

**Institute of Primate Research**

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**STANDARD OPERATING PROCEDURE (SOP) DOCUMENT**

## **Bioinformatics pipelines (from raw sequence data to analysis)**

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| **Approvals** |  |  |  |
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# 

# PURPOSE

To define standardized workflows for building and running bioinformatics pipelines that ensure reproducibility, accuracy, and efficiency.

# SCOPE

Covers raw sequence data (DNA/RNA) through processing, alignment, annotation, and downstream analysis.

# PERSONS RESPONSIBLE:

* **Bioinformatician:** Designs and runs pipelines.
* **Computational Biologist:** Interprets results.
* **Head of DS&AS:** Approves workflows before deployment.

# FREQUENCY

* Pipeline validation prior to first use.
* Updates whenever new tools, methods, or reference builds are introduced.

# MATERIALS

* Workflow management systems (Nextflow, Snakemake, Galaxy).
* Analysis tools (BWA, GATK, DESeq2, BLAST).
* HPC/Cloud infrastructure.
* Version control (Git).

# PROCEDURE

1. **Pipeline Design:** Define steps (QC, alignment, variant calling, annotation).
2. **Implementation:** Build reproducible workflows using workflow managers.
3. **Testing:** Validate pipeline on benchmark datasets.
4. **Execution:** Run pipelines on HPC/Cloud, log outputs systematically.
5. **Version Control:** Maintain pipeline scripts in Git repositories.
6. **Documentation:** Archive pipeline details, parameter settings, and results in DS&AS repository.

# REFERENCES