# Package ‘minionSummaryData’

October 10, 2024

**Type** Package

**Version** 1.34.0

**Title** Summarised MinION sequencing data published by Ashton et al. 2015

**Description** Summarised MinION sequencing data for Salmonella Typhi published by Ashton et al. in 2015. Three replicate runs are each provided as Fast5Summary objects.

**biocViews** ExperimentData, SequencingData

**Depends** R (>= 3.2.0)

**License** MIT + file LICENSE

**Suggests** BiocStyle, knitr, rmarkdown

**VignetteBuilder** knitr

**LazyLoad** yes

**NeedsCompilation** no

**Author** Mike Smith [aut, cre]

**Maintainer** Mike Smith <grimbough@gmail.com>

**git_url** https://git.bioconductor.org/packages/minionSummaryData

**git_branch** RELEASE_3_19

**git_last_commit** 875b41d

**git_last_commit_date** 2024-04-30

**Repository** Bioconductor 3.19

**Date/Publication** 2024-10-10

## Contents

minionSummaryData . . . . . 2

**Index** **3**

`minionSummaryData` *Summarised MinION sequencing data published by Ashton et al. [2015]*

## Description

Summarised MinION sequencing data for Salmonella Typhi published by Ashton et al. in 2015. Three replicate runs are each provided as Fast5Summary objects.

## Usage

```
data(s.typhi.rep1)
data(s.typhi.rep2)
data(s.typhi.rep3)
```

## Format

Three `Fast5Summary` objects containing data for three replicates of Salmonella Typhi sequenced on the Oxford Nanopre MinION platform.

## Details

This dataset represents the study published by Aston et al. 2015.

- `Abstract`: Short-read, high-throughput sequencing technology cannot identify the chromosomal position of repetitive insertion sequences that typically flank horizontally acquired genes such as bacterial virulence genes and antibiotic resistance genes. The MinION nanopore sequencer can produce long sequencing reads on a device similar in size to a USB memory stick. Here we apply a MinION sequencer to resolve the structure and chromosomal insertion site of a composite antibiotic resistance island in Salmonella Typhi Haplotype 58. Nanopore sequencing data from a single 18-h run was used to create a scaffold for an assembly generated from short-read Illumina data. Our results demonstrate the potential of the MinION device in clinical laboratories to fully characterize the epidemic spread of bacterial pathogens.

## Value

Loading this data file provides access to three `Fast5Summary` objects called: `s.typhi.rep1`, `s.typhi.rep2` and `s.typhi.rep3`.

## Source

The original data can be downloaded from here: http://www.ebi.ac.uk/ena/data/view/PRJEB7681

## References

Ashton, Philip, Satheesh Nair, Tim Dallman, Salvatore Rubino, Wolfgang Rabsch, Solomon Mwaigwisya, John Wain, and Justin O'Grady. 2014. "MinION Nanopore Sequencing Identifies the Position and Structure of a Bacterial Antibiotic Resistance Island." *Nature Biotechnology* **33**, 296-300 (2015).

# Index

∗ **datasets**
    minionSummaryData, 2

Fast5Summary, *2*

minionSummaryData, 2

s.typhi.rep1 *(*minionSummaryData*)*, 2
s.typhi.rep2 *(*minionSummaryData*)*, 2
s.typhi.rep3 *(*minionSummaryData*)*, 2