

Azure Custom Tasks (ACT) - simplifying cloud-based bioinformatics with efficient parallel computing on Microsoft Azure

Pablo Alessandro B. Viana^{1,2}, Pedro M. Meirelles^{3,4}, and Pablo Ivan P. Ramos^{1,2}✉

1 Center for Data and Knowledge Integration for Health (CIDACS), Gonçalo Moniz Institute, Oswaldo Cruz Foundation (Fiocruz Bahia), Salvador, Bahia, Brazil. **2** Postgraduate Course in Biotechnology in Health and Investigative Medicine (PgBSMI), Gonçalo Moniz Institute, Oswaldo Cruz Foundation (Fiocruz Bahia), Salvador, Bahia, Brazil. **3** Institute of Biology, Federal University of Bahia, Salvador, Bahia, Brazil. **4** National Institute for Interdisciplinary and Transdisciplinary Studies in Ecology and Evolution (IN-TREE), Salvador, Bahia, Brazil. ✉ Corresponding author

DOI: [10.xxxxxx/draft](https://doi.org/10.xxxxxx/draft)

Software

- [Review](#) ✉
- [Repository](#) ✉
- [Archive](#) ✉

Editor: [Open Journals](#) ✉

Reviewers:

- [@openjournals](#)

Submitted: 01 January 1970

Published: unpublished

License

Authors of papers retain copyright and release the work under a Creative Commons Attribution 4.0 International License ([CC BY 4.0](#)).

Summary

Bioinformatics applications often encounter computational bottlenecks due to the vast volume of data generated by omics technologies. Cloud solutions like Microsoft Azure offer scalable infrastructures to manage these processing demands, but their complexity and associated costs can hinder adoption. Azure Custom Tasks (ACT) is a Python-based wrapper developed to simplify the deployment of parallelized bioinformatics tasks on Azure. By abstracting the complexities of the Azure Batch API, ACT reduces setup time through automated resource provisioning and simplified configuration, and lowers operational costs by optimizing task distribution and resource utilization, providing a scalable and reproducible solution. As an open-source tool under the MIT license, ACT minimizes technical barriers, promoting efficient and accessible large-scale data analysis in bioinformatics workflows. ACT's architecture is also suitable to other domains that require large-scale parallel data analysis, including fields such as physics, engineering, and data science, making it a versatile tool for diverse computational challenges.

Statement of need

The exponential growth of omics technologies generates vast datasets, challenging computational biology, particularly regarding data processing and analysis ([Da Silva et al., 2019](#)). Cloud computing has emerged as a flexible, cost-effective solution, providing scalable access to computational resources without the need for physical infrastructure investments ([Sikeridis et al., 2017](#)). Despite this, the complexity of configuring and managing cloud environments—such as Microsoft Azure—remains a barrier to widespread adoption in bioinformatics ([Shanahan et al., 2014](#)).

Azure Batch, a core Azure service for parallel computing, is well-suited for large-scale bioinformatics workflows. However, configuring and deploying tasks via Azure Batch requires managing complex parameters like virtual machines (VMs), input/output operations, and resource allocation ([Stein, 2010](#)).

To simplify this process, we developed Azure Custom Tasks (ACT), an open-source Python wrapper that abstracts Azure Batch configurations. ACT enables researchers to leverage cloud scalability with minimal technical overhead, supporting reproducible and efficient bioinformatics

41 workflows.

42 Features

43 ACT is implemented in Python and leverages the Azure Batch API to simplify the deployment
44 of parallelized bioinformatics tasks. Users can specify cloud resources, storage configurations,
45 and task parameters via a single JSON configuration file. Key features include:

- 46 ▪ **Centralized Configuration:** Simplifies deployment by centralizing parameters for Azure
47 Batch resources (Pools, Jobs, Tasks) in a single JSON file, reducing the need for multiple
48 API calls.
- 49 ▪ **Comprehensive Azure Batch Support:** Provides streamlined access to essential Azure
50 Batch features, simplifying task management and configuration.
- 51 ▪ **Automatic Storage Mounting:** Automatically mounts Azure storage containers to
52 compute nodes, facilitating direct reading and writing of input/output data.
- 53 ▪ **Flexible Input Options:** Supports input data as storage blobs or local file strings, with
54 customizable filtering based on task criteria.
- 55 ▪ **Custom Resource Management:** Allows users to define functions in the configuration file
56 to calculate required computing slots for tasks, optimizing resource usage and reducing
57 operational costs.
- 58 ▪ **Built-in Debugging:** Displays detailed information about task execution (inputs, outputs,
59 scripts, and commands) for troubleshooting.
- 60 ▪ **Custom Logging:** Provides detailed logs for monitoring task progress and profiling
61 execution efficiency.

