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| **{ Title }** | |
| **Responsible Department: CLS-NGS** | **Effective Date: { Publication Date }** |
| **Policy Basis for Procedure**  This SOP describes the standard processes for monitoring and troubleshooting bioinformatics workflow. | |
| **Applicability**  This applies to the bioinformatics personnel of the NGS Lab. | |
| **Description of Standard Procedure**  **PROCEDURE**  1) Nextflow Process Completion  Ensure workflow completion has no process errors by changing to the process output directory and entering the command ‘cat nextflow\_alignment.log’ for the alignment workflow, ‘cat nextflow\_tumoronly.log’ for the tumor only workflow, ‘cat nextflow\_rnaseq.log’ for the rnaseq workflow, and ‘cat nextflow\_somatic.log’ for the somatic workflow. If errors have occurred, an error message will be displayed. To resolve these issues, you first need to identify the process and source of the issue. Below is a list of files that could give insight to the cause of the error. Troubleshooting is not limited to this list.   * Nextflow process   Process termination. View the complete command output by changing to the process work directory and entering the command ‘cat .command.out’, ‘cat .command.log’ and/or ‘cat .command.err’. Processes may be manually run by entering the command ‘sh .command.sh’ inside the process work directory. If available, search error logs generated by tools used within process.   * Nextflow run   Process/Run termination. View nextflow run logs and errors by changing to the nextflow run directory and entering the command ‘cat .nextflow.log’.   * Sbatch   Sbatch errors. View sbatch run logs and errors by changing to the user’s home directory directory and entering the command ‘cat {RunID}.log’ and ‘cat {RunID}.err’   * 4) Task/Nodes   Task and Node information: View process task information by opening the pipeline.trace\* file. Node information can be viewed by the command ‘sacct -j {JobID} --format=JobID,JobName,NNodes,NodeList,State’.  **IMPLEMENTATION**  The Workflow used in this SOP can be downloaded here: <https://git.biohpc.swmed.edu/brandi.cantarel/clinseq_workflows> | |
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| **Applicable Forms**   |  |  | | --- | --- | | Document ID# | Title of Document | |  | Bioinformatics\_Troubleshooting | |  |  | |  |  |   **Related Documents**   |  |  | | --- | --- | | Document ID# | Title of Document | |  | DNA\_Analysis | |  | RNA\_Analysis | |  | Overview\_Bioinformatics\_SOP | | |
| **References** | |
| **Review, Revision, and Approval History**   |  |  |  |  | | --- | --- | --- | --- | | **History of Document** | | | | | Version | Date | Description of Change | Authored/Revised by | | 2 | 01/13/202 |  | Brandi Cantarel, Erika Villa | |  |  |  |  | | |
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| **Contact for Further Information** | |

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