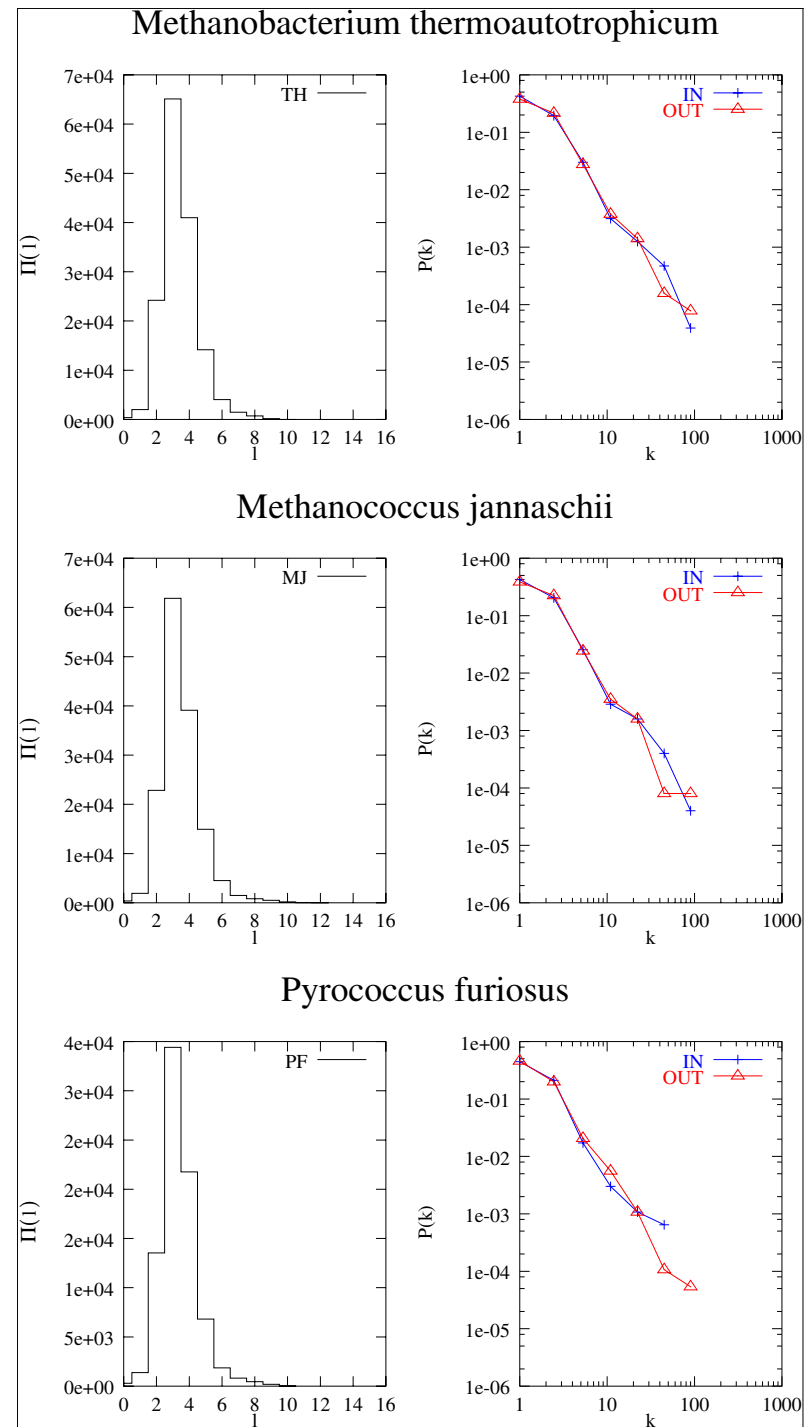
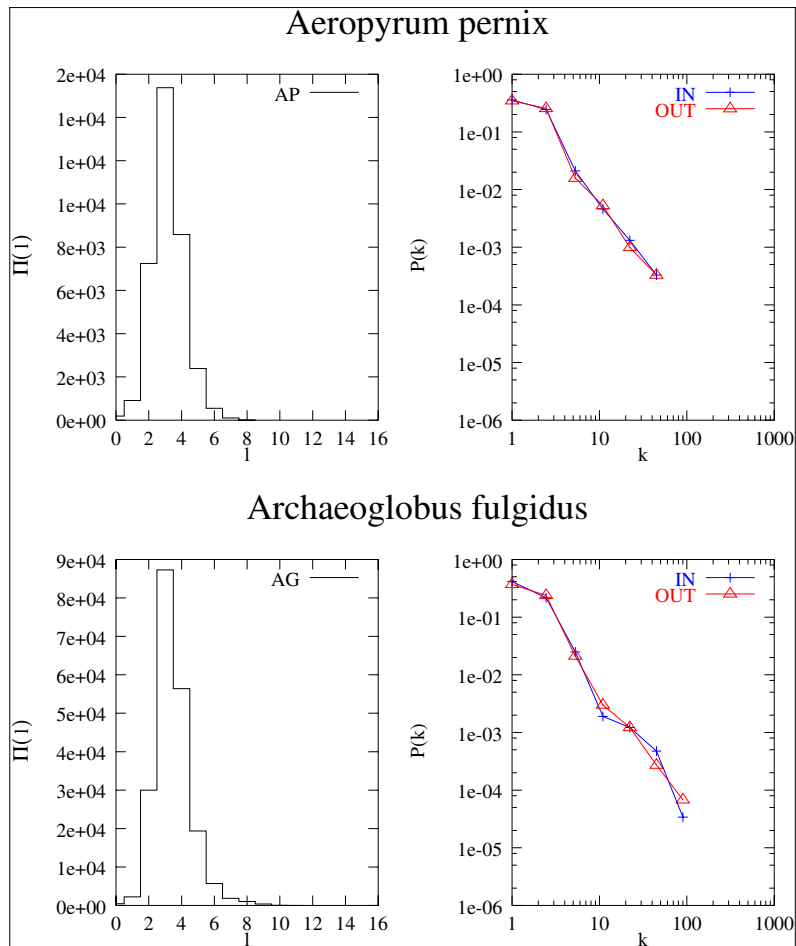
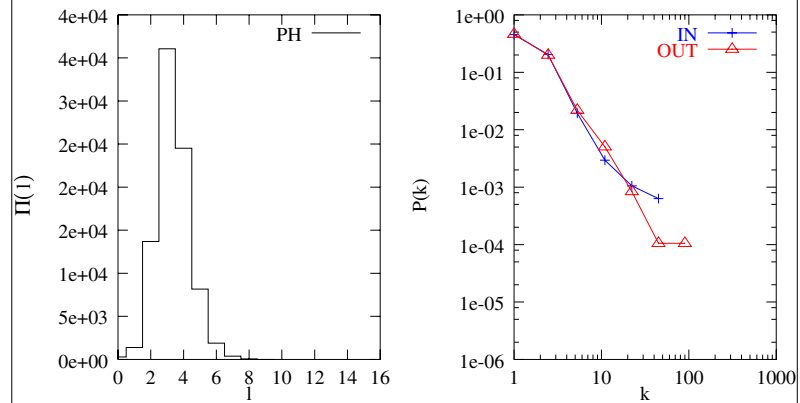


