

Interaction contrast

	contrast	estimate	SE	df	t.ratio	p.value
## 1	Inside,Dsp - Inside,Dsuz	68.66250	20.3062	714	3.3813570	3.802858e-03
## 2	Inside,Dsp - Outside,Dsp	-159.80417	20.3062	714	-7.8697241	1.055241e-13
## 3	Inside,Dsp - Outside,Dsuz	-149.49583	20.3062	714	-7.3620794	3.499553e-12
## 4	Inside,Dsp - Soil,Dsp	79.07917	20.3062	714	3.8943367	6.462476e-04
## 5	Inside,Dsp - Soil,Dsuz	-172.06667	20.3062	714	-8.4736038	1.220157e-15
## 6	Inside,Dsuz - Outside,Dsp	-228.46667	20.3062	714	-11.2510811	4.303516e-26
## 7	Inside,Dsuz - Outside,Dsuz	-218.15833	20.3062	714	-10.7434364	4.645217e-24
## 8	Inside,Dsuz - Soil,Dsp	10.41667	20.3062	714	0.5129797	1.000000e+00
## 9	Inside,Dsuz - Soil,Dsuz	-240.72917	20.3062	714	-11.8549608	1.418348e-28
## 10	Outside,Dsp - Outside,Dsuz	10.30833	20.3062	714	0.5076447	1.000000e+00
## 11	Outside,Dsp - Soil,Dsp	238.88333	20.3062	714	11.7640608	3.253668e-28
## 12	Outside,Dsp - Soil,Dsuz	-12.26250	20.3062	714	-0.6038797	1.000000e+00
## 13	Outside,Dsuz - Soil,Dsp	228.57500	20.3062	714	11.2564161	4.303516e-26
## 14	Outside,Dsuz - Soil,Dsuz	-22.57083	20.3062	714	-1.1115244	1.000000e+00

```

## 15      Soil,Dsp - Soil,Dsuz -251.14583 20.3062 714 -12.3679405 8.481637e-31
##   sig.
## 1   **
## 2   ***
## 3   ***
## 4   ***
## 5   ***
## 6   ***
## 7   ***
## 8
## 9   ***
## 10
## 11  ***
## 12
## 13  ***
## 14
## 15  ***

Sum = as.data.frame(m5)
clList(p.value ~ contrast, data=Sum) ### alfa level = 0.05

##          Group Letter MonoLetter
## 1  Inside,Dsp     a     a
## 2  Inside,Dsuz    b     b
## 3  Outside,Dsp   c     c
## 4  Outside,Dsuz  c     c
## 5   Soil,Dsp     b     b
## 6   Soil,Dsuz    c     c

m6 <- art.con(m4, "hab", adjust="holm") %>%
  summary() %>% # add significance stars to the output
  mutate(sig. = symnum(p.value, corr=FALSE, na=FALSE,
    cutpoints = c(0, .001, .01, .05, .10, 1),
    symbols = c("***", "**", "*", ".", " ")))

```

Habitat Contrast

```

## NOTE: Results may be misleading due to involvement in interactions
m6

##          contrast estimate    SE  df t.ratio p.value sig.
## 1 Inside - Outside -219.4875 16.83026 714 -13.041243 1.518095e-34  ***
## 2   Inside - Soil -126.8750 16.83026 714 -7.538505 2.891193e-13  ***
## 3   Outside - Soil  92.6125 16.83026 714  5.502737 5.215604e-08  **

Sum = as.data.frame(m6)
clList(p.value ~ contrast, data=Sum) ### alfa level = 0.05

##          Group Letter MonoLetter
## 1   Inside     a     a
## 2   Outside    b     b
## 3     Soil     c     c

