Introduction

As a pandemic replacement for the cross-division-chance-encounter in the coffee kitchen, it has become common to use a virtual social mixer format, where the \(n\) participants are randomly divided into groups of at least \(m\) people, e.g., for a video meeting or Zoom breakout rooms. Software exists to institutionalize such Random Lunches for, e.g., Slack. In this post we shall be interested in the properties of such group assignment algorithms.

A practical experience is that all too often, the algorithm assigns me to a group where at least one of the participants was already in my group the last time. Before accusing the programmers of writing a poor grouping algorithm: can we determine mathematically what the probability for such a “reunion” is? How can we modify the algorithm to avoid this?

Survey of the field

Arranging a fixed set of \(n=k\times m\) individuals into \(k\) groups of size \(m\) in subsequent rounds ensuring that no overlap occurs between the groups for as many rounds as possible is also known as the social golfer problem or round robin scheduling in combinatorics – and can be solved using constraint programming. Compared to the social golfer problem, we have the additional challenge that the group of people between rounds may be subject to change. Furthermore, \(m\) might not be a divisor of \(n\). Hence, somewhat closer to our problem is the so called maximally diverse grouping problem, where the grouping is to be done such that the requirements on group size are met and a diversity score over the elements in each group is maximized. For our setup, the score could, e.g., be time since the last meet between individuals. Integer programming can be used to solve the NP-complete problem.

However, in our application we will either ignore the diversity score altogether (i.e. set it to 1 always) or use a 0/1 diversity score (met last time or not). Furthermore, we are interested in random assignment algorithms selecting uniformly among the valid configurations. As a consequence, we choose a more probabilistic approach and instead use a custom group assignment algorithm as described in the next section.

The Grouping

We want to split the \(n\) individuals into groups of preferably \(m\) members. However, if \(m\) is not a divisor of \(n\) then after making \(\lfloor n/m \rfloor\) groups of \(m\) members we would have \(l = n – \lfloor n/m \rfloor\) individuals left. Instead of assigning these to a single leftover group, which would be of size less than \(m\) (particularly critical is size 1), we assign the remaining individuals to the \(l\) groups in round robin fashion. This ensures that each group has size at least \(m\). Note: Depending on \(n\) and \(m\) the resulting sizes might be larger \(m+1\), but the difference in the resulting group size will never be larger than 1[1]. Let `people` be a tibble with a column `id` denoting a primary identifier key – this could, e.g., be the people’s email address. An R function to perform a random assignment of the \(n\)=`nrow(people)` individuals into groups of at least \(m\) could look like:

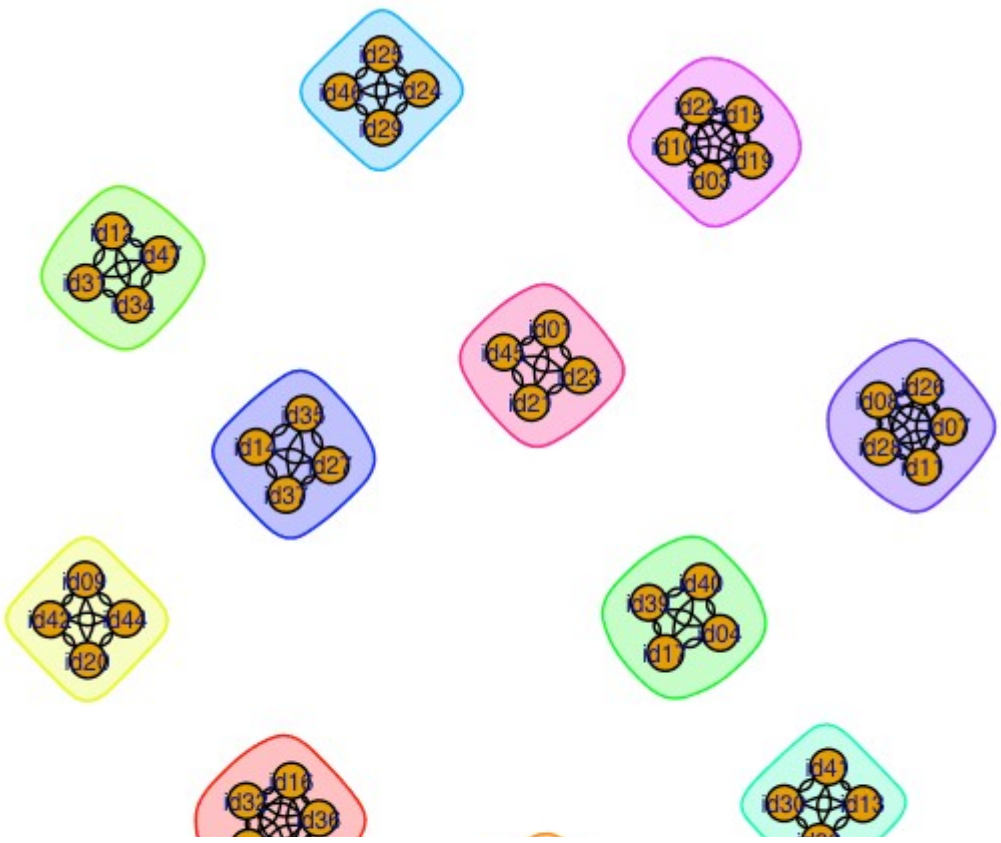
```
#' Sample people into groups (original algorithm)
#'
#' @param people tibble containing name and email of available ppl
#' @param m requested group size. If m not a divisor of nrow(people)
then put leftovers in existing groups
#'
```

```
#' @return A list of vectors where each vector containing the ids (row
number in ppl) of those belonging to the same group
#'
sample_groups <- function(people, m) {
  # Number of groups needed
  n_g <- nrow(people) %/% m
  # Group membership indicator
  g <- rep(seq_len(n_g), length.out=nrow(people))
  # Permutation order
  perm <- sample(seq_len(nrow(people)))

  # Make a list of ids in each group
  groups <- map(seq_len(n_g), function(i) {
    idx <- perm[which(g == i)]
    people %>% slice(idx) %>% pull(id)
  })

  return(groups)
}
```