## Supplementary material II

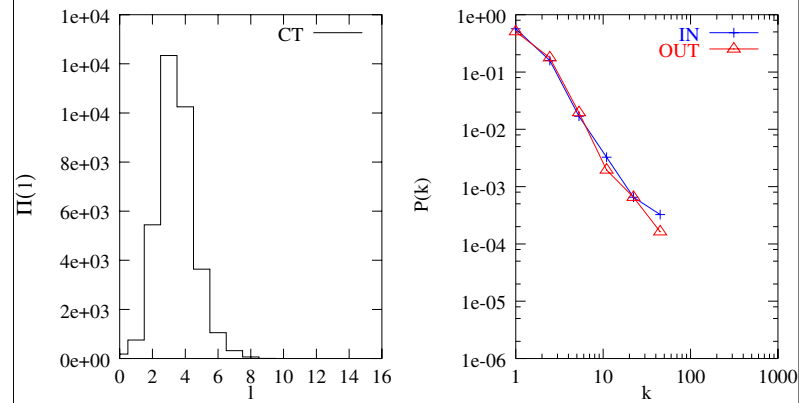
The attached graphs show the path length distribution  $\Pi(l)$  (see Fig. 3a in the manuscript) and the connectivity distribution  $P(k)$  (see Fig. 2 in the manuscript) for each of the 43 investigated organisms.



