Analysis for the Nature of our Literature

Aaron R. Caldwell

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# Summary

Within this document I have included a summary of all the analyses included within our manuscript, “The Nature of Our Literature A Registered Report on the Positive Result Rate and Reporting Practices in Kinesiology”

library(readr)  
library(tidyverse)  
library(tidyselect)  
library(brms)  
library(ggdist)  
library(distributional)  
library(broom)  
library(ggpubr)  
library(epitab)  
  
# Testing out data analysis  
# import data ------------  
df\_all = read\_csv("df\_all.csv") %>%  
 mutate(support = factor(support,  
 levels = c("Unclear or not stated",   
 "Not supported",  
 "Partial support",   
 "Full support"))) %>%  
 # Coding error in 20 cases  
 mutate(sig\_test = ifelse(is.na(sig\_test), "No", sig\_test))  
# Get hypothesis tested set ------------  
hyp\_tested = df\_all %>%  
 filter(hypo\_tested == "Yes")

# Import brms analysis 1 (positive) ---------  
m\_final = read\_rds("m\_final.rds")  
# Import brms analysis 2 (prop. of hyp. tested) ------  
m\_final2 = read\_rds("m\_final2.rds")  
  
h\_test <- hypothesis(m\_final, "Intercept > 0.8")  
#knitr::kable(h\_test$hypothesis, caption = "Hypothesis Test #1")  
h\_ci = fixef(m\_final)  
test\_pos = posterior\_interval(m\_final,  
 prob = .95)  
#knitr::kable(test\_pos, caption = "Hyp Test #1: 95% Posterior C.I.")  
  
h\_test2 <- hypothesis(m\_final2, "Intercept > 0.6")  
h\_ci2 = fixef(m\_final2)  
test\_pos2 = posterior\_interval(m\_final2,  
 prob = .95)  
  
# Main Figures  
  
dat\_mfinal = posterior\_samples(m\_final, "b") %>%  
 mutate(Test = "Positive Result Rate")  
dat\_mfinal2 = posterior\_samples(m\_final2, "b") %>%  
 mutate(Test = "Rate of Hypothesis Tests")  
  
df\_mfinal = rbind(dat\_mfinal, dat\_mfinal2)

# figure 1  
p\_f1a = df\_mfinal %>%  
 ggplot(aes(x=b\_Intercept,  
 fill = Test)) +  
 stat\_halfeye(alpha = .75) +  
 #scale\_fill\_brewer(direction = -1, na.translate = FALSE) +  
 #scale\_fill\_viridis\_d() +  
 #scale\_fill\_brewer(direction = -1, na.translate = FALSE) +  
 labs(fill = "Interval",  
 x = "Probability",  
 y = "") +  
 theme\_bw() +  
 facet\_wrap(~Test) +  
 scale\_fill\_manual(values =c("lightgreen","skyblue2")) +  
 theme(legend.position = "none",  
 #axis.title.y=element\_blank(),  
 axis.text.y=element\_blank(),  
 axis.ticks.y=element\_blank(),  
 text = element\_text(size = 14,  
 face = "bold"))  
  
fig\_1b = df\_all %>%  
 select(support) %>%  
 drop\_na() %>%  
 ggplot(aes(support,  
 fill = support)) +  
 geom\_bar(aes(y = (..count..) / sum(..count..)),  
 color = "black") +  
 scale\_y\_continuous(labels = scales::percent,  
 limits = c(0,.5),  
 breaks = c(0,.1,.2,.3,.4,.5),  
 expand = c(0,0)) +  
 labs(x = "Level of Hypothesis Support",  
 y = "Relative Frequency",  
 fill = "Hypothesis Support") +  
 theme\_classic() +  
 scale\_fill\_viridis\_d(option = "E") +  
 theme(legend.position = "none")  
  
fig\_1c = df\_all %>%  
 select(hypo\_tested) %>%  
 drop\_na() %>%  
 ggplot(aes(hypo\_tested,  
 fill = hypo\_tested)) +  
 geom\_bar(aes(y = (..count..) / sum(..count..)),  
 color = "black") +  
 scale\_y\_continuous(labels = scales::percent,  
 limits = c(0,.75),  
 breaks = c(0,.25,.5,.75),  
 expand = c(0,0)) +  
 labs(x = "Hypothesis Tested",  
 y = "Relative Frequency",  
 fill = "") +  
 theme\_classic() +  
 scale\_fill\_viridis\_d(option = "E") +  
 theme(legend.position = "none")  
fig1 = ggarrange(p\_f1a,  
 fig\_1b,  
 hjust = -0.2,  
 ncol = 1,  
 labels = "AUTO")

