

Figure 1: Year of publication of the articles in the core papers set. Bar fills and numbers refer to the number of articles within each research aim category. Note that only articles indexed by Web of Science by 3rd November 2020 were included.

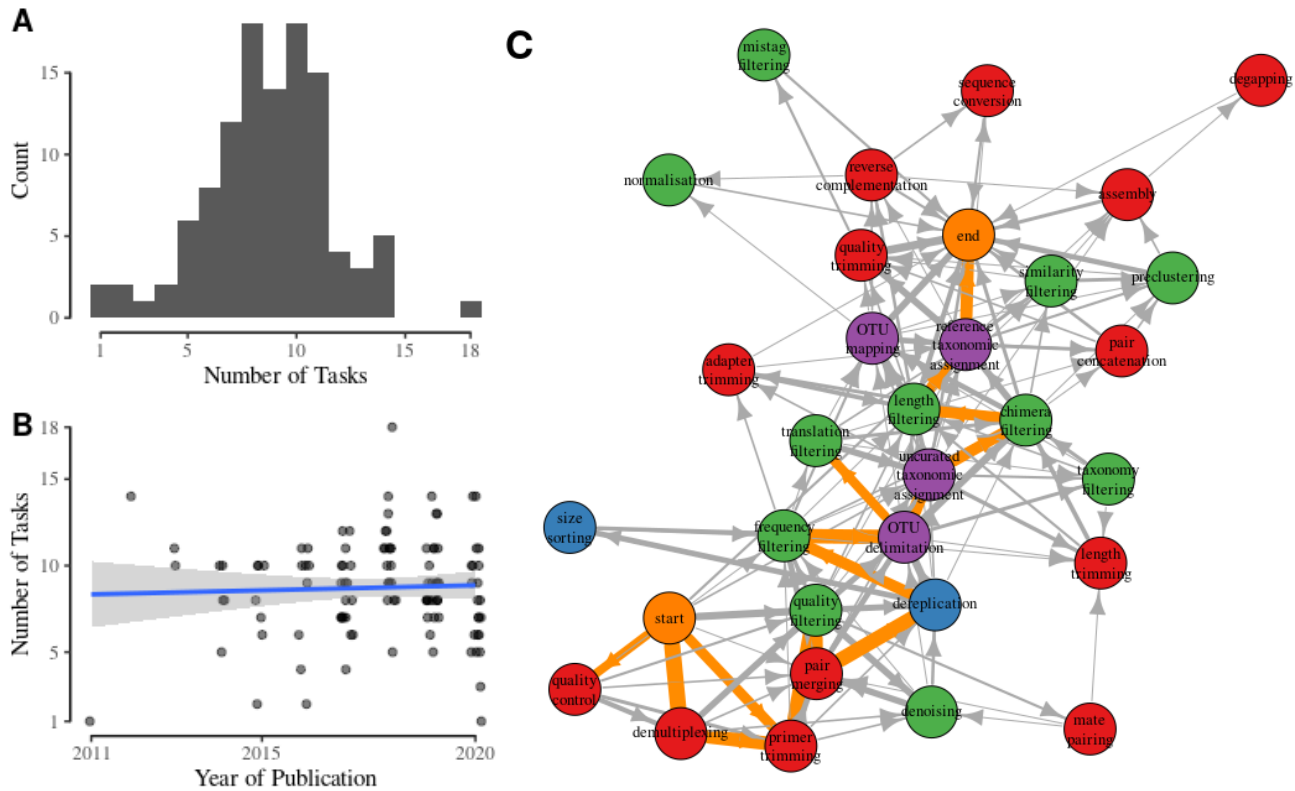


Figure 2: Bioinformatic pipelines implemented by the core papers set. Left: A) Frequency distribution of the number of tasks by study, B) Number of tasks by study against the year of publication, with best fit regression line in blue with shaded 95% confidence intervals around the line. Slight horizontal jitter added to points to better show density. Right: C) Network diagram of tasks and different pipeline routes through these tasks. All pipelines start and end on the respective orange nodes. All other nodes are coloured according to the four main categories of bioinformatic tasks; red for read preparation tasks, blue for sequence processing, green for filtering and purple for data generation tasks. Arrows link tasks performed consecutively, with direction of arrow showing order of tasks. Thickness of arrows shows relative frequency of pairs of consecutive tasks. Arrows coloured orange are the top 10% of consecutive task pairs by relative frequency. Note that while this illustrates a possible complete pipeline from Start to End, this “average” pipeline is not in fact performed by any of the papers assessed by this review.