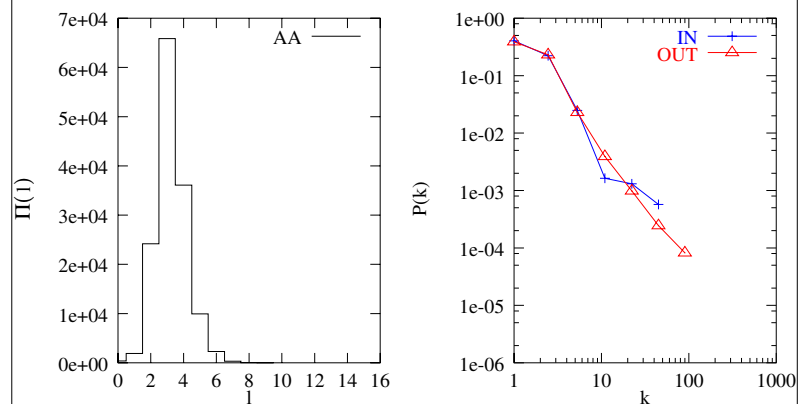
### *Pyrococcus horikoshii*



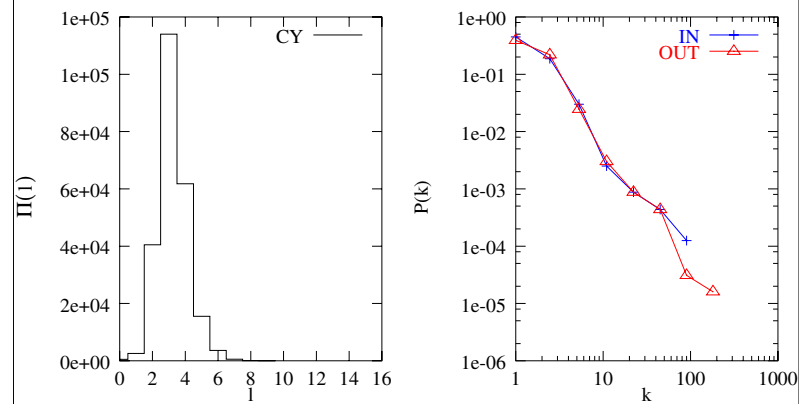
### *Chlamydia trachomatis*



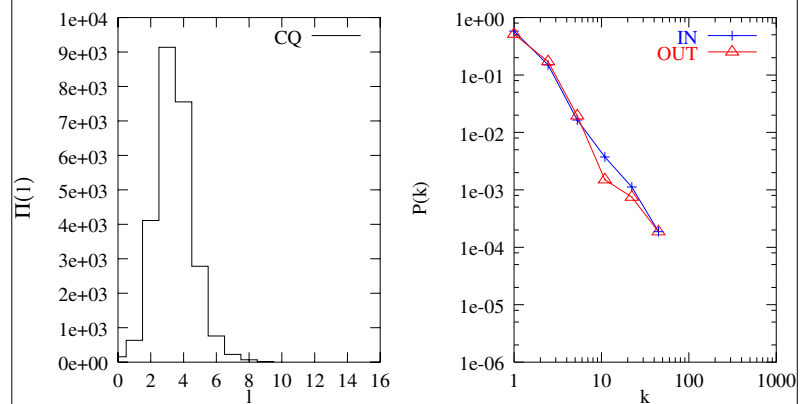
### *Aquifex aeolicus*



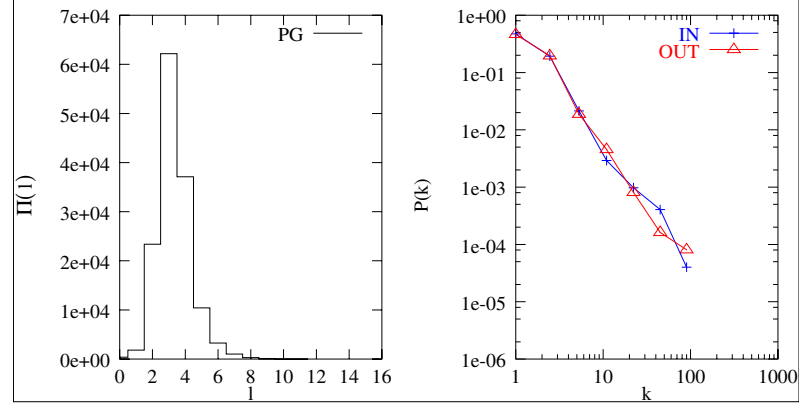
### *Synechocystis* sp.