fig1

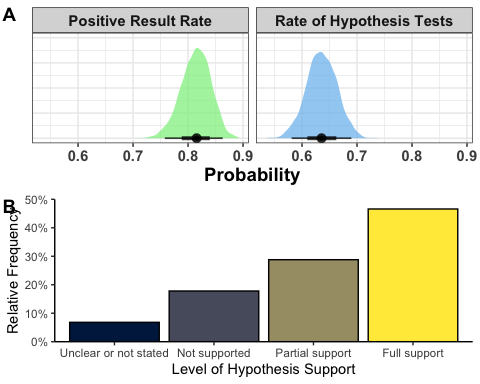


Figure 1. A) Posterior distributions from Bayesian model with the 50% and 95% percent compatibility intervals represented by the error bars at the bottom and B) Relative frequencies of the level of support reported for manuscripts with hypotheses (N = 191) with 17.8% report no support, 28.8% stating partial support, 46.6% stating full support, and 6.81% for which support was unclear or not stated.

tab\_sup = df\_all %>%  
 select(hypo\_tested, support) %>%  
 drop\_na() %>%  
 group\_by(support) %>%  
 summarize(n = n())  
tots\_sup = sum(tab\_sup$n)  
tab\_sup$perc = tab\_sup$n/tots\_sup\*100  
   
  
# Contingency Table 1 ----  
  
ctab1 = df\_all %>%   
 #filter(hypo\_tested == "Yes") %>%  
 select(effect\_size, sig\_test, hypo\_tested) %>%  
 mutate\_all(as.factor) %>%  
 drop\_na() %>%  
 epitab::contingency\_table(independents=list("Significance Testing" = "sig\_test",  
 "Effect Size Reported" = "effect\_size"),  
 outcomes=list("Hypothesis Tested" = "hypo\_tested"),  
 crosstab\_funcs=list(freq())) #%>%

ct\_effsize = table(df\_all$effect\_size)  
  
binom\_eff = binom.test(ct\_effsize[2], sum(ct\_effsize))  
eff\_pr = paste0(round(binom\_eff$estimate\*100,2),"\\% [",  
 round(binom\_eff$conf.int[1]\*100,2),", ",   
 round(binom\_eff$conf.int[2]\*100,2)  
 ,"]")  
  
ct\_sig = table(df\_all$sig\_test)  
  
binom\_sig = binom.test(ct\_sig[2], sum(ct\_sig))  
sig\_pr = paste0(round(binom\_sig$estimate\*100,2),"\\% [",  
 round(binom\_sig$conf.int[1]\*100,2),", ",   
 round(binom\_sig$conf.int[2]\*100,2)  
 ,"]")  
  
ct\_sig2 = table(subset(df\_all, hypo\_tested == "No")$sig\_test)  
  
binom\_sig2 = binom.test(ct\_sig2[2], sum(ct\_sig2))  
sig\_pr2 = paste0(round(binom\_sig2$estimate\*100,2),"\\% [",  
 round(binom\_sig2$conf.int[1]\*100,2),", ",   
 round(binom\_sig2$conf.int[2]\*100,2)  
 ,"]")  
  
ct\_sig3 = table(subset(df\_all, hypo\_tested == "Yes")$sig\_test)  
  
binom\_sig3 = binom.test(ct\_sig3[2], sum(ct\_sig3))  
sig\_pr3 = paste0(round(binom\_sig3$estimate\*100,2),"\\% [",  
 round(binom\_sig3$conf.int[1]\*100,2),", ",   
 round(binom\_sig3$conf.int[2]\*100,2)  
 ,"]")

ct\_ptype = table(df\_all$pval\_type)  
binom\_ptype = binom.test(ct\_ptype[[2]],sum(ct\_ptype))  
ptype\_pr = paste0(round(binom\_ptype$estimate\*100,2),"\\% [",  
 round(binom\_ptype$conf.int[1]\*100,2),", ",   
 round(binom\_ptype$conf.int[2]\*100,2)  
 ,"] of manuscripts reported exact p-values for all results (p = .045) versus only relative p-values (p < .05)")  
  