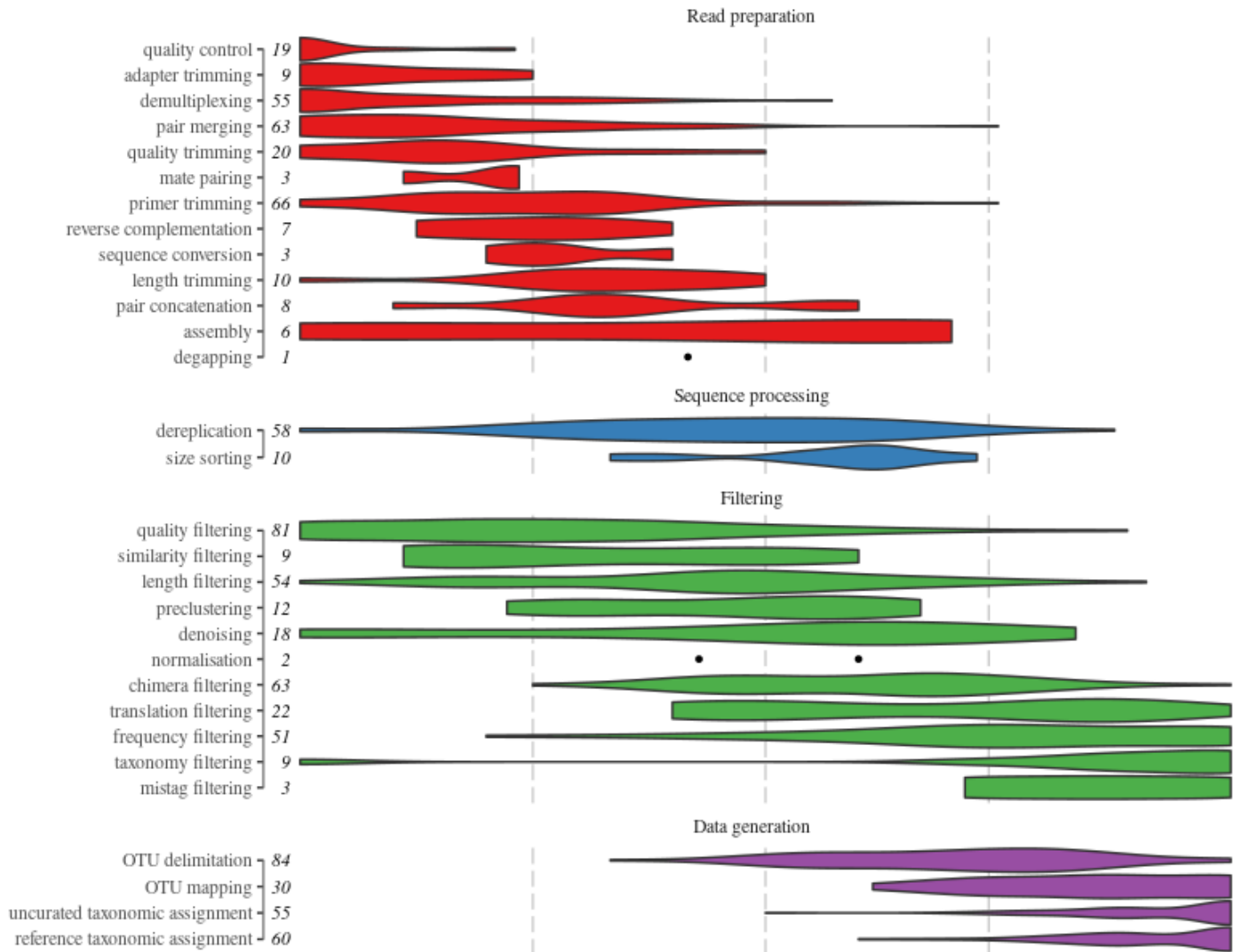


Figure 3: Violin plot of standardised task position within pipelines. Increasing x-axis position denotes later placement of task within pipelines, vertical dashed lines denote 25%, 50% and 75% of the way through the pipeline respectively. Tasks are separated into task groups and ordered within task group by mean standardised pipeline position. Points denote task positions where tasks occurred too infrequently to compute density profile for violin plots. Values report the total number of papers implementing each task.

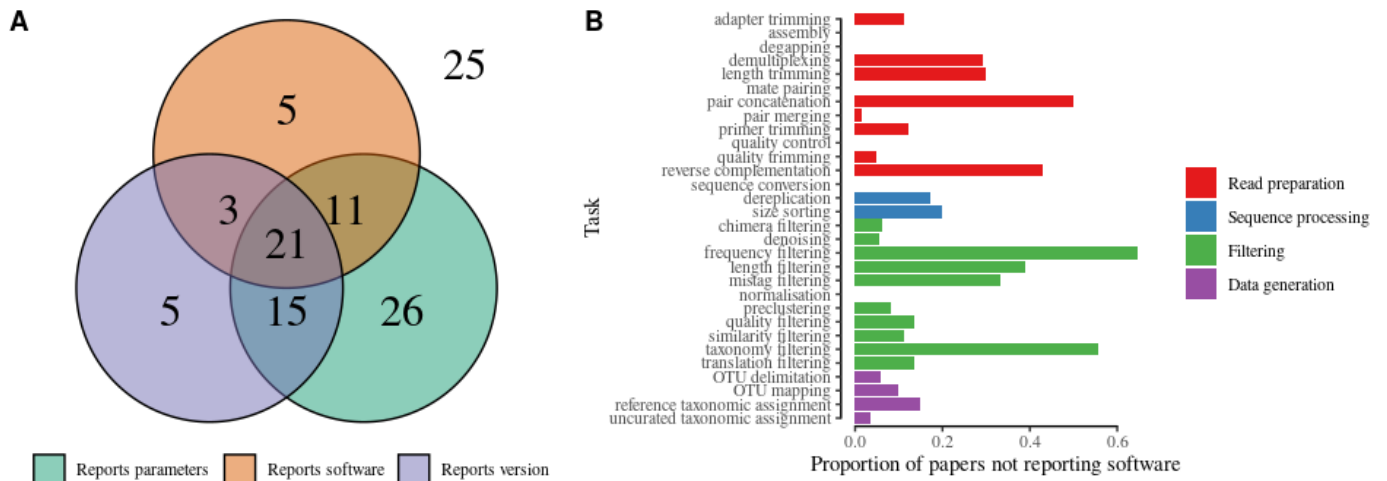


Figure 4: Plots summarising the reporting of 3 key methodological details by papers. A) Venn diagram shows the number of papers fully reporting each detail, i.e. giving the software used for every task reported, and giving the parameters and version for each task where software is given; 86 papers reported at least one of the three details for all steps, 25 further papers failed to fully report all three details in all steps. B) Bar chart details the proportion of papers employing a specific task that failed to report the software used for that task, with longer bars denoting a greater proportion of papers not reporting software for that specific task.