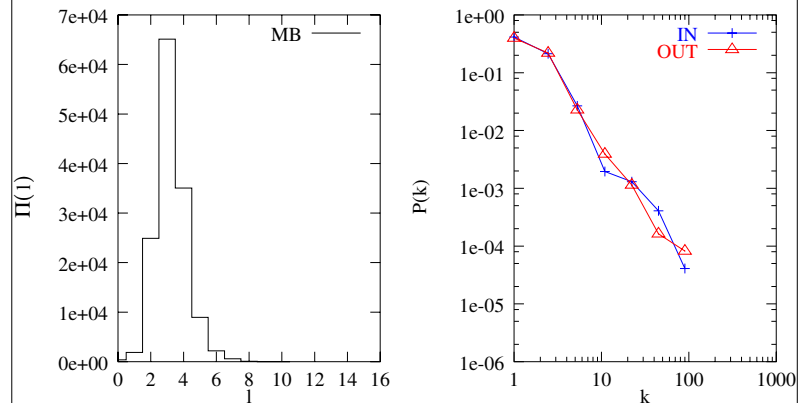
### *Chlamydia pneumoniae*



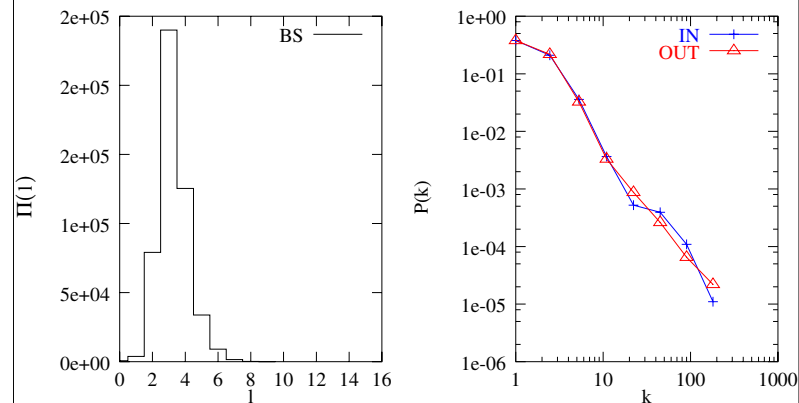
### *Porphyromonas gingivalis*



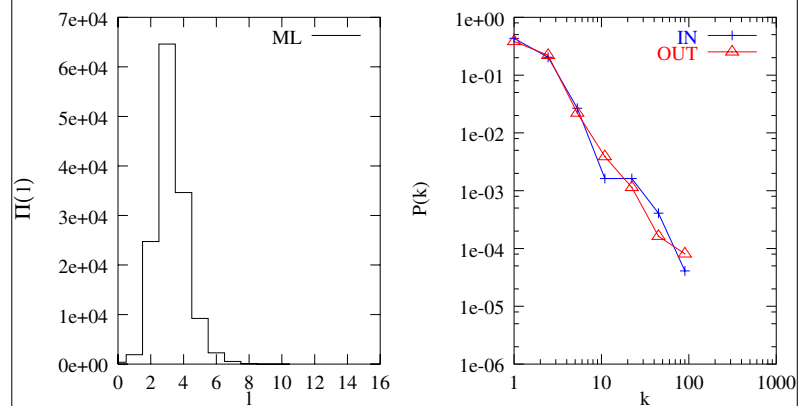
*Mycobacterium bovis*



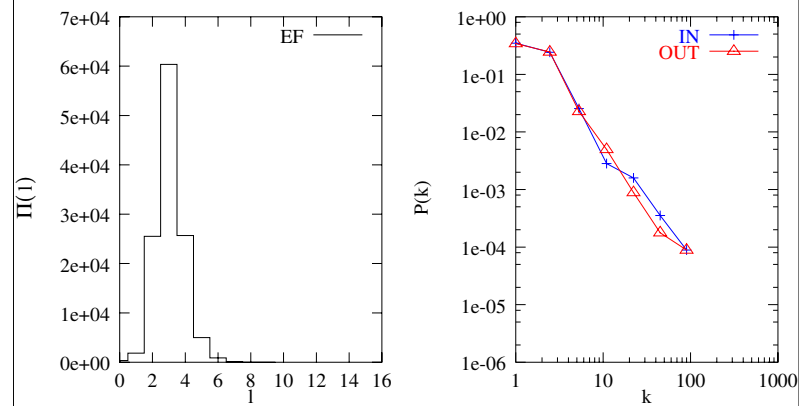
*Bacillus subtilis*



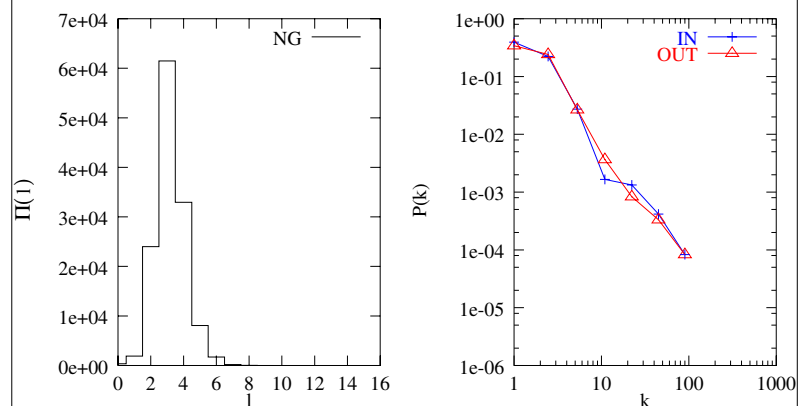
*Mycobacterium leprae*



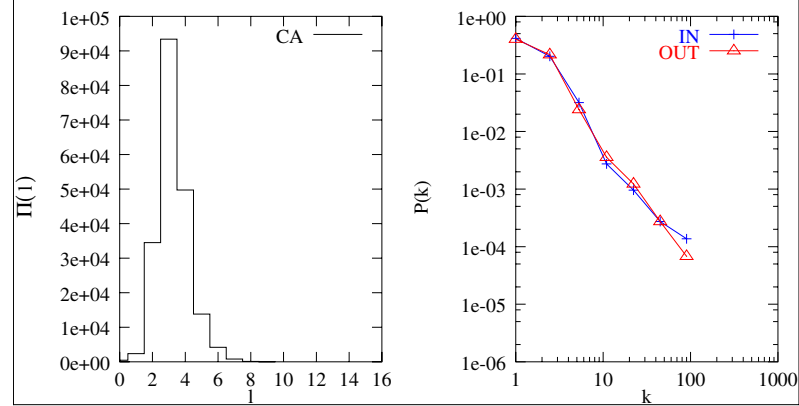
*Enterococcus faecalis*



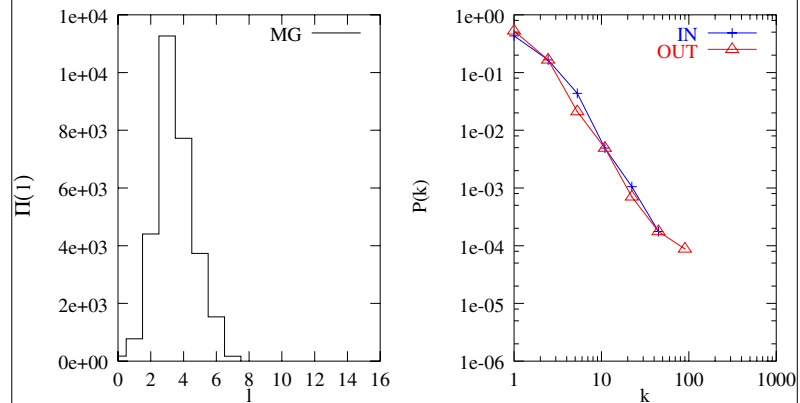
