

Statistical tests pairwise growth

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```
d.18 <- readRDS(here("wrangled_data/all_pairwise.rds"))
d.18.summ <- readRDS(here("wrangled_data/pairwise_summary_stats.rds"))
```

Wilcoxon Rank-Sums tests to compare the shift in two samples.

population size shift in coculture versus monoculture

```
# define all conditions to run through
spec <- levels(d.18$species)
cond <- levels(d.18$condition)[which(levels(d.18$condition) != "alone")]
pH <- levels(d.18$pH)

# initiate list to store data, one list element for each species
l.tests <- list()

# for each species in each condition at each pH at each time, t-test against alone cfus
for (s in spec) {
  dat.tests <- d.18[0,-c(4,6:11)]
  for (c in cond[which(cond != s)]) {
    for (p in pH) {
      for (d in c(3,10,21)) {
        # get cfu data for growth with partners
        dat.part <- d.18 %>%
          filter(species == s, condition == c, pH == p, day == d)
        # get cfu data for growth alone
        dat.alone <- d.18 %>%
          filter(species == s, condition == "alone", pH == p, day == d)
        dat.tests[nrow(dat.tests)+1, "percent.change"] <-
          (mean(dat.part$total.CFUs) - mean(dat.alone$total.CFUs)) / mean(dat.alone$total.CFUs) #
        # set up dataframe with metadata
        dat.tests[nrow(dat.tests), "condition"] <- c
        dat.tests[nrow(dat.tests), "species"] <- s
        dat.tests[nrow(dat.tests), "pH"] <- p
        dat.tests[nrow(dat.tests), "day"] <- d
        dat.tests[nrow(dat.tests), "ave.ph.cond"] <- mean(d.18 %>%
          filter(species == s, condition == c, day == d,
            !is.na(measured.pH)) %>%
          pull(measured.pH))
        dat.tests[nrow(dat.tests), "ave.ph.alone"] <- mean(d.18 %>%
          filter(species == s, condition == "alone", day ==
```

```

                                !is.na(measured.pH)) %>%
                                pull(measured.pH))
dat.tests[nrow(dat.tests), "cond.median"] <- median(dat.part$total.CFUs)
dat.tests[nrow(dat.tests), "alone.median"] <- median(dat.alone$total.CFUs)
# mean fold-change
dat.tests[nrow(dat.tests), "cfus.part.alone"] <-
  mean(dat.part$total.CFUs) / mean(dat.alone$total.CFUs)
# median fold-change
fcs <- vector()
for(i in intersect(dat.part$replicate, dat.alone$replicate)) {
  part.cfus <- dat.part %>% filter(replicate == i) %>% pull(total.CFUs)
  alone.cfus <- dat.alone %>% filter(replicate == i) %>% pull(total.CFUs)
  fcs[length(fcs)+1] <- part.cfus / alone.cfus
}
dat.tests[nrow(dat.tests), "med.fc.part.alone"] <- median(fcs)
# do mann-whitney-wilcoxon tests on raw data
ttest <- wilcox.test(dat.part$total.CFUs, dat.alone$total.CFUs,
  alternative = "two.sided", var.equal = F, conf.int = T)
# back-calculate confidence intervals
dat.tests[nrow(dat.tests), "times.diff.CI.low"] <- ttest$"conf.int"[1]
dat.tests[nrow(dat.tests), "times.diff.CI.high"] <- ttest$"conf.int"[2]
# record p-value testing whether two samples look like they're from the same population
dat.tests[nrow(dat.tests), "pval"] <- ttest$p.value
if(ttest$p.value < 0.05 & ttest$p.value >= 0.01) dat.tests[nrow(dat.tests), "sig"] = "*"
if(ttest$p.value < 0.01 & ttest$p.value >= 0.001) dat.tests[nrow(dat.tests), "sig"] = "**"
if(ttest$p.value < 0.001) dat.tests[nrow(dat.tests), "sig"] = "***"
}
}
}
l.tests[[length(l.tests)+1]] <- dat.tests
}

names(l.tests) <- spec
# turn into dataframe
d.tests <- lapply(l.tests, as.data.frame) %>% bind_rows()

