Dear Editor,

We would like to present the manuscript titled “NGSANE: A Lightweight Production Informatics Framework for High Throughput Data Analysis” for the “Applications Notes” section of Bioinformatics.

The paper introduces a novel Linux bash-based pipelining tool for high-throughput analysis of sequencing data. It is specifically designed to enable robust and documented processing on high-performance compute systems in today’s fast pace environment where individual components deprecate rapidly due to evolving technology and algorithms. NGSANE enables rapid development of new pipeline components without the overhead of implementing graphical user interfaces or high-level program language wrapper as required by comparable published pipelining software tools.

We expect the toolkit to be a valuable resource for a wide range of Bioinformatics readers, as the need for rapidly deployable yet robust documented software-processing lies at the heart of a wide range of research applications.

Our software is freely available from <https://github.com/BauerLab/ngsane>.

Thank you in advance for your consideration.

Sincerely,

**Denis C. Bauer and Fabian A. Buske**

(on behalf of all authors)