Genome analysis is no longer a field reserved for specialists and experimental laboratories are doing groundbreaking research using genome sequencing and analysis. In this new era, it is essential that data, analysis and results are shared between scientists. But this can be a challenge, even more so with no computational specialist. Here we present a setup for analysis and publication of genome data of 70 species of Aspergillus fungi. The platform is based on R, Python and uses the RShiny framework to create interactive web-applications. It allows all participants to create interactive analysis which can be shared with the team and in connection with publications. We present analysis for investigation of genetic diversity, secondary and primary metabolism and general data overview. The platform, the Aspergillus Mine, is a collection of analysis tools based on data from collaboration with the Joint Genome Institute. The Aspergillus Mine is not intended as a genomic data sharing service but instead focuses on creating an environment where the results of bioinformatic analysis is made available for inspection. The data and code is public upon request and figures can be obtained directly from the web-app. This resource will be of great benefit to the Aspergillus community which is in a rapid development in regards to genome sequencing and analysis. At the moment, the service includes analysis of more than 70 genomes, and is expected to double in the next 6 months, with the final goal of the project is the analysis of 300 Aspergillus species.

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