## species condition day times.diff.CI.low.pH5 times.diff.CI.high.pH5 sig.ph5
## 1 135E BC10 3 -11696000 4000000 <NA>
## 2 135E BC10 10 4200000 13800000 *
## 3 135E BC10 21 7000000 26500000 *
## times.diff.CI.low.pH7 times.diff.CI.high.pH7 sig.ph7
## 1 -110000 3940000 <NA>
## 2 -1500000 10700000 <NA>
## 3 -16500000 25700000 <NA>
## species condition day times.diff.CI.low.pH5 times.diff.CI.high.pH5 sig.ph5
## 1 135E BC9 3 -4200000 9300000 <NA>
## 2 135E BC9 10 -5800000 12300000 <NA>
## 3 135E BC9 21 5700000 26100000 *
## times.diff.CI.low.pH7 times.diff.CI.high.pH7 sig.ph7
## 1 -810000 2300000 <NA>
## 2 -2000000 2300000 <NA>
## 3 -14500000 35700000 <NA>
## species condition day times.diff.CI.low.pH5 times.diff.CI.high.pH5 sig.ph5
## 1 135E JB5 3 -5.0e+06 4600000 <NA>

```

## 2	135E	JB5	10	-5.3e+06	14300000	<NA>
## 3	135E	JB5	21	-1.2e+07	-2100000	**
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1		-540000	2660000	<NA>		
## 2		2900000	10100000	*		
## 3		-12300000	8300000	<NA>		
##	species condition day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5		
## 1	135E JB7 3	-5600000	5800000	<NA>		
## 2	135E JB7 10	-10500000	7800000	<NA>		
## 3	135E JB7 21	-11300000	1400000	<NA>		
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1		-760000	3360000	<NA>		
## 2		2500000	7500000	*		
## 3		-11800000	11600000	<NA>		
##	species condition day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5		
## 1	135E JBC 3	-2700000	7700000	<NA>		
## 2	135E JBC 10	-20170000	-10880000	**		
## 3	135E JBC 21	-27700000	-17999600	*		
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1		-1320000	1010000	<NA>		
## 2		-5300000	-3100000	**		
## 3		-24000000	-3400000	**		
##	species condition day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5		
## 1	135E JB370 3	-3300000	5500000	<NA>		
## 2	135E JB370 10	-6400000	5900000	<NA>		
## 3	135E JB370 21	-18800000	-3500000	*		
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1		-1500000	1320000	<NA>		
## 2		-3760000	-1000000	*		
## 3		-21670000	13600000	<NA>		
##	species condition day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5		
## 1	BC10 135E 3	-132900000	-12900000	*		
## 2	BC10 135E 10	-72000000	106000000	<NA>		
## 3	BC10 135E 21	-51000000	172000000	<NA>		
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1		-1.32e+08	3.23e+08	<NA>		
## 2		-1.28e+08	4.97e+08	<NA>		
## 3		-2.34e+08	3.09e+08	<NA>		
##	species condition day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5		
## 1	BC10 BC9 3	-74800000	4.52e+07	<NA>		
## 2	BC10 BC9 10	-53000000	7.60e+07	<NA>		
## 3	BC10 BC9 21	-15000000	1.04e+08	<NA>		
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1		-1.55e+08	3.62e+08	<NA>		
## 2		-6.30e+07	1.86e+08	<NA>		
## 3		-1.93e+08	1.35e+08	<NA>		
##	species condition day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5		
## 1	BC10 JB5 3	-1.15e+08	12400000	<NA>		
## 2	BC10 JB5 10	-6.30e+07	33000000	<NA>		
## 3	BC10 JB5 21	-7.00e+07	99000000	<NA>		
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1		-2.02e+08	2.90e+07	<NA>		
## 2		-1.23e+08	9.90e+07	<NA>		
## 3		-1.89e+08	1.59e+08	<NA>		

##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	BC10	JB7	3	-103200000	4.2e+07	<NA>
## 2	BC10	JB7	10	-56000000	3.3e+07	<NA>
## 3	BC10	JB7	21	-74000000	3.9e+07	<NA>
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1	-1.33e+08	1.02e+08	<NA>			
## 2	-9.50e+07	7.90e+07	<NA>			
## 3	-1.50e+08	2.26e+08	<NA>			
##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	BC10	JBC	3	-66000000	68000000	<NA>
## 2	BC10	JBC	10	-96000000	-14000000	**
## 3	BC10	JBC	21	-83700000	-22300000	*
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1	-1.70e+08	389000000	<NA>			
## 2	-1.71e+08	23000000	<NA>			
## 3	-2.90e+08	-8000000	*			
##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	BC10	JB370	3	-7.7e+07	4.30e+07	<NA>
## 2	BC10	JB370	10	9.8e+07	2.92e+08	**
## 3	BC10	JB370	21	3.6e+07	2.31e+08	*
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1	-1.98e+08	4.20e+07	<NA>			