ct\_ptype2 = table(df\_all$pval\_type)  
  
binom\_ptype2 = binom.test(ct\_ptype2[[2]]+ct\_ptype2[[1]],sum(ct\_ptype2))  
ptype\_pr2 = paste0(round(binom\_ptype2$estimate\*100,2),"\\% [",  
 round(binom\_ptype2$conf.int[1]\*100,2),", ",   
 round(binom\_ptype2$conf.int[2]\*100,2)  
 ,"] of manuscripts reported at least \*some\* exact p-values (e.g., p = .045) versus relative p-values (e.g., p < .05)")  
  
  
ctab2 = df\_all %>%   
 filter(sig\_test == "Yes") %>%  
 select(effect\_size, pval\_sig, pval\_type) %>%  
 mutate\_all(as.factor) %>%  
 drop\_na() %>%  
 contingency\_table(independents=list("Effect Size Reported" = "effect\_size",  
 "p-value Type" = "pval\_type"),  
 outcomes=list("Significant p-value" = "pval\_sig"),  
 crosstab\_funcs=list(freq())) #%>%  
 #neat\_table(caption = "Statistics Reported")   
  
# Prereg Descriptives -----  
  
ctab\_prereg = df\_all %>%   
 select(clin\_trial, rct, animal, prereg) %>%  
 mutate\_all(as.factor) %>%  
 drop\_na() %>%  
 contingency\_table(  
 independents = list(  
 "Clinical Trial" = "clin\_trial",  
 "RCT" = "rct",  
 "Animal Study" = "animal"  
 ),  
 outcomes = list("Preregistration" = "prereg"),  
 crosstab\_funcs=list(freq()))  
  
ct\_prereg = table(df\_all$prereg)  
  
binom\_prereg = binom.test(ct\_prereg[[2]],sum(ct\_prereg))  
prereg\_pr = paste0(round(binom\_prereg$estimate\*100,2),"\\% [",  
 round(binom\_prereg$conf.int[1]\*100,2),", ",   
 round(binom\_prereg$conf.int[2]\*100,2)  
 ,"] of manuscripts reporting preregistration or clinical trial registration information")  
  
# Sample Size Information -----------  
  
ctab\_ss = df\_all %>%  
 select(journal, n\_just, sample\_info) %>%  
 mutate\_all(as.factor) %>%  
 drop\_na() %>%  
 contingency\_table(  
 independents = list(  
 "Sample Size Justification" = "n\_just",  
 "Sample Size Reported" = "sample\_info"  
 ),  
 outcomes = list("Journal" = "journal"),  
 crosstab\_funcs = list(freq())  
)   
  
ct\_njust = table(df\_all$n\_just)  
  
binom\_njust = binom.test(ct\_njust[[2]], sum(ct\_njust))  
njust\_pr = paste0(  
 round(binom\_njust$estimate \* 100, 2),  
 "% [",  
 round(binom\_njust$conf.int[1] \* 100, 2),  
 ", ",  
 round(binom\_njust$conf.int[2] \* 100, 2)  
 ,  
 "]"  
)  
  
ct\_samp = table(df\_all$sample\_info)  
  
binom\_samp = binom.test(ct\_samp[[3]], sum(ct\_samp))  
samp\_pr = paste0(  
 round(binom\_samp$estimate \* 100, 2),  
 "% [",  
 round(binom\_samp$conf.int[1] \* 100, 2),  
 ", ",  
 round(binom\_samp$conf.int[2] \* 100, 2)  
 ,  
 "] of manuscripts reported all the required sample size information (total and group sample sizes)."  
)  
  
# Sample Size Analysis ------  
  
  
# problems with med1way not sure if result is accurate  
samp\_1way = df\_all %>%  
 select(n, sci\_cat) %>%  
 mutate(n = as.numeric(n)) %>%  
 drop\_na() %>%  
 WRS2::med1way(formula = n ~ sci\_cat)  
  
