

A Closer Look at Particle Counts

30/06/2020

Background

Expt D in the Transfer studies shows high variability and much higher transfer ratio, T_r , values than the others, especially with wool. On closer inspection it appears that it (as well as expt B to some extent) shows quite high values for Photo 1, P_1 , - median ~ 100 - when the A,C & E are much near to zero.

With that information can simulate or reproduce the behaviour on simulated data. As all the data are raw counts of independent events it is sensible to assume a Poisson distribution. Poisson distributions are dependent on two parameters k , the number of occurrences, and λ , the mean (which is equal to the variance).

The hypothesis being are relatively high P_1 counts causative of high Transfer Ratios independently of other photo counts?

So we can model the counts for photos P_1 , P_2 and P_3 assuming a Poisson distribution and taking equivalent means from the Transfer experiment. Photos P_4 and P_5 are a function of these starting counts based on the amount of transfer. A 35% transfer of particles is consistent with the data. A random normal sampling around this mean with a standard deviation of 4 is used.

$n = 20$ for the number of times each transfer ‘experiment’ is simulated.

Loss and ‘declumping’ of particles is not simulated.

Simulation

```
# function to produce the starting data
makeData <- function(p1 = 45, p2 = 6, p3 = 120, n = 20, transfer.pc = 35) {
  # create donor background data
  p1.dist = rpois(n, p1)

  # low background on receiver
  p2.dist = rpois(n, p2)
  # add some particles
  p3.dist = rpois(n, p3)

  # assume 30-40 percent transfer
  trans = round(rnorm(n, transfer.pc, sd = 4))/100

  # create modelled data for particulate transfer
  df = data.frame(p1.dist, p2.dist, p3.dist, p4 = p1.dist + round(p3.dist * trans),
    p5 = p1.dist + round(p3.dist * (1 - trans)))

  return(df)
}
```

With the function for creating the distributions defined a range of values will be parameterised:

- $P_1 = 5, 30, 55, 80, 105$
- $P_2 = 5, 30, 55, 80, 105$

- $P_3 = 100, 150, 200, 250, 300$

```
df.dat = data.frame()
for (p1 in seq(5, 105, 25)) {
  for (p2 in seq(5, 105, 25)) {
    for (p3 in seq(100, 300, 50)) {
      df = makeData(p1, p2, p3)
      if (nrow(df.dat) > 0) {
        tmp = data.frame(p1.m = as.character(p1), p2.m = as.character(p2),
                          p3.m = as.character(p3), df)
        df.dat = rbind(df.dat, tmp)
      } else {
        df.dat = data.frame(p1.m = as.character(p1), p2.m = as.character(p2),
                          p3.m = as.character(p3), df)
      }
    }
  }
}
```

The Transfer Ratio is calculated as previous described:

$$t_r = (P_5 - P_2)/(P_3 - P_1)$$

```
# calc transfer ratio
df.dat$tr = (df.dat$p5 - df.dat$p2.dist)/(df.dat$p3.dist - df.dat$p1.dist)
```

Note: If $P_1 = P_3$ the denominator is 0 which results in a non-finite T_r .

Results

If we fix $P_2 = 5$ and simulate P_1 and P_3 we can visualise the effect on T_r as a function of both counts.

```
df.dat %>% filter(p2.m == "5") %>% ggplot(aes(x = factor(p1.m, levels = c(seq(5,
  105, 25))), y = tr)) + labs(title = "Simulation of Transfer Ratio as a Function of P1 & P3 Counts",
  subtitle = "n = 20, Mean P2 counts = 5, % particles transferred = 35% (+/- 4 s.d.)",
  x = "Mean P1 Counts", y = "Transfer Ratio", caption = "Y-axes are not the same") +
  geom_boxplot() + facet_wrap(p3.m ~ ., scales = "free_y")
```

```
## Warning: Removed 2 rows containing non-finite values (stat_boxplot).
```

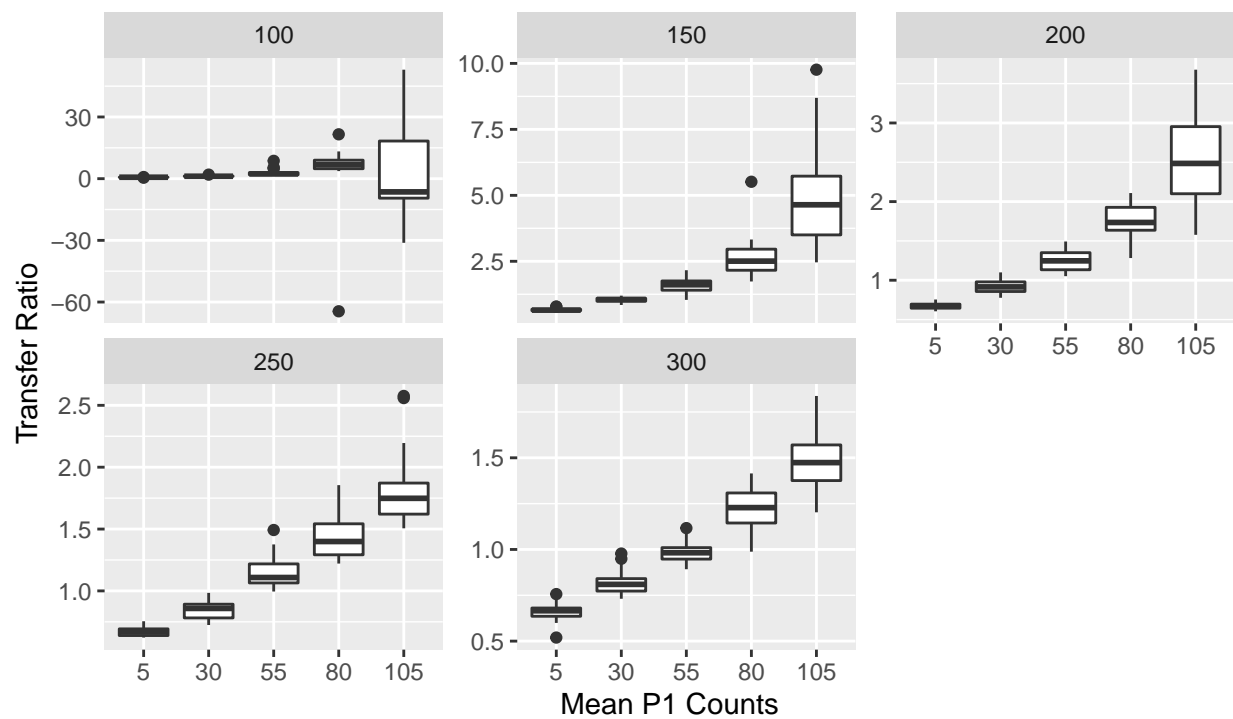
Figure 1 shows that for $P_3 > 150$ there is a predictable, linear relationship between P_1 and P_3 counts. However, with $P_3 \leq 150$ and mean P_1 increasing the T_r relationship gets very unstable - high positive and negative values. This suggests that it's not just high P_1 counts that are the problem, but it's when $P_1 \approx P_3$ then T_r is extreme.