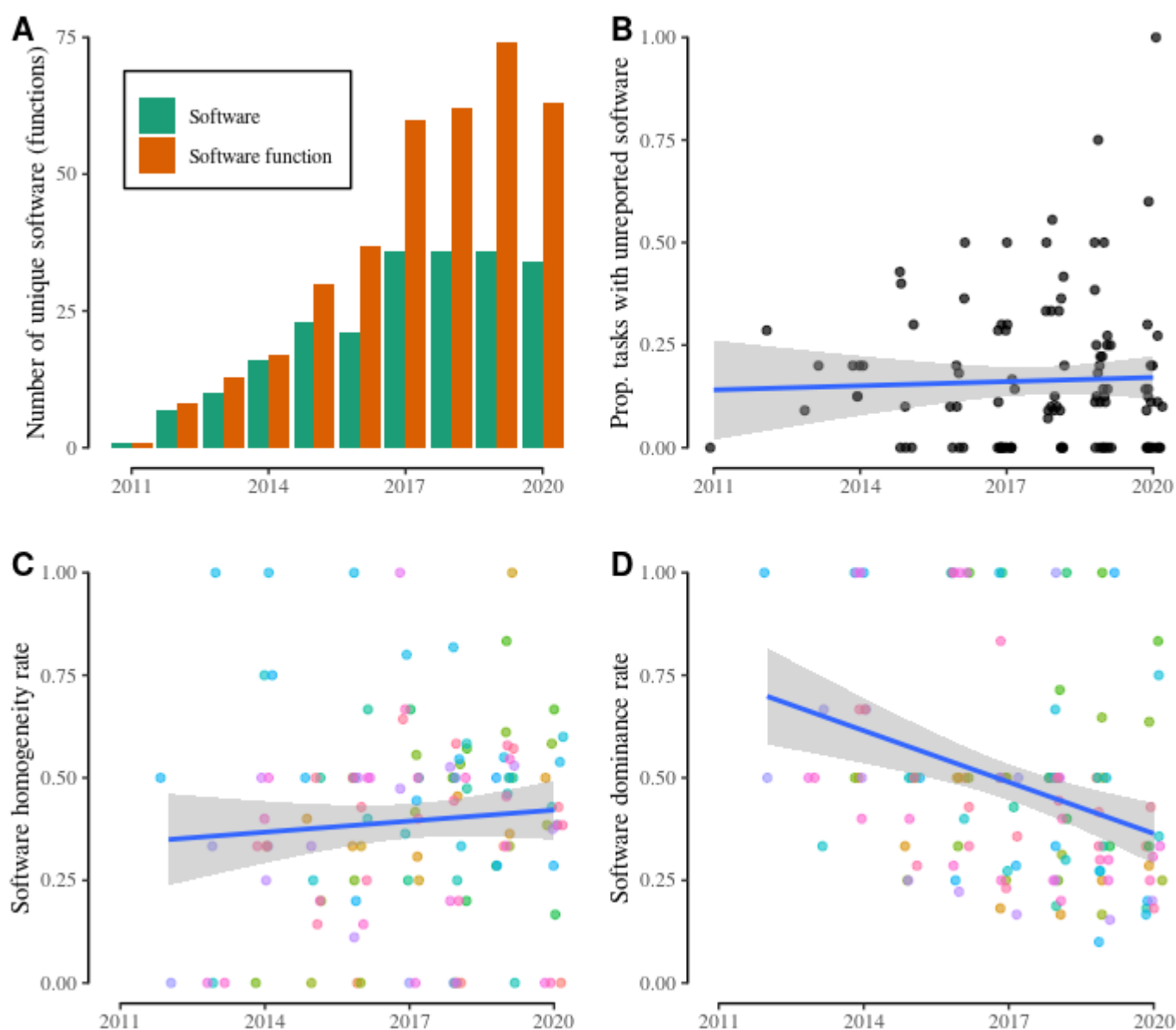


Figure 5: Consistency in software reporting and use over time. *A)* The total number of unique software functions reported across all papers for each year of publication. *B)* For each paper, the proportion of the total number of bioinformatic tasks for which the software used for a task was not reported. *C)* The software homogeneity rate is one minus the number of different software tools used for a given task in a given year, divided by the number of papers employing the task in that year, calculated only when more than one paper reported a task in a given year. A value of 1 means all papers used the same tool for a given task in a given year. *D)* The software dominance rate is the proportion of papers that use the most common software tool for a given task in a given year, calculated only when more than one paper reported a task in a given year. A value of 1 means all papers used the same tool for a given task in a given year. *B-D)* Best fit regression lines are shown in blue with shaded 95% confidence intervals around the line. Horizontal jitter added to points to illustrate density within years; *C & D)* colours denote different tasks, see Figure S1.