Example: Let `people` denote the population of 47 individuals to be assigned into groups of at least \(m=4\) according to the above description.

```
n <- 47
people <- tibble(id = str_c("id", sprintf("%0.2d",seq_len(n))))
m <- 4
groups <- sample_groups(people, m=m)
```

This leads to 11 groups with between 4 and 5 members. We can visualize the group allocation as a graph, where each group will correspond to a fully connected sub-graph, but with no connections between the sub-graphs.



Mathematical Formulation

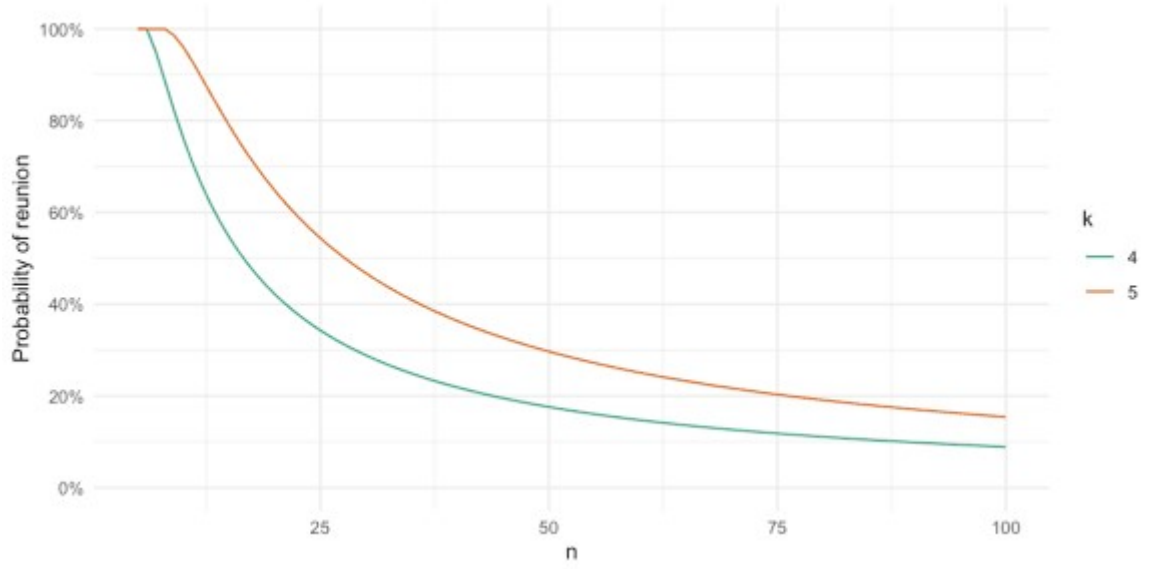
The mathematical question is now: Given you were in the group with \(l\) other persons the last time, what is the probability that after assigning \(n\) individuals into groups of preferred size \(m\geq 2\), that you will be in the same group with at least one of them again this time[2]. Let \(m \leq k\) be the size of your group in the current assignment. Combinatorical considerations tell us the probability to meet at least one of the \(l\) persons again is:

\[p(k, l, n) = 1 - \frac{1\cdot\prod_{i=2}^{k} (n-(l+i-1))}{1\cdot\prod_{i=2}^{k} (n-i+1)}. \] In order to determine the overall probability for a reunion after assignment, we need to determine the PMF \(f_{n,m}\) of the group size, i.e. what is the probability that the algorithm dividing \(n\) individuals into groups of size at least \(m\) will assign me to a group of size \(k, k\geq m\). The probability of interest is then: \[p(n,m,l) = \sum_{k=1}^\infty p(k,l,n) f_{n,m}(k) \] Note: Even though we write the summation to be from 1 to \(\infty\), the PMF will only have support on at most two integers.

