

# AWS HealthOmics? Nf-core ????? ?????? ?? (scrnaseq)

📄 : <https://catalog.us-east-1.prod.workshops.aws/workshops/76d4a4ff-fe6f-436a-a1c2-f7ce44bc5d17/en-US>

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2025 📄 4 📄 18 📄 📄 scrnaseq 📄 History 2.7.1 > 3.0.0 > 4.0.0

📄 📄 📄 2.7.0, 2.7.1 📄 📄 .

## ???? ??

📄 📄 📄 **Bash** 📄 📄

```
cd ~

export yourbucket="your-bucket-name"
export your_account_id="your-account-id"
export region="your-region"
export workflow_name="your-workflow-name"
export omics_role_name="your_omics_rolename"

# if not exist the bucket, let's create.
#aws s3 mb $yourbucket
```

nf-core repository??? ????? ??

```
git clone https://github.com/nf-core/scrnaseq --branch 2.7.1 --single-branch
```

```
cp ~/amazon-ecr-helper-for-aws-healthomics/lib/lambda/parse-image-uri/public_registry_properties.json namespace
```

```
python3 amazon-omics-tutorials/utlils/scripts/inspect_nf.py \
--output-manifest-file scrnaseq_271_docker_images_manifest.json \
-n namespace.config \
--output-config-file omics.config \
--region $region \
~/scrnaseq/
```

scrnaseq\_271\_docker\_images\_manifest.json       :

???? ??? (into Amazon ECR)

```
aws stepfunctions start-execution \  
--state-machine-arn arn:aws:states:$region:$your_account_id:stateMachine:omx-container-puller \  
--input file://scrnaseq_271_docker_images_manifest.json
```

Step Functions

State machines

Activities

Developer resources

Online learning workshop

Local Development

Data flow simulator

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Updated extension for VS Code

With the latest AWS Toolkit extension for Visual Studio Code, you can edit and test workflows graphically with Workflow Studio. [Learn more](#).

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State machines (2)

View execution counts

View details

Edit

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Search for state machines

Any type

| Name                                  | Type     | Creation date                      | Status |
|---------------------------------------|----------|------------------------------------|--------|
| <a href="#">omx-container-builder</a> | Standard | Apr 15, 2025, 15:44:36 (UTC+09:00) | Active |
| <a href="#">omx-container-puller</a>  | Standard | Apr 15, 2025, 14:55:08 (UTC+09:00) | Active |

Executions

Monitoring

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Definition

Aliases

Versions

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Executions (5)

View details

Stop execution

Redrive

Start execution

Filter executions by property or value

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Last 15 months

5 matches

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| Name                                                 | Status    | Start Time (local)     | End Time (local)       | Duration     |
|------------------------------------------------------|-----------|------------------------|------------------------|--------------|
| <a href="#">465b6f92-b88a-4277-8465-8f45bbd8755c</a> | Succeeded | Aug 20, 2024, 15:31:10 | Aug 20, 2024, 15:32:25 | 00:01:15.021 |
| <a href="#">14ad44ec-264a-49ca-bb2e-04bde507ac7e</a> | Succeeded | Aug 19, 2024, 21:18:42 | Aug 19, 2024, 21:21:41 | 00:02:59.204 |
| <a href="#">6bb79dab-d511-41a0-8ba1-db9e905b8fb0</a> | Succeeded | Jun 21, 2024, 21:09:49 | Jun 21, 2024, 21:15:16 | 00:05:26.831 |
| <a href="#">edc05886-0499-4b95-baa4-4ca995d97e2f</a> | Succeeded | Jun 17, 2024, 13:19:44 | Jun 17, 2024, 13:20:45 | 00:01:00.931 |
| <a href="#">83eda741-4152-4fa9-a5ae-5ed29ba0941c</a> | Succeeded | Jun 14, 2024, 18:30:55 | Jun 14, 2024, 18:31:54 | 00:00:59.321 |

nf-core project ?? ?????

```
mv omics.config scrnaseq/conf
```

```
echo "includeConfig 'conf/omics.config'" >> scrnaseq/nextflow.config
```

AWS HealthOmics ?????? ????

## ??1. AWS HealthOmics ???? ??

parameter-description.json      .

```
cat << EOF > parameter-description.json
{
  "input": {"description": "Samplesheet with sample locations.",
    "optional": false},
  "protocol": {"description": "10X Protocol used: 10XV1, 10XV2, 10XV3",
    "optional": false},
  "aligner": {"description": "choice of aligner: alevin, star, kallisto",
    "optional": false},
  "barcode_whitelist": {"description": "Optional whitelist if 10X protocol is not used.",
    "optional": true},
  "gtf": {"description": "S3 path to GTF file",
    "optional": false},
  "fasta": {"description": "S3 path to FASTA file",
    "optional": false},
  "skip_emptydrops": {"description": "module does not work on small dataset",
    "optional": true}
}
EOF
```

## ??2. ?????? ???? ?

```
zip -r scrnaseq-workflow.zip scrnaseq -x "**/\.*" "**/\.*/**"
```

```
aws s3 cp scrnaseq-workflow.zip s3://${yourbucket}/workshop/scrnaseq-workflow.zip
```

```
aws omics create-workflow \
  --name ${workflow_name} \
  --definition-uri s3://${yourbucket}/workshop/scrnaseq-workflow.zip \
  --parameter-template file://parameter-description.json \
  --engine NEXTFLOW
```

## ??3. ?????? ?? ??

```
workflow_id=$(aws omics list-workflows --name ${workflow_name} --query 'items[0].id' --output text)
echo $workflow_id
```

????? ?????