## 2	-1.20e+08	2.11e+08	<NA>			
## 3	-3.12e+08	1.30e+08	<NA>			
##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	BC9	135E	3	7990000	34450000	**
## 2	BC9	135E	10	55900000	143000000	*
## 3	BC9	135E	21	115300000	306700000	**
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1	-1.15e+08	142000000	<NA>			
## 2	-1.29e+08	-46000000	**			
## 3	-4.80e+07	170000000	<NA>			
##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	BC9	BC10	3	-1480000	5850000	<NA>
## 2	BC9	BC10	10	-30000000	-21700000	*
## 3	BC9	BC10	21	-18500000	41300000	<NA>
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1	-1.28e+08	1.70e+07	<NA>			
## 2	-2.71e+08	-2.05e+08	**			
## 3	-2.75e+08	-7.50e+07	**			
##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	BC9	JB5	3	-1027000	2030000	<NA>
## 2	BC9	JB5	10	-16900000	8200000	<NA>
## 3	BC9	JB5	21	-7700000	25900000	<NA>
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1	3.00e+06	1.98e+08	*			
## 2	-6.00e+07	4.50e+07	<NA>			
## 3	-2.04e+08	2.40e+08	<NA>			
##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	BC9	JB7	3	-1201000	2890000	<NA>
## 2	BC9	JB7	10	-23600000	281100000	<NA>
## 3	BC9	JB7	21	-14000000	24900000	<NA>
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1	-3.50e+07	1.99e+08	<NA>			

## 2				-3.80e+07	2.06e+08	<NA>
## 3				-2.09e+08	2.90e+08	<NA>
##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	BC9	JBC	3	5850000	55150000	**
## 2	BC9	JBC	10	-29000000	-17000000	*
## 3	BC9	JBC	21	-24900000	28900000	<NA>
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1				3.10e+07	5.49e+08	*
## 2				-2.60e+08	6.00e+06	<NA>
## 3				-2.35e+08	8.80e+07	<NA>
##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	BC9	JB370	3	2250000	31050000	**
## 2	BC9	JB370	10	306900000	540000000	*
## 3	BC9	JB370	21	-17400000	605700000	<NA>
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1				-1.60e+07	3.27e+08	<NA>
## 2				-1.59e+08	1.40e+07	<NA>
## 3				-1.79e+08	1.76e+08	<NA>
##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	JB5	135E	3	319610	9599890	*
## 2	JB5	135E	10	819988700	1559995600	*
## 3	JB5	135E	21	159830000	2899830000	**
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1				-2.174e+07	1.566e+07	<NA>
## 2				-1.950e+09	5.900e+08	<NA>
## 3				-1.800e+09	1.400e+09	<NA>
##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	JB5	BC10	3	290	779690	**
## 2	JB5	BC10	10	832200	22992200	**
## 3	JB5	BC10	21	17470000	3899900000	*
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1				-2.167e+07	8.00e+04	<NA>
## 2				-1.630e+09	2.50e+08	<NA>
## 3				-2.530e+09	2.02e+09	<NA>
##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	JB5	BC9	3	-290	589.9999	<NA>
## 2	JB5	BC9	10	-12300	600.0000	<NA>
## 3	JB5	BC9	21	-34099100	-58900.0000	*
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1				-1.995e+07	2.6e+06	<NA>
## 2				-1.650e+09	1.3e+09	<NA>
## 3				-2.720e+09	1.6e+09	<NA>
##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	JB5	JB7	3	-210	350	<NA>
## 2	JB5	JB7	10	-9400	8800	<NA>
## 3	JB5	JB7	21	-33930000	910000	<NA>
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1				-1.29e+07	24160000	<NA>
## 2				-1.97e+09	310000000	<NA>
## 3				-3.20e+09	-610000000	**
##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	JB5	JBC	3	-180	1190	<NA>
## 2	JB5	JBC	10	-13890	-940	*
## 3	JB5	JBC	21	-34100000	-60000	*

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## times.diff.CI.low.pH7 times.diff.CI.high.pH7 sig.ph7
