Capacity-Building Request for Colleagues interested in Benchmarking WGS-AMR Workflows and Results.

Dear Colleagues,

- The use of different workflows to generate antimicrobial resistance (AMR) gene lists and AMR phenotype from identical bacterial whole genome sequencing (WGS) data may yield different results.

- Therefore, JPIAMR networks B2B2B AMR Dx and Seq4AMR would like to start the process of capacity building in this area for collaboration and joint grant applications, thereby requiring the input and enthusiasm from stakeholders interested in this field of research.

- As a starting point, and In order to illustrate the current problem, a free to use Galaxy-based web pilot application *BenchAMRking**** has been developed, which allows the results of WGS to be compared between 4 different workflows (including the ISO certified workflow abritAMR). Additionally, *BenchAMRking* is open to all interested parties to try out, develop and improve.
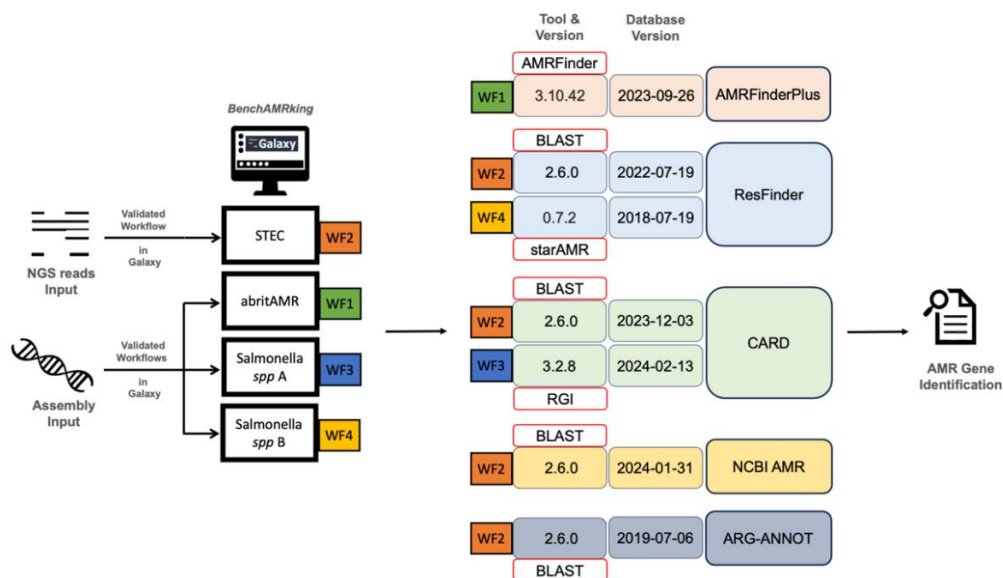

Figure 1. Overview of *BenchAMRking* and its 4 workflows

*https://erasmusmc-bioinformatics.github.io/benchAMRking/

- Importantly, the pilot *BenchAMRking* application is only the start of the process towards international standardisation and capacity building, networking and collaboration in this field, having been built by a team of dedicated programmers, bioinformaticians and AMR experts at little cost.

- Therefore, this one-pager has been developed to request comments and potential contributions from <u>dedicated, enthusiastic and contributing stakeholders</u> to help improve international benchmarking standards related to this pilot application, thereby helping: 1) promote the implementation of international benchmarking standards, 2) participate in joint comparative workflow programming activities and 3) applications for international grant funding to take the next steps forward.

Thank you for your interest! Contact Details: for questions and comments please email:

j.hays@erasmusmc.nl (on behalf of all B2B2B AMR DX and Seq4AMR participants).