# checking residuals; aov are fair  
library(afex)  
aov\_1way = df\_all %>%  
 select(n, sci\_cat, doi) %>%  
 mutate(n = as.numeric(n)) %>%  
 drop\_na() %>%  
 afex::aov\_4(formula = log(n) ~ sci\_cat + (1|doi))  
  
  
library(emmeans)  
emm\_samps = emmeans::emmeans(aov\_1way, ~ sci\_cat,  
 type = "response")  
  
   
# Other open Science Practices -----  
  
ct\_datstat = table(df\_all$data\_state)  
  
binom\_datstat = binom.test(ct\_datstat[[2]],300)  
datstat\_pr = paste0(round(binom\_datstat$estimate\*100,2),"% [",  
 round(binom\_datstat$conf.int[1]\*100,2),", ",   
 round(binom\_datstat$conf.int[2]\*100,2)  
 ,"] of manuscripts had a data accessibility statement")  
  
ct\_odat = table(df\_all$open\_data)  
  
binom\_odat = binom.test(ct\_odat[[2]],300)  
odat\_pr = paste0(round(binom\_odat$estimate\*100,2),"% [",  
 round(binom\_odat$conf.int[1]\*100,2),", ",   
 round(binom\_odat$conf.int[2]\*100,2)  
 ,"] of manuscripts reported some form of data sharing or open data")  
  
  
ct\_replic = table(df\_all$replic)  
  
binom\_replic = binom.test(0,300)  
replic\_pr = paste0(  
 round(binom\_replic$estimate \* 100, 2),  
 "% [",  
 round(binom\_replic$conf.int[1] \* 100, 2),  
 ", ",  
 round(binom\_replic$conf.int[2] \* 100, 2)  
 ,  
 "] of manuscripts explicitly stated they were replicating a previous study."  
)  
  
p\_n = df\_all %>%  
 ggplot(aes(x = as.numeric(n))) +  
 geom\_boxplot(fill = "skyblue3",  
 alpha = 0.55) +  
 labs(title = "Sample Size by Discipline",  
 x = "Total Sample Size (log scale)") +  
 theme\_bw() +  
 facet\_wrap(~sci\_cat,  
 scales ="free",  
 ncol = 2) +  
 scale\_x\_continuous(trans = "log10") +  
 theme(axis.ticks.y = element\_blank(),  
 axis.text.y = element\_blank())  
  
# By Journal ----  
  
## Hypothesis Support -----  
tab\_jhyp = table(df\_all$journal,df\_all$support)  
chisq\_support = chisq.test(tab\_jhyp)  
  
## Hypothesis Tested -----  
tab\_jtest = table(df\_all$journal,df\_all$hypo\_tested)  
chisq\_jtest = chisq.test(tab\_jtest)  
  
## Significance Testing -----  
tab\_jsig = table(df\_all$journal,df\_all$sig\_test)  
chisq\_jsig = chisq.test(tab\_jsig)  
  
## Effect Size -----  
tab\_jes = table(df\_all$journal,df\_all$effect\_size)  
chisq\_jes = chisq.test(tab\_jes)  
  
## Sample Size Justification -----  
tab\_jjust = table(df\_all$journal,df\_all$n\_just)  
chisq\_jjust = chisq.test(tab\_jjust)  
  
# Clinical Trial breakdown ------  
df\_clin = subset(df\_all, clin\_trial == "Yes")  
  
## Hypothesis Support (di)  
tab\_clindisup = table(df\_clin$di\_sup)  
binom\_clindisup = binom.test(tab\_clindisup[2], sum(tab\_clindisup),  
 p = .8)  
tab\_clinsup = table(df\_clin$support)  
  
## Hypothesis Tested  
tab\_clinhypo = table(df\_clin$hypo\_tested)  
binom\_clinhypo = binom.test(tab\_clinhypo[2], sum(tab\_clinhypo),  
 p = .6)  
  
## Sample Size Just ---------  
tab\_clinjust = table(df\_clin$n\_just)  
binom\_clinjust = binom.test(tab\_clinjust[2], sum(tab\_clinjust))  
  
## Pregreg -------  
  
tab\_clinreg = table(df\_clin$prereg)  
  
binom\_clinreg = binom.test(tab\_clinreg[2], sum(tab\_clinreg))  
  
