

Running wsl commands using system2() function in R

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Using “wsl” command in system2() to run commands in wsl

```
system2("wsl", "cd ~/bioinfor/; ls", stdout = TRUE)
```

```
## [1] "AF086833.gb"      "RNASeqByExample" "chr22.fa"
```

We can retrieve the SARS-coronavirus 2 gene sequences using efetch

```
system2("wsl", "efetch -db=nuccore -format=gb -id=NC_045512", stdout = "../ ../ ../NC_045512.gb")
```

```
system2("wsl", "cat ../ ../ ../NC_045512.gb | head", stdout = TRUE)
```

```
## [1] "LOCUS          NC_045512          29903 bp ss-RNA      linear   VRL 18-JUL-2020"
## [2] "DEFINITION    Severe acute respiratory syndrome coronavirus 2 isolate Wuhan-Hu-1,"
## [3] "              complete genome."
## [4] "ACCESSION     NC_045512"
## [5] "VERSION      NC_045512.2"
## [6] "DBLINK       BioProject: PRJNA485481"
## [7] "KEYWORDS     RefSeq."
## [8] "SOURCE       Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2)"
## [9] "  ORGANISM   Severe acute respiratory syndrome coronavirus 2"
## [10] "            Viruses; Riboviria; Orthornavirae; Pisuviricota; Pisoniviricetes;"
```