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Deep sequencing targeted for strain identification of trypanosomatids

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Trypanosomatidae is a group of kinetoplastid excavates distinguished by having only a single flagellum. All members are exclusively parasitic, found primarily in insects. A few genera have life-cycles involving a secondary host, which may be a vertebrate, invertebrate or plant. These include several species that cause major diseases in humans. The three major human diseases caused by trypanosomatids are: African trypanosomiasis (sleeping sickness, caused by *Trypanosoma brucei* and transmitted by tsetse flies), South American trypanosomiasis (Chagas disease, caused by *Trypanosoma cruzi* and transmitted by triatomine bugs), and leishmaniasis (a set of trypanosomal diseases caused by various species of *Leishmania* transmitted by sandflies).

Through a next generation sequencing approach, various variations in several genes were detected as well as important biological features in clinical samples of patients affected by the *Leishmania* disease. The custom reads form Ilumina sequencing platform are aligned to reference genomes of different *Leishmania* species taken from TriTryp dabatase to be used for bioinformatics analysis.

The applications of this tool is essential for the potential identification of somatic mutations, important polymorphisms of the disease as well as the identification of structural variants of protein amongst other applications. Bioinformatic analysis are carried out through Galaxy Server Bioinformatics Platform and related bioinformatics open source tools. Due to the sheer size of the genetic data collated, cloud infrastructure will be set up.

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