### by journal -----  
tab\_clinregj = table(df\_clin$prereg, df\_clin$journal)  
  
  
# RCT breakdown ---------  
  
df\_rct = subset(df\_all, rct == "Yes")  
  
## Hypothesis Support (di)  
tab\_rctdisup = table(df\_rct$di\_sup)  
binom\_rctdisup = binom.test(tab\_rctdisup[2], sum(tab\_rctdisup),  
 p = .8)  
tab\_rctsup = table(df\_rct$support)  
  
## Hypothesis Tested  
tab\_rcthypo = table(df\_rct$hypo\_tested)  
binom\_rcthypo = binom.test(tab\_rcthypo[2], sum(tab\_rcthypo),  
 p = .6)  
  
## Sample Size Just ---------  
tab\_rctjust = table(df\_rct$n\_just)  
binom\_rctjust = binom.test(tab\_rctjust[2], sum(tab\_rctjust))  
  
tab\_rctreg = table(df\_rct$prereg)  
  
binom\_rctreg = binom.test(tab\_rctreg[2], sum(tab\_rctreg))  
  
## Sample Size Info -------  
# All studies reported sample size information  
#tab\_clinssj = table(df\_clin$sample\_info)  
#binom\_clinssj = binom.test(tab\_clinssj)  
  
  
# Breakdown by Discipline ----------  
  
## Hypothesis Tested ---------  
  
tab\_dissupp = table(df\_all$sci\_cat, df\_all$support)  
chisq\_dissupp = chisq.test(tab\_dissupp)  
  
tab\_dishypop = table(df\_all$sci\_cat, df\_all$hypo\_tested)  
chisq\_dishypop = chisq.test(tab\_dishypop)  
  
p\_dissup = df\_all %>%  
 group\_by(support, sci\_cat) %>%  
 summarize(count = n(),  
 .groups = 'drop') %>%  
 filter(!is.na(support)) %>%  
 ggplot( aes(fill=support, y=count, x=sci\_cat)) +   
 geom\_bar(position="fill", stat="identity",  
 color = "black")+  
 scale\_y\_continuous(labels = scales::percent) +  
 labs(x = "",  
 y = "Relative Frequency",  
 fill = "") +  
 theme\_classic() +  
 scale\_fill\_viridis\_d(option = "E") +  
 theme(legend.position = "bottom") +  
 coord\_flip()+  
 theme(text = element\_text(face = "bold"))  
  
p\_dishypo = df\_all %>%  
 group\_by(hypo\_tested, sci\_cat) %>%  
 summarize(count = n(),  
 .groups = 'drop') %>%  
 filter(!is.na(hypo\_tested)) %>%  
 ggplot( aes(fill=hypo\_tested, y=count, x=sci\_cat)) +   
 geom\_bar(position="fill", stat="identity",  
 color = "black")+  
 scale\_y\_continuous(labels = scales::percent) +  
 labs(x = "",  
 y = "Relative Frequency",  
 fill = "Hypothesis Tested") +  
 theme\_classic() +  
 scale\_fill\_viridis\_d(option = "E") +  
 theme(legend.position = "bottom") +  
 coord\_flip() +  
 theme(text = element\_text(face = "bold"))  
  
emm\_plot = plot(emm\_samps) +  
 scale\_x\_continuous(trans = "log",  
 breaks = c(10,15,20,30,40,50,65,80,110,150,1095)) +  
 labs(x = "Estimated Mean Sample Size (log scale)",  
 y = "") +  
 theme\_bw() +  
 theme(text = element\_text(face = "bold"))  
  
fig3 = ggarrange(p\_dishypo,p\_dissup,emm\_plot,  
 ncol = 1,  
 labels = "AUTO")

# Figure 3

fig3

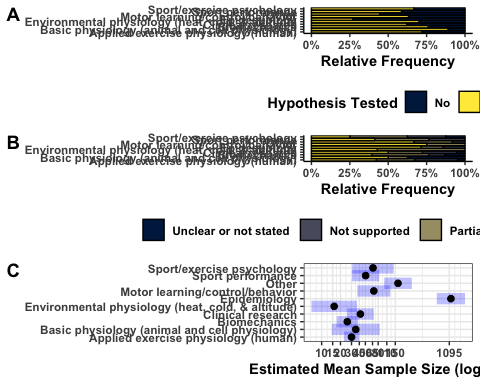


Figure 3. The breakdown, by discipline, for A) indication of whether a hypothesis was tested B) level of reported support for hypotheses, and C) the estimated total sample size (grey bands indicate 95% confidence intervals).