The calculations in R and verified by 1000 Monte Carlo simulations:

```
# Group membership indicator for the n individuals
g <- rep(seq_len(n %/% m), length.out=n)

# Which previous group sizes to consider. Note:
# can be way beyond m, even if m was selected
p_groupsize <- prop.table(table(table(g)))

p_kln <- sapply(as.numeric(names(p_groupsize)), prob_reunion, l=l, n=n)
c(p_analytical = sum(p_kln * p_groupsize), p_mc = p_reunion_mc)
## p_analytical         p_mc
##    0.2024913    0.2010000
```

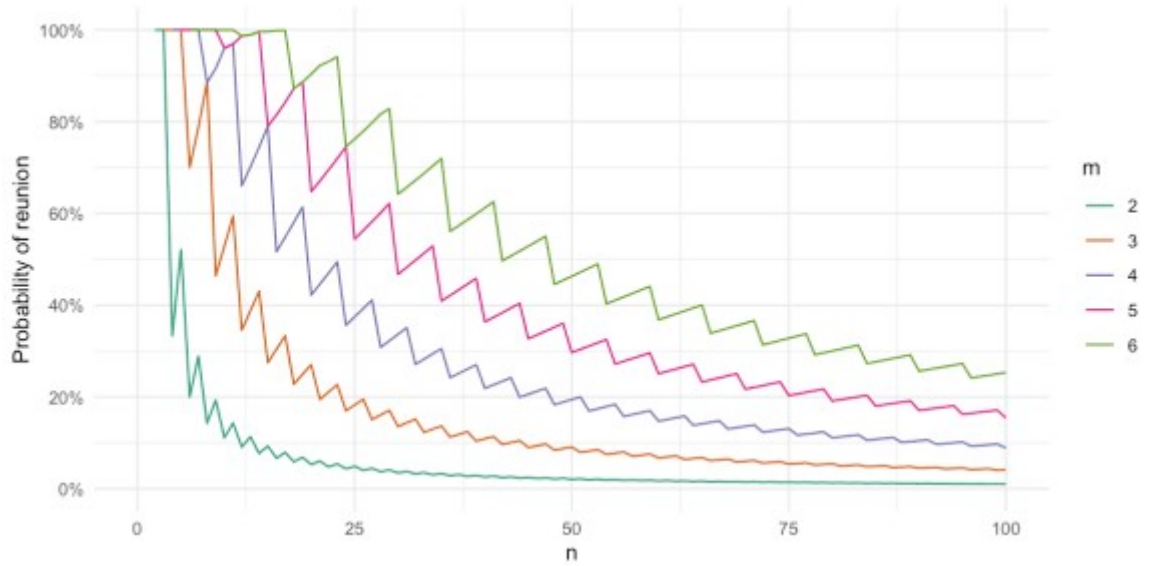
We can illustrate this reunion probability as a function of \(k\) and \(n\).



As a next step we need to marginalise out the previous group size \(l+1\). For simplicity, we will

assume that exactly the same participants participate in each round. Hence, we can use the same group size PMF as before when summing out \(l\): \[p(n,m) = \sum_{l=1}^\infty \sum_{k=1}^\infty p(k,l,n) f_{n,m}(k) f_{n,m}(l+1) \]

The result thus denotes the probability that you in two consecutive assigments of \(n\) individuals into groups of at least \(m\) individuals will be in the same group with someone twice. We will denote this the *reunion probability*.



Given our \(n=47\) and \(m=4\) we note the high probability of 22% for a reunion, which confirms our empirical experience. Thus there seems to be a need to impose some additional constraints on the grouping in order to optimize social diversity. For a translation of \(m\) into the number of breakout rooms used in Zoom, see Appendix A.

Grouping with avoidance

Let `pairs` be a tibble with columns `id1` and `id2` denoting all pairs of individuals who were placed in the same group the last time. We now want to enhance our group allocation algorithm to only assign people into groups, if they were not in the same group the last time. We do this by a simple rejection sampling algorithm, where we draw a configuration with `sample_groups`, check if it has overlaps with the last allocation, and if so, draw again. This method is not very efficient and might take a while. Even worse: it might not finish at all, if no configuration satisfying the constraint exist. An example is, if 9 individuals are to be divided into groups of at least 4 two times without any reunions. The corresponding code of such a `sample_groups_avoid` function is available in the R code from GitHub. This can then be used to generate the desired grouping without reunions:

```
# Sampling in round1 and round2
groups_r1 <- sample_groups(people, m=m)
groups_r2 <- sample_groups_avoid(people, m=m, avoid_pairs =
make_pairs(groups_r1))

# Check if there are any re-unions. Note: There should be none.
inner_join( make_pairs(groups_r1) %>% select(hash),
make_pairs(groups_r2) %>% select(hash), by="hash")
## # A tibble: 0 x 1
## # … with 1 variable: hash
```

In other words: No reunions, just as we wanted.