

The nematode *Caenorhabditis elegans* and diverse potential invertebrate vectors predominantly interact opportunistically

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load required packages

```
library(readr)
library(plyr)
library(ggplot2)
```

load data

```
data <- read_csv("Wash_example.csv")
```

omit samples that should be excluded (e.g. threshold not reached)

```
data <- data[!(data$include == "no"),]
```

perform non-parametric Wilcoxon-signed rank test per group against 0 (no attraction or repulsion) and correct for multiple comparisons using FDR

```
wilcox.result <- ddply(data,.(choice_treat, worm_strain, solvent), function(sub_data){
  wilcox.result <- wilcox.test(sub_data$index, mu = 0.0)
  p.val <- wilcox.result$p.value
  return(data.frame(p.val))
})

wilcox.result$p.val_corrected <- p.adjust(wilcox.result$p.val, method = 'fdr'); wilcox.result
```

##	choice_treat	worm_strain	solvent	p.val	p.val_corrected
## 1	isoamylalc	MY2079	DMSO	0.001953125	0.003515625
## 2	isoamylalc	MY2079	EtOH	0.001953125	0.003515625
## 3	isoamylalc	MY2079	H2O	0.001953125	0.003515625
## 4	isoamylalc	N2	DMSO	0.001953125	0.003515625
## 5	isoamylalc	N2	EtOH	0.001953125	0.003515625
## 6	isoamylalc	N2	H2O	0.001953125	0.003515625
## 7	octanol	MY2079	DMSO	0.001953125	0.003515625
## 8	octanol	MY2079	EtOH	0.001953125	0.003515625
## 9	octanol	MY2079	H2O	0.001953125	0.003515625
## 10	octanol	N2	DMSO	0.001953125	0.003515625
## 11	octanol	N2	EtOH	0.003906250	0.006392045
## 12	octanol	N2	H2O	0.009029911	0.013544866
## 13	wash	MY2079	DMSO	0.064453125	0.089242788
## 14	wash	MY2079	EtOH	0.113893311	0.136671973
## 15	wash	MY2079	H2O	0.833634883	0.882672229
## 16	wash	N2	DMSO	0.625000000	0.703125000
## 17	wash	N2	EtOH	0.959327237	0.959327237
## 18	wash	N2	H2O	0.113893311	0.136671973

change order of factors for graph

```
data$choice_treat <- factor(data$choice_treat, levels = c("wash", "isoamylalc", "octanol"))
data$solvent <- factor(data$solvent, levels = c("H2O", "EtOH", "DMSO"))
data$worm_strain <- factor(data$worm_strain, levels = c("N2", "MY2079"))
```

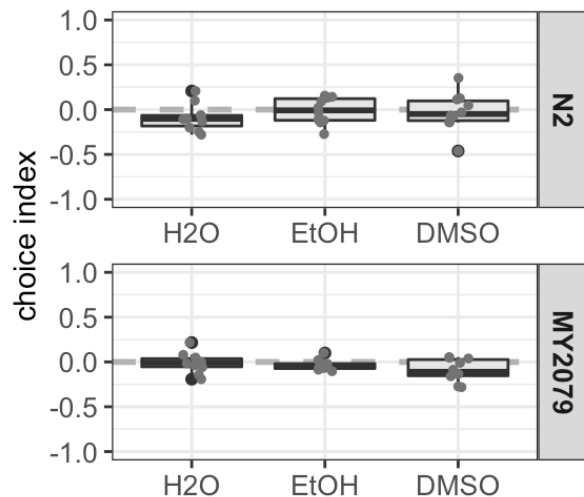
split data into two data frames: treatment and controls

```
data_treatment <- data[!(data$choice_treat == "isoamylalc"),]
data_treatment <- data_treatment[!(data_treatment$choice_treat == "octanol"),]

data_controls <- data[!(data$choice_treat == "wash"),]
```

generate boxplot for treatment without controls

```
ggplot(data_treatment, aes(x = solvent, y = index, fill = choice_treat)) +
  theme_bw() +
  theme(legend.position = "none") +
  scale_y_continuous(limits = c(-1, 1)) +
  geom_hline(yintercept = 0, linetype = "dashed", color = "grey70", size = 1) +
  geom_boxplot() +
  facet_wrap(~ worm_strain, scales = "free", nrow = 2, strip.position = "right") +
  geom_point(position = position_jitterdodge(), color = "grey45", size = 1) +
  labs(y = "choice index", x = "", title = "") +
  scale_fill_manual(name = "", values = "grey90") +
  theme(axis.text.x = element_text(size = 10), strip.text.x = element_text(size = 10, face = "bold"),
        strip.text.y = element_text(size = 10, face = "bold"), axis.text.y = element_text(hjust = 1, size = 10))
```



generate boxplot for controls

```
ggplot(data_controls, aes(x = solvent, y = index, fill = choice_treat)) +
  theme_bw() +
  theme(legend.position = "none") +
  scale_y_continuous(limits = c(-1, 1)) +
  geom_hline(yintercept = 0, linetype = "dashed", color = "grey70", size = 1) +
  geom_boxplot() +
  facet_wrap(~ worm_strain, scales = "free", nrow = 2, strip.position = "right") +
  geom_point(position = position_jitterdodge(), color = "grey45", size = 1) +
  labs(y = "choice index", x = "", title = "") +
  scale_fill_manual(name = "", values = c("grey90", "grey30")) +
  theme(axis.text.x = element_text(size = 10), strip.text.x = element_text(size = 10, face = "bold"),
        strip.text.y = element_text(size = 10, face = "bold"), axis.text.y = element_text(hjust = 1, size = 10))
```