As a comparison if we look at the P_2 , the receiver background, relationship with T_r there is no issue either at high counts or when $P_2 \approx P_3$.

```
df.dat %>% filter(p1.m == 5) %>% ggplot(aes(x = factor(p2.m, levels = c(seq(5, 105,
  25))), y = tr)) + labs(title = "Simulation of Transfer Ratio as a Function of P2 Counts",
  subtitle = "n = 20, Mean P1 counts = 5, % particles transferred = 35% (+/- 4 s.d.)",
  x = "Mean P2 Counts", y = "Transfer Ratio", caption = "Y-axes is the same") +
  geom_boxplot() + facet_wrap(p3.m ~ .)
```

Simulation of Transfer Ratio as a Function of P1 & P3 Counts

$n = 20$, Mean P2 counts = 5, % particles transferred = 35% (± 4 s.d.)

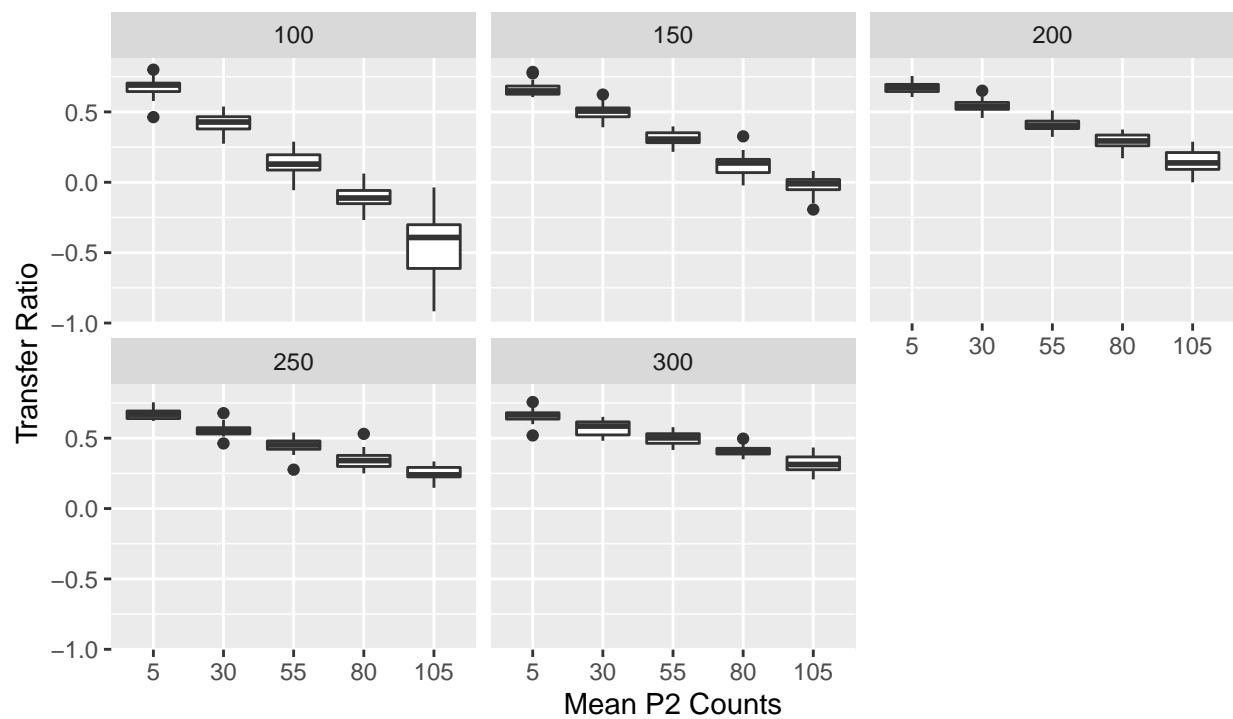


Y-axes are not the same

Figure 1: Simulation of Transfer Ratio as a Function of P1 & P3 Counts

Simulation of Transfer Ratio as a Function of P2 Counts

$n = 20$, Mean P1 counts = 5, % particles transferred = 35% (± 4 s.d.)



Y-axes is the same

Figure 2: Simulation of Transfer Ratio as a Function of P2 Counts