# Main Figures --------------  
  
p\_2a = df\_all %>%  
 group\_by(journal, support) %>%  
 summarize(count = n(),  
 .groups = 'drop') %>%  
 filter(!is.na(support)) %>%  
 ggplot( aes(fill=support, y=count, x=journal)) +   
 geom\_bar(position="fill", stat="identity",  
 color = "black")+  
 scale\_y\_continuous(labels = scales::percent) +  
 labs(x = "Journal",  
 y = "Relative Frequency",  
 fill = "Hypothesis Support") +  
 theme\_classic() +  
 scale\_fill\_viridis\_d(option = "E") +  
 theme(legend.position = "top",  
 text = element\_text(face = "bold"))  
  
p\_2b = df\_all %>%  
 group\_by(journal, hypo\_tested) %>%  
 summarize(count = n(),  
 .groups = 'drop') %>%  
 filter(!is.na(hypo\_tested)) %>%  
 ggplot( aes(fill=hypo\_tested, y=count, x=journal)) +   
 geom\_bar(position="fill", stat="identity",  
 color = "black")+  
 scale\_y\_continuous(labels = scales::percent) +  
 labs(x = "Journal",  
 y = "Relative Frequency",  
 fill = "Hypothesis Tested") +  
 theme\_classic() +  
 scale\_fill\_viridis\_d(option = "E") +  
 theme(legend.position = "top",  
 text = element\_text(face = "bold"))  
  
p\_2c = df\_all %>%  
 group\_by(journal, effect\_size) %>%  
 summarize(count = n(),  
 .groups = 'drop') %>%  
 filter(!is.na(effect\_size)) %>%  
 ggplot( aes(fill=effect\_size, y=count, x=journal)) +   
 geom\_bar(position="fill", stat="identity",  
 color = "black")+  
 scale\_y\_continuous(labels = scales::percent) +  
 labs(x = "Journal",  
 y = "Relative Frequency",  
 fill = "Effect Size Reported") +  
 theme\_classic() +  
 scale\_fill\_viridis\_d(option = "E") +  
 theme(legend.position = "top",  
 text = element\_text(face = "bold"))  
  
p\_2d = df\_all %>%  
 group\_by(journal, n\_just) %>%  
 summarize(count = n(),  
 .groups = 'drop') %>%  
 filter(!is.na(n\_just)) %>%  
 ggplot( aes(fill=n\_just, y=count, x=journal)) +   
 geom\_bar(position="fill", stat="identity",  
 color = "black")+  
 scale\_y\_continuous(labels = scales::percent) +  
 labs(x = "Journal",  
 y = "Relative Frequency",  
 fill = "Sample Size Justification") +  
 theme\_classic() +  
 scale\_fill\_viridis\_d(option = "E") +  
 theme(legend.position = "top",  
 text = element\_text(face = "bold"))  
  
  
fig\_2 = ggarrange(p\_2b, p\_2a, p\_2c, p\_2d,  
 ncol = 1,  
 labels = "AUTO")

# Figure 2

fig\_2

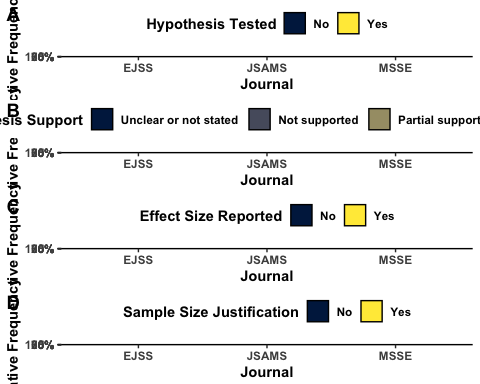


Figure 2. Relative frequencies, by journal, for A) level of reported support for hypotheses, B) indication of whether a hypothesis was tested, C) indication of whether an effect size was reported, or D) indication of if sample size was justified by the authors. Journals included the European Journal of Sport Science (EJSS), the Journal of Science and Medicine in Sport (JSAMS), and Medicine and Science in Sport and Exercise (MSSE),