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<b>Title</b>	MGkit: A Metagenomic Framework For The Study Of Microbial Communities
<b>Author</b>	<i>Francesco Rubino</i> , Chris Creevey
<b>Affiliation</b>	<a href="http://www.aber.ac.uk/en/ibers/">http://www.aber.ac.uk/en/ibers/</a>
<b>Contact</b>	frr11@aber.ac.uk
<b>URL</b>	<a href="https://bitbucket.org/setsuna80/mgkit">https://bitbucket.org/setsuna80/mgkit</a>
<b>License</b>	GPL-2.0

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Metagenomics is a relatively new field, in which environmental samples are studied, offering insights into a microbial community as a whole. The wide range of sample types and possible experiments, as well as the scale of the sequencing data, make the creation of new pipelines or the adaptation of a pre-existing one a complex and time consuming task.

Moreover, while metagenomics has been used extensively to study microbial communities from a taxonomic and functional perspective, little has been done to address how the species in a microbiome are adapted to and maintain specific roles in dynamic environments like the rumen. Identifying and assessing the level of this biological adaptation for function is an important aspect that has not been addressed by any currently available metagenomic pipelines.

To address these problems, we have developed a framework that can be used to create and adapt metagenomic analysis workflows, making it faster to implement or prototype different analysis approaches.

Example workflows are included that can scale in size and can be customised with ease. Moreover, we implemented approaches to estimate SNP diversity in metagenomic samples and carry out statistical tests to identify where differences exist, making it possible to apply evolutionary approaches to metagenomic datasets.

The framework does not tie the user to any specific tool, providing templates and documentation that can be used to customise any metagenomic workflow. It is implemented in Python and can be installed on any operating system that supports its library dependencies. The framework is open source, and licensed under GPL-2.0.