**Filtering Reads Made Easy**

# **Abstract**

Recent advances in sequencing and informatics technologies have led to a deluge of sequencings. This has dramatically changed our understanding the genome and our understating of biology. While it is now relatively easy to sequence, extracting only the meaningful reads are still a challenge. Here we introduce a new webserver to facilitates the filtering process. Three of the main features implemented in <Name> are: (1) automate updating of the latest bacteria database; (2) fast comparing the input reads to the database; (3) a simple web page to analyses the results and filter the reads.

**Introduction**

Over the past decades, the price of sequencing rapidly decreased (Check Hayden 2014). This allowed research groups all over the world to sequence different species [ref]. With the increase of sequencing new challenges arises and one of the main is confounding contaminant DNA.

**References**

Check Hayden, Erika. 2014. “Technology: The $1,000 Genome.” *Nature* 507 (7492): 294–95. https://doi.org/10.1038/507294a.