## 1 -15100000 20860000 <NA>
## 2 -2769983000 -1059983000 **
## 3 -5051100000 -2710000000 *
## species condition day times.diff.CI.low.pH5 times.diff.CI.high.pH5 sig.ph5
## 1 JB5 JB370 3 -2.000003e+01 390 <NA>
## 2 JB5 JB370 10 6.392200e+06 28692200 **
## 3 JB5 JB370 21 2.147000e+07 216830000 *
## times.diff.CI.low.pH7 times.diff.CI.high.pH7 sig.ph7
## 1 -6.40e+06 7.866e+07 <NA>
## 2 -2.02e+09 -2.500e+08 **
## 3 -4.42e+09 -2.120e+09 **
## species condition day times.diff.CI.low.pH5 times.diff.CI.high.pH5 sig.ph5
## 1 JB7 135E 3 3.585e+04 659850 *
## 2 JB7 135E 10 1.240e+09 1639999900 *
## 3 JB7 135E 21 1.480e+09 3709999880 **
## times.diff.CI.low.pH7 times.diff.CI.high.pH7 sig.ph7
## 1 -7.28e+07 2.61e+07 <NA>
## 2 4.00e+07 2.15e+09 *
## 3 1.05e+09 3.59e+09 *
## species condition day times.diff.CI.low.pH5 times.diff.CI.high.pH5 sig.ph5
## 1 JB7 BC10 3 40 280 <NA>
## 2 JB7 BC10 10 699850 51399880 *
## 3 JB7 BC10 21 80999880 1719999880 **
## times.diff.CI.low.pH7 times.diff.CI.high.pH7 sig.ph7
## 1 -7.68e+07 3.08e+07 <NA>
## 2 -5.00e+08 7.30e+08 <NA>
## 3 4.10e+08 1.49e+09 *
## species condition day times.diff.CI.low.pH5 times.diff.CI.high.pH5 sig.ph5
## 1 JB7 BC9 3 -49.99994 530 <NA>
## 2 JB7 BC9 10 -199.99994 100 <NA>
## 3 JB7 BC9 21 -130.00005 129890 <NA>
## times.diff.CI.low.pH7 times.diff.CI.high.pH7 sig.ph7
## 1 -7.59e+07 3.80e+06 <NA>
## 2 -1.02e+09 4.00e+07 <NA>
## 3 3.00e+08 1.33e+09 *
## species condition day times.diff.CI.low.pH5 times.diff.CI.high.pH5 sig.ph5
## 1 JB7 JB5 3 -70.0000 119.99997 <NA>
## 2 JB7 JB5 10 -190.0001 80.00003 <NA>
## 3 JB7 JB5 21 -30.0000 1490.00001 <NA>
## times.diff.CI.low.pH7 times.diff.CI.high.pH7 sig.ph7
## 1 -3.72e+07 146800000 <NA>
## 2 -2.80e+08 780000000 <NA>
## 3 -3.60e+08 530000000 <NA>
## species condition day times.diff.CI.low.pH5 times.diff.CI.high.pH5 sig.ph5
## 1 JB7 JBC 3 -9.999965 200 <NA>
## 2 JB7 JBC 10 -280.000000 730 <NA>
## 3 JB7 JBC 21 -130.000000 15999880 <NA>
## times.diff.CI.low.pH7 times.diff.CI.high.pH7 sig.ph7
## 1 -5.490e+07 1.462e+08 <NA>
## 2 -1.845e+09 -1.060e+09 **
## 3 -6.600e+08 2.500e+08 <NA>
## species condition day times.diff.CI.low.pH5 times.diff.CI.high.pH5 sig.ph5
## 1 JB7 JB370 3 -9.999994e+01 250 <NA>

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## 2	JB7	JB370	10	3.998500e+05	1239880	*
## 3	JB7	JB370	21	1.099988e+07	551999880	**
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1		-3.62e+07	132800000	<NA>		
## 2		-8.80e+08	-100000000	*		
## 3		-7.20e+08	240000000	<NA>		
##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	JBC	135E	3	-15060	-7560	**
## 2	JBC	135E	10	-38000000	-16000000	**
## 3	JBC	135E	21	-47000000	166000000	<NA>
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1		-4.1e+03	3700	<NA>		
## 2		-3.0e+06	330700000	<NA>		
## 3		-5.5e+07	12000000	<NA>		
##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	JBC	BC10	3	-1.1e+04	3.3e+03	<NA>
## 2	JBC	BC10	10	-1.6e+07	7.0e+06	<NA>
## 3	JBC	BC10	21	-3.9e+07	1.3e+07	<NA>
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1		-5170	1100	<NA>		
## 2		-13000000	10700000	<NA>		
## 3		-53000000	14000000	<NA>		
##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	JBC	BC9	3	-11260	-1400	*
## 2	JBC	BC9	10	-20000000	25000000	<NA>
## 3	JBC	BC9	21	-26000000	26000000	<NA>
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1		-5110	4.900000e+02	<NA>		
## 2		-12900000	1.000000e+07	<NA>		
## 3		-71000000	2.332915e-05	<NA>		
##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	JBC	JB5	3	-8.4e+03	1.4e+03	<NA>
## 2	JBC	JB5	10	-1.0e+07	2.3e+07	<NA>
## 3	JBC	JB5	21	-2.4e+07	4.1e+07	<NA>
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1		-3.5e+03	3400	<NA>		
## 2		1.0e+05	23700000	*		
## 3		-6.2e+07	11000000	<NA>		
##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	JBC	JB7	3	-9.2e+03	-1.1e+03	**
## 2	JBC	JB7	10	-2.2e+07	2.2e+07	<NA>
## 3	JBC	JB7	21	-1.9e+07	2.5e+08	<NA>
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1		-4.3e+03	2800	<NA>		
## 2		-8.0e+05	21000000	<NA>		
## 3		-6.8e+07	-1000000	*		
##	species	condition	day	times.diff.CI.low.pH5	times.diff.CI.high.pH5	sig.ph5
## 1	JBC	JB370	3	-10700	7.8e+03	<NA>
## 2	JBC	JB370	10	-24000000	7.0e+06	<NA>
## 3	JBC	JB370	21	-39000000	1.2e+07	<NA>
##	times.diff.CI.low.pH7	times.diff.CI.high.pH7	sig.ph7			
## 1		-4.3e+03	1.3e+03	<NA>		
## 2		9.0e+06	3.7e+07	*		
## 3		-6.7e+07	3.2e+07	<NA>		