*Neisseria gonorrhoeae*



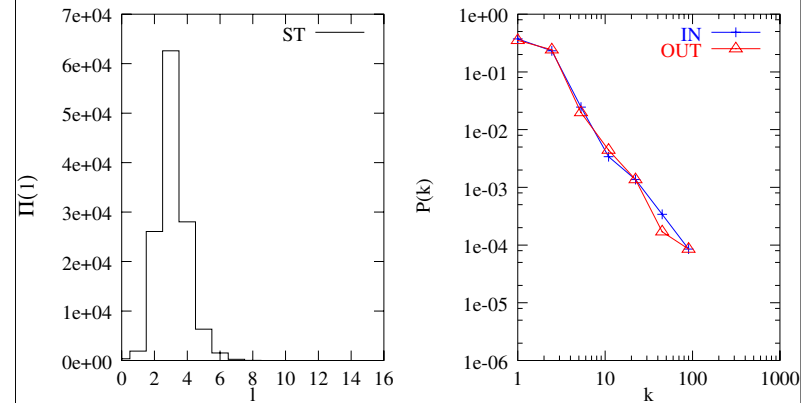
*Clostridium acetobutylicum*



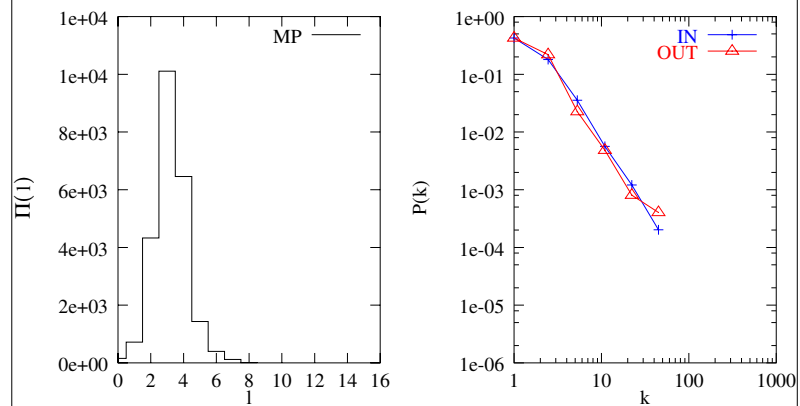
### Mycoplasma genitalium



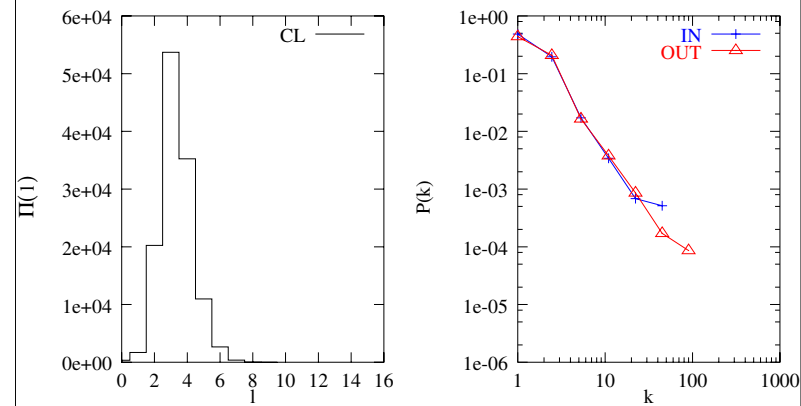
### Streptococcus pyogenes



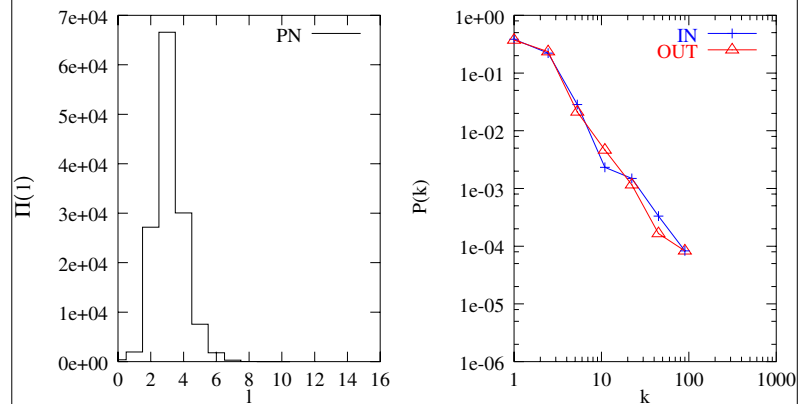
### Mycoplasma pneumoniae



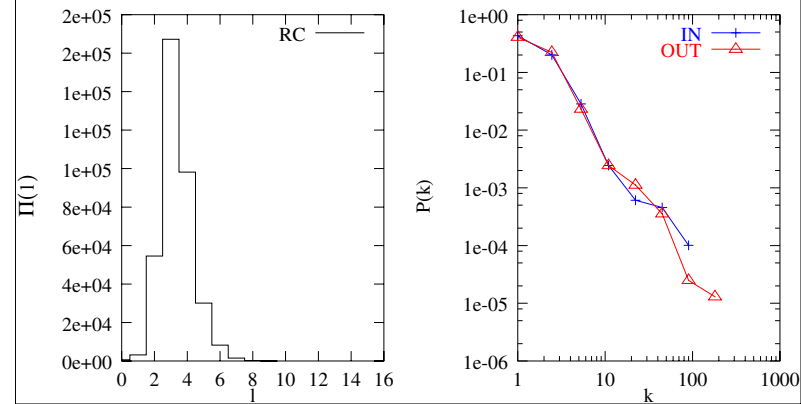
### Chlorobium tepidum



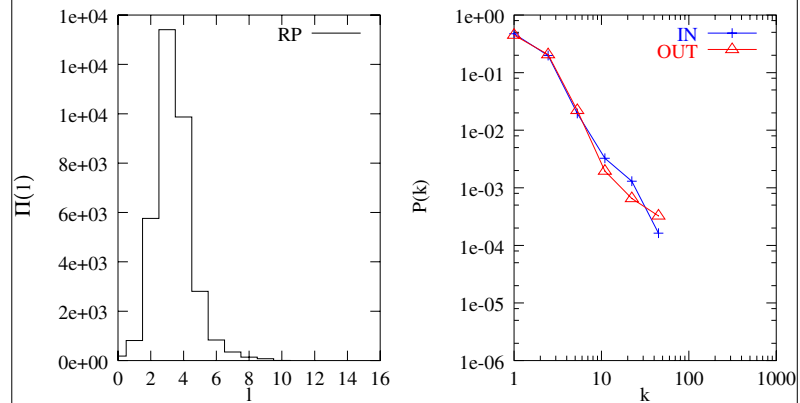