```

Fly species contrast

```
m7 <- art.con(m4, "fly_sp", adjust="holm") %>%
  summary() %>% # add significance stars to the output
  mutate(sig. = symnum(p.value, corr=FALSE, na=FALSE,
                       cutpoints = c(0, .001, .01, .05, .10, 1),
                       symbols = c("***", "**", "*", ".", " ")))

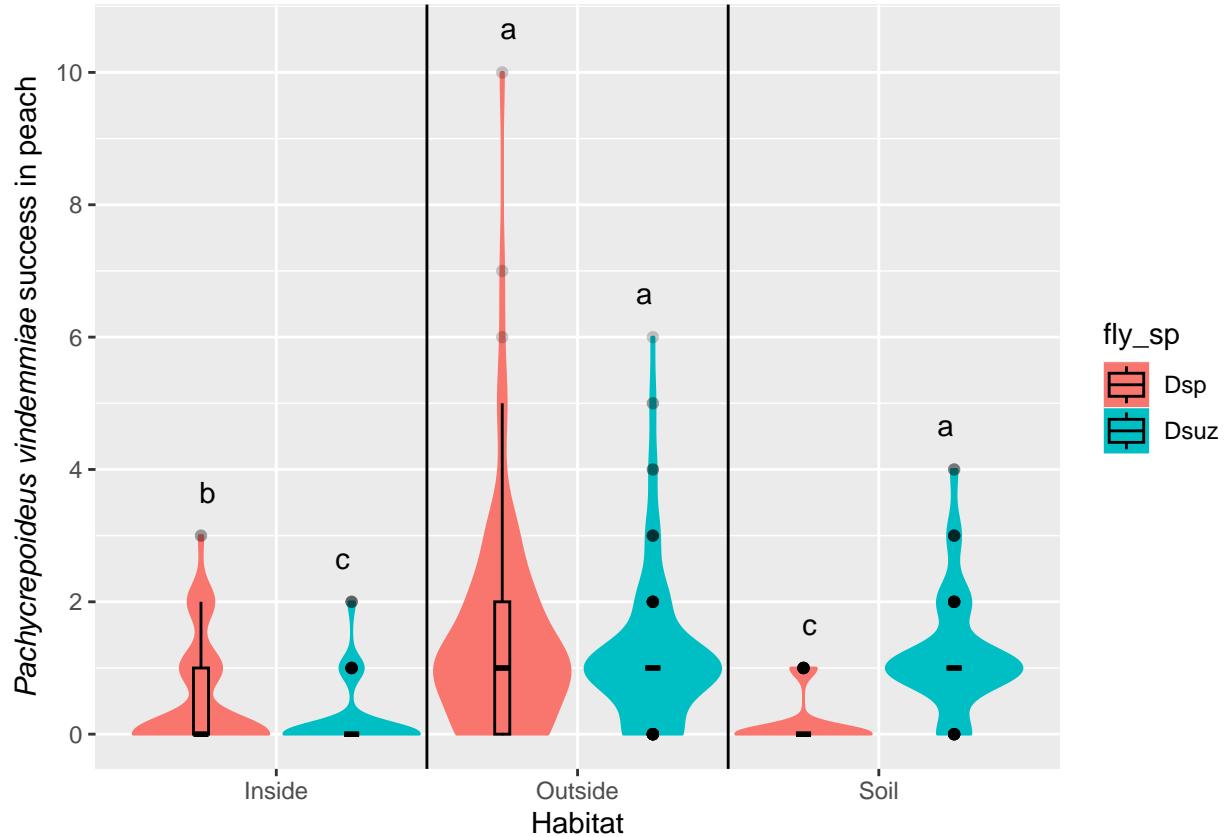
## NOTE: Results may be misleading due to involvement in interactions
m7

##   contrast estimate      SE df t.ratio     p.value sig.
## 1 Dsp - Dsuz -134.1556 14.60406 714 -9.186183 4.346913e-19 ***
Sum = as.data.frame(m7)
cldList(p.value ~ contrast, data=Sum) #### alfa level = 0.05

##   Group Letter MonoLetter
## 1   Dsp      a          a
## 2   Dsuz     b          b
```

Graphic of *P. vindemmiae* success with interactions

```
ggplot(dt, aes(x = factor(hab), y = pach_suc, fill = fly_sp, colour = fly_sp)) +
  geom_violin(trim = T, position=position_dodge(1), scale = "width") +
  scale_y_continuous(breaks=seq(0, 10, 2)) +
  labs(x = "Habitat",
       y = italic('Pachycrepoideus vindemmiae')~ "success in peach") +
  annotate('text', label='b',
           x=0.75, y=3.5, hjust=0.1, vjust=0, size=4, color='black') +
  annotate('text', label='c',
           x=1.20, y=2.5, hjust=0.1, vjust=0, size=4, color='black') +
  annotate('text', label='a',
           x=1.75, y= 10.5, hjust=0.1, vjust=0, size=4, color='black') +
  annotate('text', label='a',
           x=2.20, y= 6.5, hjust=0.1, vjust=0, size=4, color='black') +
  annotate('text', label='c',
           x=2.75, y= 1.5, hjust=0.1, vjust=0, size=4, color='black') +
  annotate('text', label='a',
           x=3.20, y= 4.5, hjust=0.1, vjust=0, size=4, color='black') +
  geom_boxplot(width=0.1, color="black", alpha=0.2, position=position_dodge(1)) +
  geom_vline(xintercept = 1.5) +
  geom_vline(xintercept = 2.5)
```



Elkin, Lisa A., Matthew Kay, James J. Higgins, and Jacob O. Wobbrock. 2021. “An Aligned Rank Transform Procedure for Multifactor Contrast Tests.” *The 34th Annual ACM Symposium on User Interface Software and Technology*, October. <https://doi.org/10.1145/3472749.3474784>.

Wobbrock, Jacob O., Leah Findlater, Darren Gergle, and James J. Higgins. 2011. “The Aligned Rank Transform for Nonparametric Factorial Analyses Using Only Anova Procedures.” *Proceedings of the SIGCHI Conference on Human Factors in Computing Systems*, May. <https://doi.org/10.1145/1978942.1978963>.