```

## species condition day times.diff.CI.low.pH5 times.diff.CI.high.pH5 sig.ph5
## 1 JB370 135E 3 -2000 760 <NA>
## 2 JB370 135E 10 -796000 -350000 **
## 3 JB370 135E 21 -8200000 -1500000 *
## times.diff.CI.low.pH7 times.diff.CI.high.pH7 sig.ph7
## 1 -1300 250 <NA>
## 2 -126000 -17000 **
## 3 -1690000 2010000 <NA>
## species condition day times.diff.CI.low.pH5 times.diff.CI.high.pH5 sig.ph5
## 1 JB370 BC10 3 -2520 660 <NA>
## 2 JB370 BC10 10 120000 2070000 *
## 3 JB370 BC10 21 -6200000 3100000 <NA>
## times.diff.CI.low.pH7 times.diff.CI.high.pH7 sig.ph7
## 1 -1280 -2.036127e-08 *
## 2 -131000 2.000000e+03 <NA>
## 3 -2060000 -1.900000e+05 *
## species condition day times.diff.CI.low.pH5 times.diff.CI.high.pH5 sig.ph5
## 1 JB370 BC9 3 -1640 3900 <NA>
## 2 JB370 BC9 10 -30000 410000 <NA>
## 3 JB370 BC9 21 -3300000 16300000 <NA>
## times.diff.CI.low.pH7 times.diff.CI.high.pH7 sig.ph7
## 1 -1230 550 <NA>
## 2 -151000 -49000 *
## 3 -1990000 140000 <NA>
## species condition day times.diff.CI.low.pH5 times.diff.CI.high.pH5 sig.ph5
## 1 JB370 JB5 3 -1920 400 <NA>
## 2 JB370 JB5 10 -340000 400000 <NA>
## 3 JB370 JB5 21 -3600000 4300000 <NA>
## times.diff.CI.low.pH7 times.diff.CI.high.pH7 sig.ph7
## 1 -1230 690 <NA>
## 2 -93000 19000 <NA>
## 3 -1380000 290000 <NA>
## species condition day times.diff.CI.low.pH5 times.diff.CI.high.pH5 sig.ph5
## 1 JB370 JB7 3 -1.460000e+03 840 <NA>
## 2 JB370 JB7 10 1.055984e-06 2570000 *
## 3 JB370 JB7 21 -5.200000e+06 3900000 <NA>
## times.diff.CI.low.pH7 times.diff.CI.high.pH7 sig.ph7
## 1 -1110 350 <NA>
## 2 -140000 8000 <NA>
## 3 -1160000 780000 <NA>
## species condition day times.diff.CI.low.pH5 times.diff.CI.high.pH5 sig.ph5
## 1 JB370 JBC 3 -2900 -640 *
## 2 JB370 JBC 10 -899860 -549760 <NA>
## 3 JB370 JBC 21 -11698800 -5400000 *
## times.diff.CI.low.pH7 times.diff.CI.high.pH7 sig.ph7
## 1 -1300 -40.00002 *
## 2 -159980 -57940.00000 *
## 3 -2498900 -828360.00000 *