### Streptococcus pneumoniae



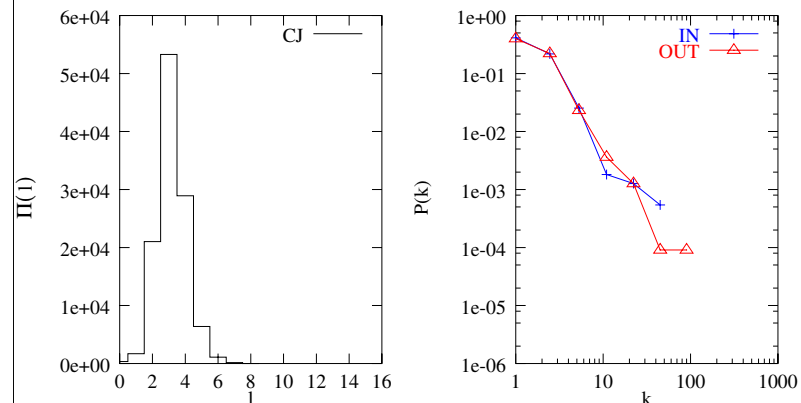
### Rhodobacter capsulatus



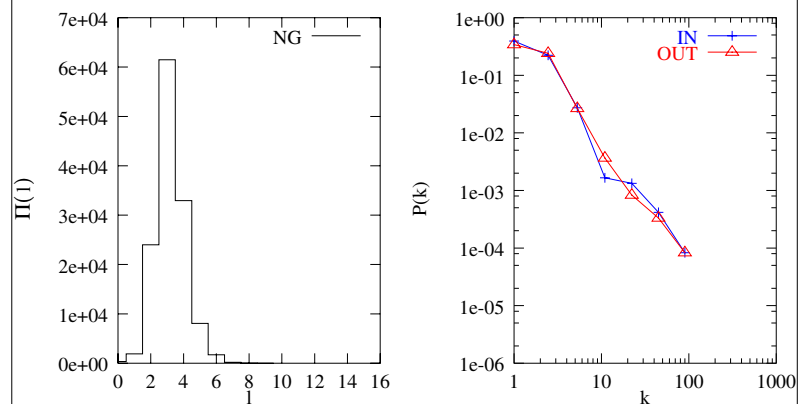
### *Rickettsia prowazekii*



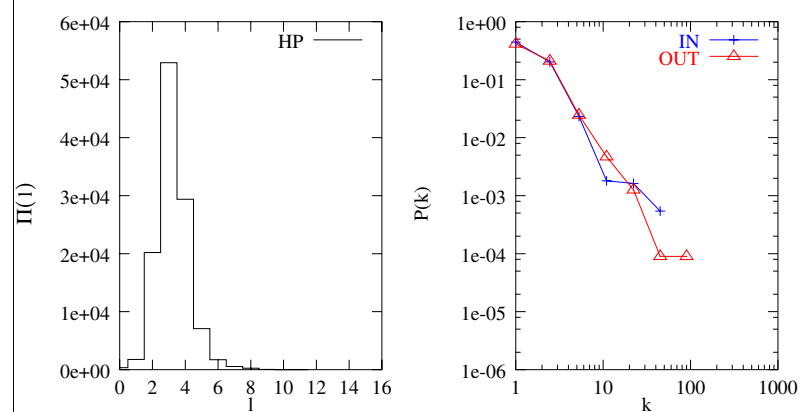
### *Campylobacter jejuni*



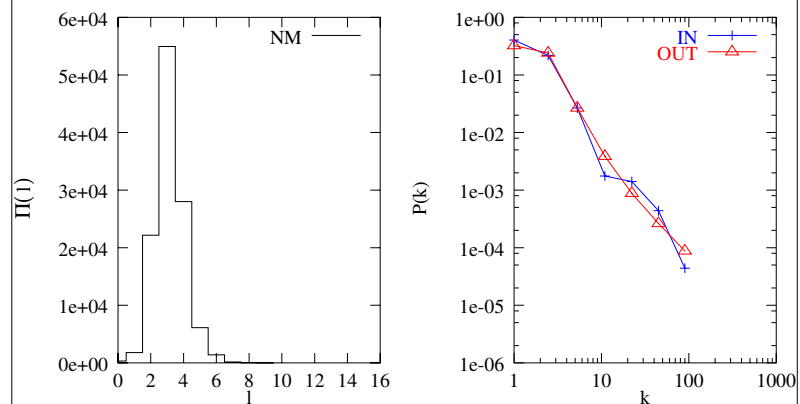
### *Neisseria gonorrhoeae*



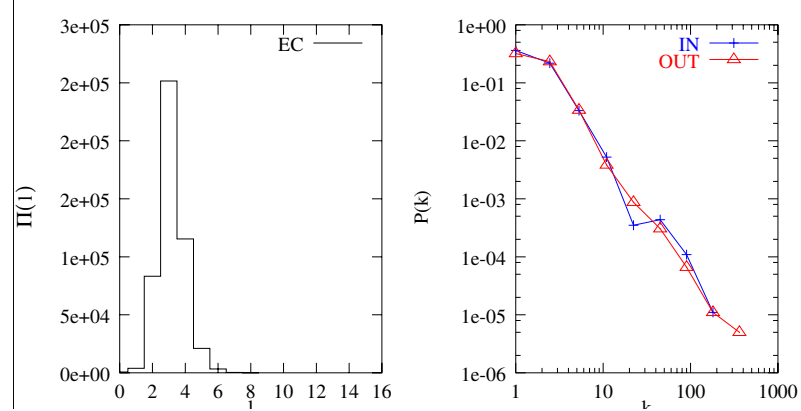
### *Helicobacter pylori*



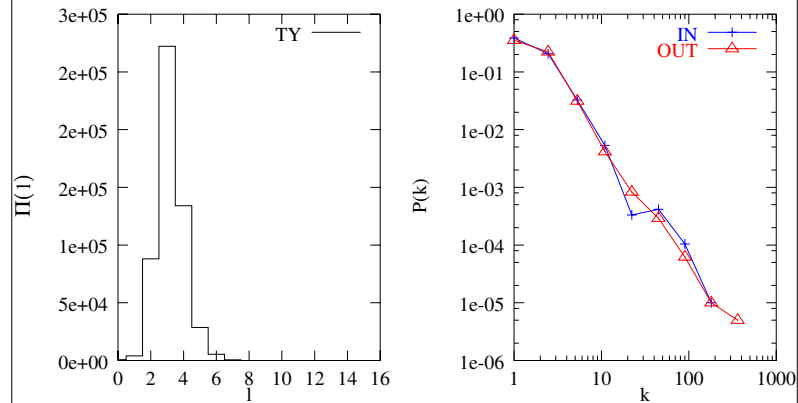
