ERRATUM

Antibiotics Methods and Protocols

Peter Sass

Peter Sass (ed.), *Antibiotics: Methods and Protocols*, Methods in Molecular Biology, vol. 1520, DOI 10.1007/978-1-4939-6634-9, © Springer Science+Business Media New York 2017

DOI 10.1007/978-1-4939-6634-9_21

In **Chapter 20** titled “Epidemiological Surveillance and Typing Methods to Track Antibiotic Resistant Strains Using High Throughput Sequencing”, table 3 is incorrect, it is corrected as follows.

The online version of the original chapter can be found at
http://dx.doi.org/10.1007/978-1-4939-6634-9_20

Peter Sass (ed.), *Antibiotics: Methods and Protocols*, Methods in Molecular Biology, vol. 1520, DOI 10.1007/978-1-4939-6634-9_21, © Springer Science+Business Media New York 2017

Table 3
Software installation procedures (see Note 1)

Name	Commands required for installation
SPAdes	<code>cd ~/methods_protocols/programs; wget http://spades.bioinf.spbau.ru/release3.9.0/SPAdes-3.9.0-Linux.tar.gz; tar xf SPAdes-3.9.0-Linux.tar.gz; cp -r ./SPAdes-3.9.0-Linux/bin/ ./; cp -r ./SPAdes-3.9.0-Linux/share/ ./; rm -rIf SPAdes-3.9.0-Linux.tar.gz SPAdes-3.9.0-Linux/</code>
BLAST+	<code>cd ~/methods_protocols/programs; wget ftp://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/2.4.0/ncbi-blast-2.4.0+-x64-linux.tar.gz; tar xf ncbi-blast-2.4.0+-x64-linux.tar.gz; cp ./ncbi-blast-2.4.0+/bin/* ./bin/; rm -rIf ncbi-blast-2.4.0+-x64-linux.tar.gz ncbi-blast-2.4.0+/</code>
MLST 2	<code>sudo apt-get install git; cd ~/methods_protocols/programs; git clone https://github.com/tseemann/mlst.git; cp ./mlst/bin/* ./bin/; cp -r ./mlst/db/ ./; cp -r ./mlst/perl5/ ./; rm -rIf mlst; sudo cpan Moo List::MoreUtils</code>
Samtools/Bcftools	<code>sudo apt-get install zlib1g-dev libncurses5-dev; cd ~/methods_protocols/programs; wget https://github.com/samtools/samtools/releases/download/1.2/samtools-1.2.tar.bz2; tar xf samtools-1.2.tar.bz2; cd samtools-1.2; make; make prefix=~/methods_protocols/programs install; cd ../; wget https://github.com/samtools/bcftools/releases/download/1.2/bcftools-1.2.tar.bz2; tar xf bcftools-1.2.tar.bz2; cd bcftools-1.2; make; make prefix=~/methods_protocols/programs install; cd ../; rm -rIf samtools-1.2.tar.bz2 samtools-1.2/ bcftools-1.2.tar.bz2 bcftools-1.2/</code>
Bowtie2	<code>cd ~/methods_protocols/programs; wget http://downloads.sourceforge.net/project/bowtiebio/bowtie2/2.2.9/bowtie2-2.2.9-linux-x86_64.zip; unzip bowtie2-2.2.9-linux-x86_64.zip; cp ./bowtie2-2.2.9/bowtie* ./bin/; rm -rIf bowtie2-2.2.9-linux-x86_64.zip bowtie2-2.2.9/</code>
Bedtools	<code>sudo apt-get install g++; cd ~/methods_protocols/programs; wget https://github.com/arq5x/bedtools2/releases/download/v2.26.0/bedtools-2.26.0.tar.gz; tar xf bedtools-2.26.0.tar.gz; cd bedtools2/; make; cd ../; cp ./bedtools2/bin/* ./bin/; rm -rIf bedtools-2.26.0.tar.gz bedtools2/</code>
GATK	<code># Download GATK software from https://software.broadinstitute.org/gatk/download/ to ~/methods_protocols/programs folder. The following commands are for GATK version 3.6 (they must be adapted to the downloaded version). sudo apt-get install openjdk-8-jdk; cd ~/methods_protocols/programs; tar xf GenomeAnalysisTK-3.6.tar.bz2; chmod +x GenomeAnalysisTK.jar; mv GenomeAnalysisTK.jar ./bin/; rm GenomeAnalysisTK-3.6.tar.bz2</code>
Picard	<code>cd ~/methods_protocols/programs; wget https://github.com/broadinstitute/picard/releases/download/2.6.0/picard.jar; chmod +x picard.jar; mv picard.jar ./bin/</code>

Table 3 (Cont'd)
Software installation procedures (see Note 1)

Aspera connect	cd ~/methods_protocols/programs; wget http://download.asperasoft.com/download/sw/connect/3.6.2/aspera-connect-3.6.2.117442-linux-64.tar.gz; tar xf aspera-connect-3.6.2.117442-linux-64.tar.gz; sh aspera-connect-3.6.2.117442-linux-64.sh; rm aspera-connect-3.6.2.117442-linux-64.sh aspera-connect-3.6.2.117442-linux-64.tar.gz; cd ~/; cp -Rn .aspera/connect/* ~/methods_protocols/programs/; rm -rIf .aspera/
ReMatCh	sudo apt-get install python-dev python-pip; pip install numpy; cd ~/methods_protocols/programs; git clone -b antibiotics_book_chapter https://github.com/miguelpmachado/ReMatCh.git; chmod +x ./ReMatCh/rematch.py; cd bin; ln -s ../ReMatCh/rematch.py ./
PHYLOViZ	cd ~/methods_protocols/programs; wget https://bitbucket.org/phyloviz/phyloviz-main/downloads/phyloviz-1.1a.zip; unzip phyloviz-1.1a.zip; rm phyloviz-1.1a.zip
R	sudo apt-get install r-base

Changes have also been made to paragraph 3.2.1 *Antibiotic Resistance Databases* in the same chapter

```
$ cd ~/methods_protocols/antibiotic_resistance/
$ wget https://card.mcmaster.ca/download/0/broadstreet-v1.1.0.tar.gz
$ tar xf broadstreet-v1.1.0.tar.gz
$ mv "nucleotide_fasta[protein homolog model].fasta"
.nucleotide_fasta_protein_homolog_model.fasta
$ rm *
$ mv .nucleotide_fasta_protein_homolog_model.fasta
nucleotide_fasta_protein_homolog_model.fasta
$ sed --in-place "s# #_#g" nucleotide_fasta_protein_
homolog_model.fasta
```

In Chapter 4 titled “Structure Elucidation of Antibiotics by NMR Spectroscopy”, the running head “Nmr” is replaced by “NMR” and the configuration of the amino acids (Note 53) is updated as “L”. Other author corrections are also updated.

The online version of the original chapter can be found at
http://dx.doi.org/10.1007/978-1-4939-6634-9_4