## $`135E`
## NULL
##
## $BC10
## NULL

```



```
##
## $BC9
## NULL
##
## $JB5
## NULL
##
## $JB7
## NULL
##
## $JBC
## NULL
##
## $JB370
## NULL
```

measured pH shift in coculture versus monoculture

Note that pH of sample was measured after homogenizing sample in a buffer solution, so is not an accurate pH reading of the sample. However, a difference in sample pH's can be detected.

```
# define all conditions to run through
spec <- levels(d.18$species)
cond.all <- levels(d.18$condition)
pH <- levels(d.18$pH)

# initiate list to store data, one list element for each species
l.tests.pH <- list()

# for each species in each condition at each pH at each time, t-test against alone
for (s in levels(d.18$species)) {
  dat.tests <- d.18[0,-c(3:4,6:10)]
  for (c in cond.all[which(cond.all != s)]) {
    for (d in c(3,10,21)) {
      # get cfu data for growth with partners; log-transform
      dat <- d.18 %>%
        filter(species == s, condition == c, day == d)
      # set up dataframe with metadata
      dat.tests[nrow(dat.tests)+1, "species"] <- s
      dat.tests[nrow(dat.tests), "condition"] <- c
      dat.tests[nrow(dat.tests), "day"] <- d
      dat.tests[nrow(dat.tests), "pH"] <- "7"
      dat.tests[nrow(dat.tests), "ph5.median"] <- median(dat %>% filter(pH==5) %>% pull(total.CFUs))
      dat.tests[nrow(dat.tests), "ph7.median"] <- median(dat %>% filter(pH==7) %>% pull(total.CFUs))
      # mean fold-change
      dat.tests[nrow(dat.tests), "cfus.ph7.v.ph5"] <-
        mean(dat %>% filter(pH==7) %>% pull(total.CFUs)) /
        mean(dat %>% filter(pH==5) %>% pull(total.CFUs))
      # median fold-change
      fcs <- vector()
      for(i in intersect(dat %>% filter(pH == 7) %>% pull(replicate),
                        dat %>% filter(pH == 5) %>% pull(replicate))) {
        ph7.cfus <- dat %>% filter(pH == 7, replicate == i) %>% pull(total.CFUs)
        ph5.cfus <- dat %>% filter(pH == 5, replicate == i) %>% pull(total.CFUs)
```

```

    fcs[length(fcs)+1] <- ph7.cfus / ph5.cfus
  }
  dat.tests[nrow(dat.tests), "med.fc.ph7.v.ph5"] <- median(fcs)

  # check similarity of variance using Levene's test
  if(mean(dat$total.CFUs)!=0) {
    levene.test <- car::leveneTest(total.CFUs ~ pH, data = dat)
    if (levene.test$"Pr(>F)"[1] <= 0.05) {
      print(paste(s, "at pH 5 versus pH 7 with", c, "on day", d,
        "do not have equal variance, with p value", levene.test$"Pr(>F)"[1]))
    }
    # do mann-whitney-wilcoxon tests on log-transformed data
    ttest <- wilcox.test(total.CFUs ~ pH, data = dat,
      alternative = "two.sided", var.equal = F, conf.int = T)
    # back-calculate confidence intervals
    dat.tests[nrow(dat.tests), "times.diff.CI.low"] <- ttest$"conf.int"[1]
    dat.tests[nrow(dat.tests), "times.diff.CI.high"] <- ttest$"conf.int"[2]