### *Neisseria meningitidis*



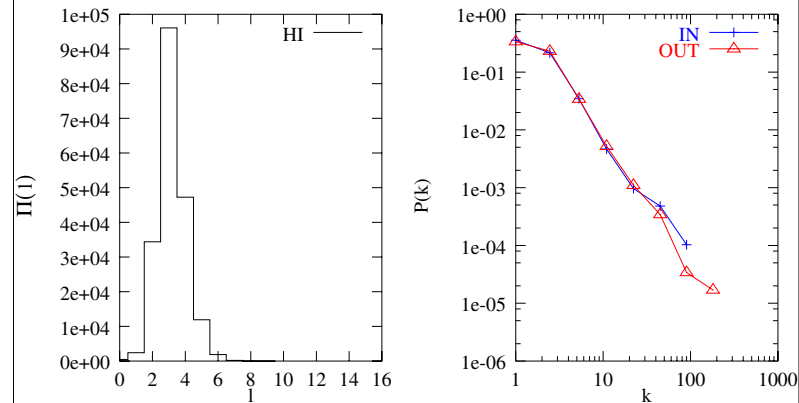
### *Escherichia coli*



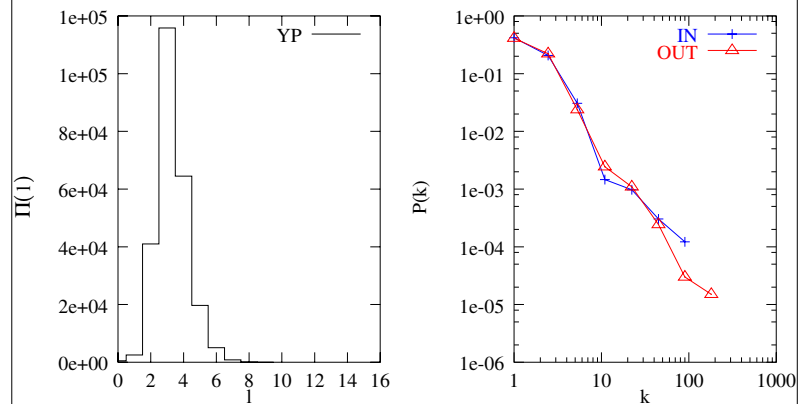
### Salmonella typhi



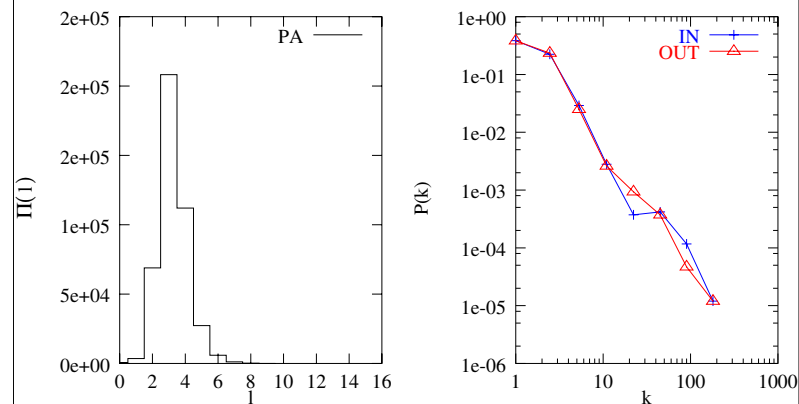
### Haemophilus influenzae



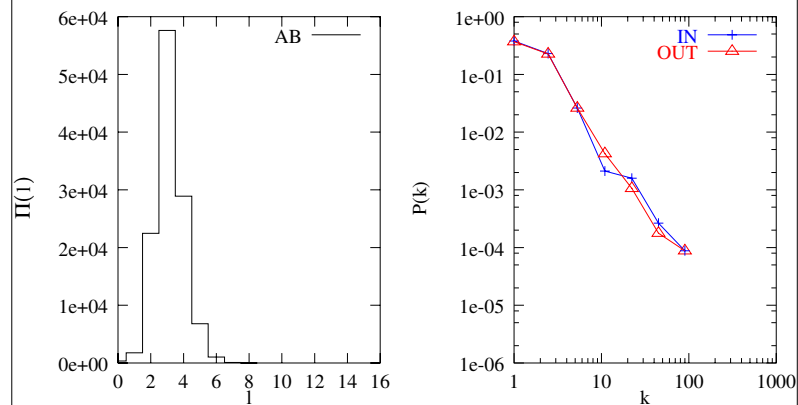
### Yersinia pestis



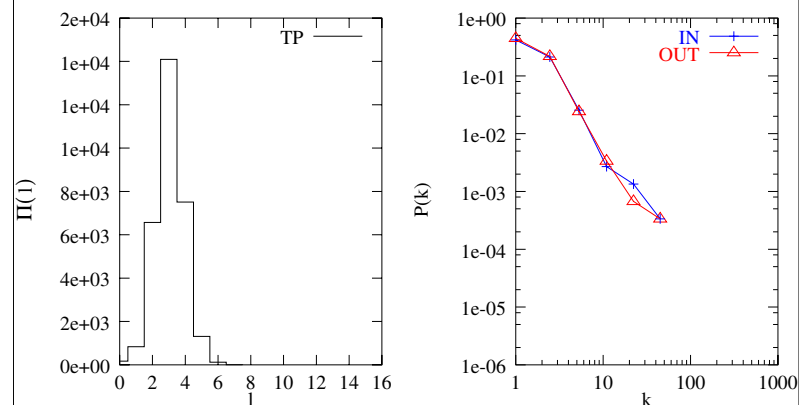
### Pseudomonas aeruginosa



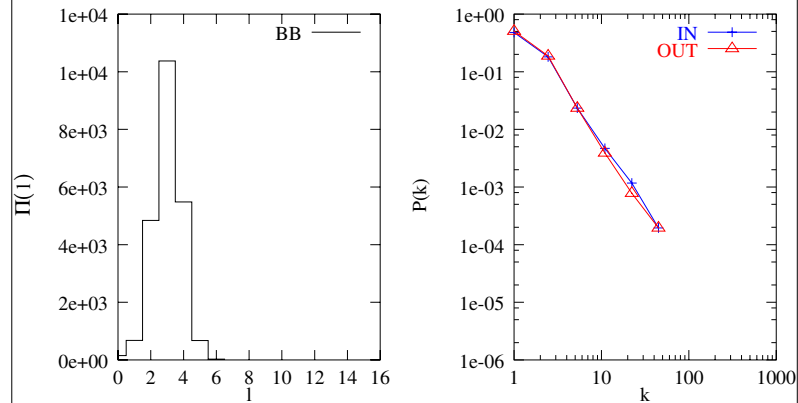
### Actinobacillus actinomycetemcomitans