62 Architecture

63 ACT follows a modular and layered architecture, where each component is designed to handle
64 distinct aspects of task orchestration and execution on Microsoft Azure Batch (Figure 1). This
65 architecture promotes separation of concerns and scalability, making ACT maintainable and
66 extensible. The core components include:

- 67 ▪ **AzureCustomTasks:** Manages task execution and resource provisioning.
- 68 ▪ **InputHandler:** Handles input parsing and user interaction.
- 69 ▪ **ConfigurationReader:** Loads configuration files and sets up authentication.
- 70 ▪ **AzureBatchUtils:** Interfaces with Azure Batch to execute jobs and manage resources.

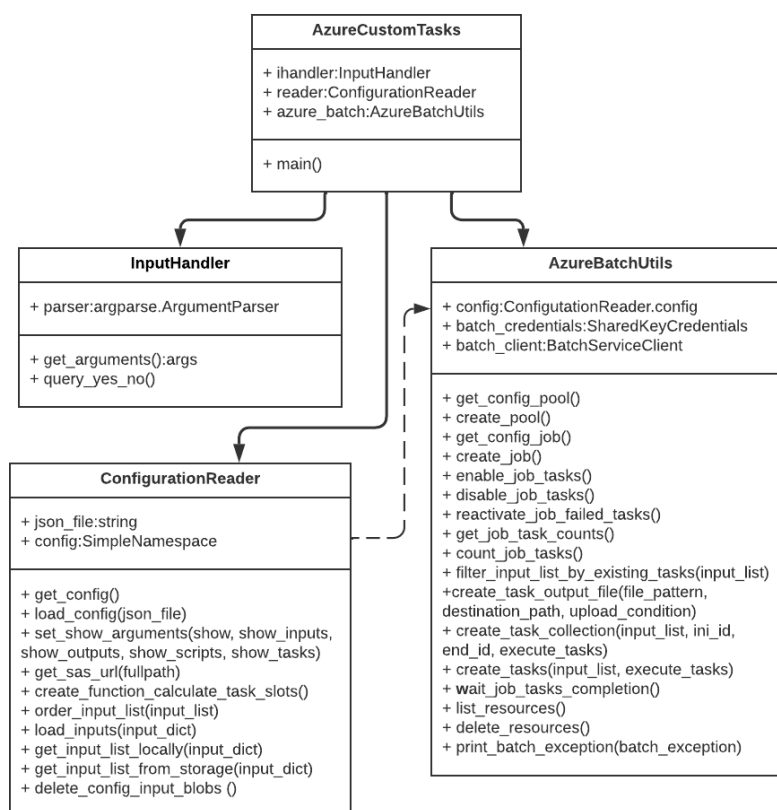


Figure 1: Figure 1. UML class diagram of Azure Custom Tasks (ACT)

Usage Information and Examples

Comprehensive documentation, including step-by-step setup instructions, configuration examples, and common use case scenarios, is available in the project's [Wiki Documentation](#)

Acknowledgements

We would like to thank Larissa Depa and Larisse Depa for thorough backtesting of the wiki examples.

References

- Da Silva, D. S. M., Da Silva, W. M. C., Ruizhe, G., Bernardi, A. P., Mariano, A. M., & Holanda, M. (2019). Big data trends in bioinformatics. *2019 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, 1862–1867. <https://doi.org/10.1109/BIBM47256.2019.8982963>
- Shanahan, H. P., Owen, A. M., & Harrison, A. P. (2014). Bioinformatics on the cloud computing platform azure. *PLOS ONE*, 9, 1–9. <https://doi.org/10.1371/JOURNAL.PONE.0102642>
- Sikeridis, D., Papapanagiotou, I., Rimal, B. P., & Devetsikiotis, M. (2017). A comparative taxonomy and survey of public cloud infrastructure vendors. *CoRR*, abs/1710.01476. <http://arxiv.org/abs/1710.01476>
- Stein, L. D. (2010). The case for cloud computing in genome informatics. *Genome Biology*, 11, 1–7. <https://doi.org/10.1186/GB-2010-11-5-207/COMMENTS>