    # record p-value testing whether two samples look like they're from the same population
    dat.tests[nrow(dat.tests), "pval"] <- ttest$p.value
    if(ttest$p.value < 0.05 & ttest$p.value >= 0.01) dat.tests[nrow(dat.tests), "sig"] = "*"
    if(ttest$p.value < 0.01 & ttest$p.value >= 0.001) dat.tests[nrow(dat.tests), "sig"] = "**"
    if(ttest$p.value < 0.001) dat.tests[nrow(dat.tests), "sig"] = "***"
  }
}
}
l.tests.pH[[length(l.tests.pH)+1]] <- dat.tests
}

```

```

## [1] "135E at pH 5 versus pH 7 with JBC on day 10 do not have equal variance, with p value 0.02169661"
## [1] "135E at pH 5 versus pH 7 with JBC on day 21 do not have equal variance, with p value 0.03262687"
## [1] "135E at pH 5 versus pH 7 with community on day 10 do not have equal variance, with p value 0.03"
## [1] "BC10 at pH 5 versus pH 7 with 135E on day 3 do not have equal variance, with p value 0.04552959"
## [1] "BC10 at pH 5 versus pH 7 with JBC on day 3 do not have equal variance, with p value 0.038424804"
## [1] "BC9 at pH 5 versus pH 7 with alone on day 3 do not have equal variance, with p value 0.03631471"
## [1] "BC9 at pH 5 versus pH 7 with 135E on day 3 do not have equal variance, with p value 0.016135850"
## [1] "BC9 at pH 5 versus pH 7 with BC10 on day 10 do not have equal variance, with p value 0.04950840"
## [1] "BC9 at pH 5 versus pH 7 with JB5 on day 3 do not have equal variance, with p value 0.0082047167"
## [1] "BC9 at pH 5 versus pH 7 with JBC on day 3 do not have equal variance, with p value 0.0347288689"
## [1] "BC9 at pH 5 versus pH 7 with JB370 on day 3 do not have equal variance, with p value 0.04881526"
## [1] "JB5 at pH 5 versus pH 7 with alone on day 10 do not have equal variance, with p value 0.0102259"
## [1] "JB5 at pH 5 versus pH 7 with alone on day 21 do not have equal variance, with p value 0.0215969"
## [1] "JB5 at pH 5 versus pH 7 with BC9 on day 3 do not have equal variance, with p value 0.0168338100"
## [1] "JB5 at pH 5 versus pH 7 with BC9 on day 10 do not have equal variance, with p value 0.006424356"
## [1] "JB5 at pH 5 versus pH 7 with BC9 on day 21 do not have equal variance, with p value 0.023689913"
## [1] "JB5 at pH 5 versus pH 7 with JB7 on day 10 do not have equal variance, with p value 0.036043421"
## [1] "JB5 at pH 5 versus pH 7 with JBC on day 21 do not have equal variance, with p value 0.007577250"
## [1] "JB5 at pH 5 versus pH 7 with community on day 21 do not have equal variance, with p value 0.038"
## [1] "JB7 at pH 5 versus pH 7 with alone on day 10 do not have equal variance, with p value 0.0348097"
## [1] "JB7 at pH 5 versus pH 7 with JBC on day 3 do not have equal variance, with p value 5.7354375809"
## [1] "JB7 at pH 5 versus pH 7 with JBC on day 21 do not have equal variance, with p value 0.029692985"
## [1] "JB7 at pH 5 versus pH 7 with community on day 3 do not have equal variance, with p value 0.0201"
## [1] "JB370 at pH 5 versus pH 7 with alone on day 10 do not have equal variance, with p value 0.04271"
## [1] "JB370 at pH 5 versus pH 7 with BC10 on day 21 do not have equal variance, with p value 0.027462"

```

```
## [1] "JB370 at pH 5 versus pH 7 with BC9 on day 10 do not have equal variance, with p value 0.0078321"
## [1] "JB370 at pH 5 versus pH 7 with JB5 on day 10 do not have equal variance, with p value 0.0086767"
# turn into dataframe
d.tests.pH <- lapply(l.tests.pH, as.data.frame) %>% bind_rows()
save(d.tests, d.tests.pH, file = here("wrangled_data/pairwise_test_summaries.RData"))
```