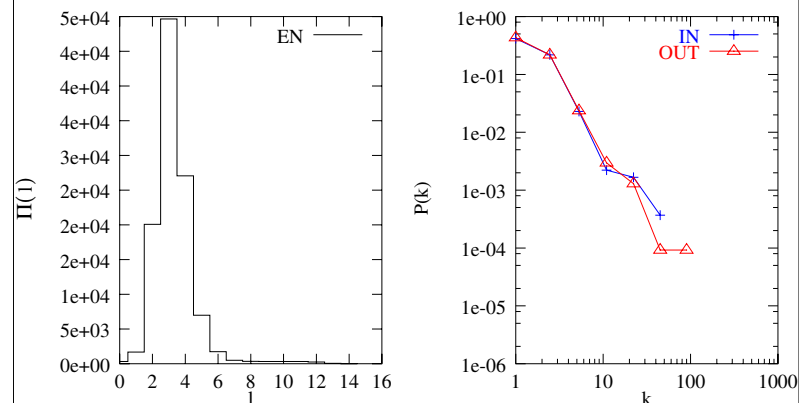
### Treponema pallidum



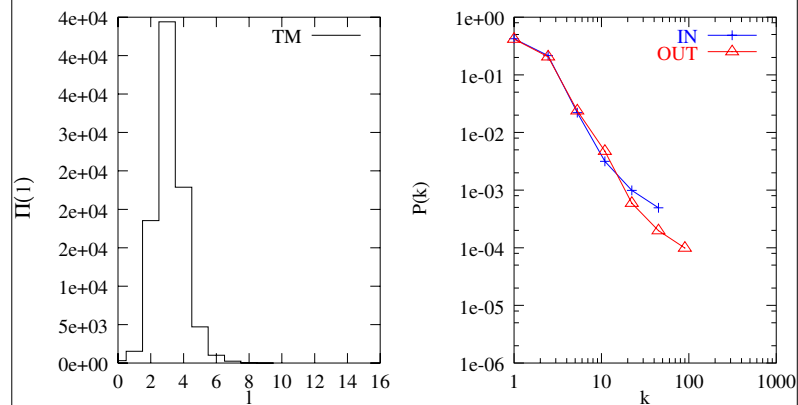
### *Borrelia burgdorferi*



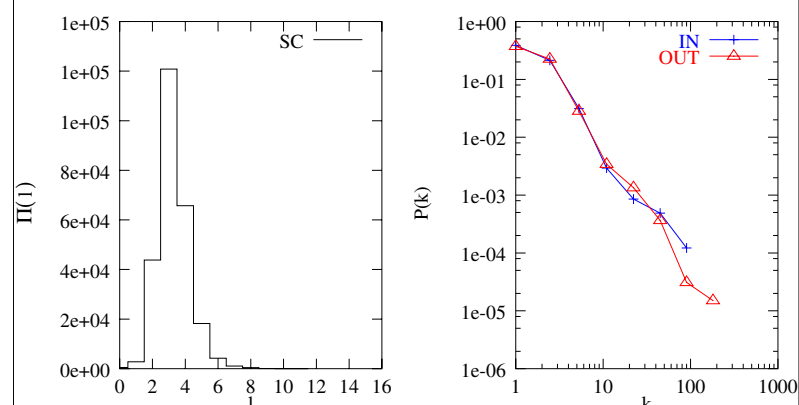
### *Emericella nidulans*



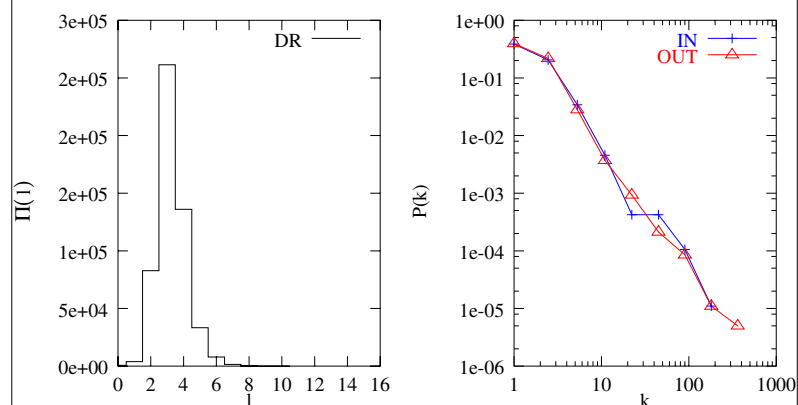
### *Thermotoga maritima*



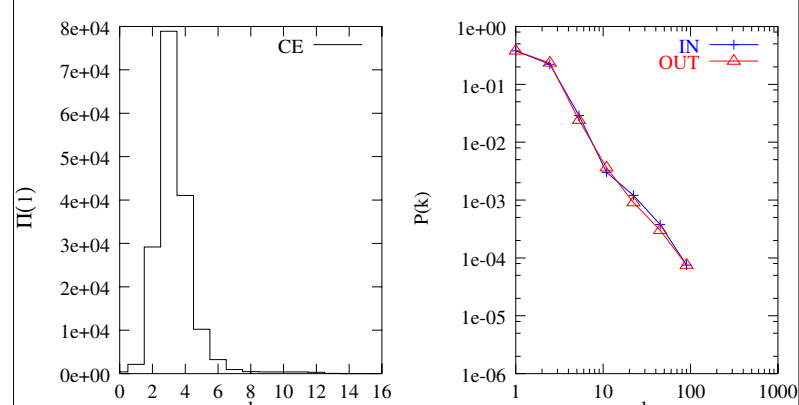
### *Saccharomyces cerevisiae*



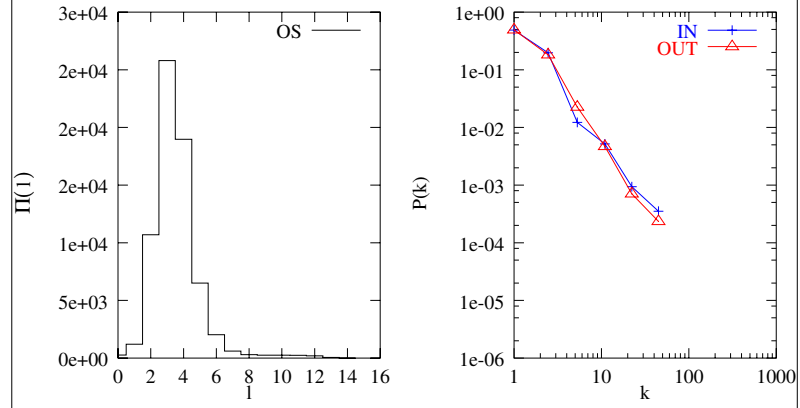
### *Deinococcus radiodurans*



### *Caenorhabditis elegans*



### Oryza sativa



### Arabidopsis thaliana

