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Professional, easy to use and robust bioinformatic tools

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To make use of Big Data software tools and computer analytics are essential. However, academic software has a bad reputation: hard to read, even harder to understand and impossible to maintain. In addition, it often does not scale up, so when faced with data sets that are increasing rapidly in size and complexity. End-users are often daunted with software that holds promises but creates complications and frustrations or incorrect analysis instead. With proper software development methodology academic software can be replaced by so-called "decent-ware". The difficulties we face with academic software development are shared within Wageningen UR and throughout the academic world. Our aim was filter and select bioinformatic tools that can perform analysis needed by different research groups and to make them easily assessable and to receive feedback of users. We validated results for bioinformatics tools using comparative assays. We enhanced their ease of use and developed robust analysis pipelines shared with mid- and end-users. We started with widely used application which does not yet hold up to decent-ware standards. Several application for bioinformatics and comparative genome analysis will be shown. We also connected to the academic software development community in The Netherlands to a) not reinvent the wheel and b) share knowledge, expertise and tools.