?? ??? ?? ??

???? ??

parameter-description.json 1 111 11 111 11 1111 input.json 111 11 1111 . 11  
11111 1111 11 S3 11 11 1111 1111 .

111 111 111 1111 11111 . (111)

111 11 11

11 1111 111 11 1111 11 1 1111 .

```
wget https://github.com/nf-core/test-datasets/raw/scrnaseq/samplesheet-2-0.csv
wget https://github.com/nf-core/test-datasets/raw/scrnaseq/reference/GRCm38.p6.genome.chr19.fa
wget https://github.com/nf-core/test-datasets/raw/scrnaseq/reference/gencode.vM19.annotation.chr19.gtf
```

11 11 11111 1111 1 1111 111 1111 1 1111 .

```
aws s3 sync . s3://omics-output-us-east-1-462922227709/workflow_migration_workshop/nfcore-scrnaseq-
v4.0.0/
```

sample sheet 111

```
cat << EOF > samplesheet-2-0.csv
sample,fastq_1,fastq_2,expected_cells,seq_center
Sample_X,s3://aws-genomics-static-${region}/workflow_migration_workshop/nfcore-scrnaseq-
v2.3.0/Sample_X_S1_L001_R1_001.fastq.gz,s3://aws-genomics-static-
${region}/workflow_migration_workshop/nfcore-scrnaseq-
v2.3.0/Sample_X_S1_L001_R2_001.fastq.gz,5000,"Broad Institute"
Sample_Y,s3://aws-genomics-static-${region}/workflow_migration_workshop/nfcore-scrnaseq-
v2.3.0/Sample_Y_S1_L001_R1_001.fastq.gz,s3://aws-genomics-static-
${region}/workflow_migration_workshop/nfcore-scrnaseq-v2.3.0/Sample_Y_S1_L001_R2_001.fastq.gz,5000,"CRG
Barcelona"
Sample_Y,s3://aws-genomics-static-${region}/workflow_migration_workshop/nfcore-scrnaseq-
```

```
v2.3.0/Sample_Y_S1_L002_R1_001.fastq.gz,s3://aws-genomics-static-
${region}/workflow_migration_workshop/nfcore-scrnaseq-v2.3.0/Sample_Y_S1_L002_R2_001.fastq.gz,5000,"CRG
Barcelona"
EOF
```

## ## **samplesheet** ## s3 ##

```
aws s3 cp samplesheet-2-0.csv s3://${yourbucket}/nfcore-scrnaseq/samplesheet-2-0.csv
```

## **json** ## (## **sample sheet**## ## ## **input**## ## )

```
cat << EOF > input.json
{
  "input": "s3://${yourbucket}/nfcore-scrnaseq/samplesheet-2-0.csv",
  "protocol": "10XV2",
  "aligner": "star",
  "fasta": "s3://aws-genomics-static-${region}/workflow_migration_workshop/nfcore-scrnaseq-
v2.3.0/GRCm38.p6.genome.chr19.fa",
  "gtf": "s3://aws-genomics-static-${region}/workflow_migration_workshop/nfcore-scrnaseq-
v2.3.0/gencode.vM19.annotation.chr19.gtf",
  "skip_emptydrops": true
}
EOF
```

?? ??? ??

(## : ##)

## ## ##

```
aws s3 sync s3://ngi-igenomes/test-data/scrnaseq/ s3://${yourbucket}/test-data/scrnaseq/ --exclude "*" --include
"pbmc8k_S1_L00*"
```

**sample sheet** ##

```
cat << EOF > samplesheet_2.0_full.csv
sample,fastq_1,fastq_2,expected_cells
```

```
pbmc8k,s3://${yourbucket}/test-data/scrnaseq/pbmc8k_S1_L007_R1_001.fastq.gz,s3://${yourbucket}/test-
data/scrnaseq/pbmc8k_S1_L007_R2_001.fastq.gz,10000
pbmc8k,s3://${yourbucket}/test-data/scrnaseq/pbmc8k_S1_L008_R1_001.fastq.gz,s3://${yourbucket}/test-
data/scrnaseq/pbmc8k_S1_L008_R2_001.fastq.gz,10000
EOF
```

samplesheet s3

```
aws s3 cp samplesheet_2.0_full.csv s3://${yourbucket}/nfcore-scrnaseq/samplesheet_2.0_full.csv
```

```













[ ] json [ ] ( [ ] sample sheet [ ] [ ] [ ] input [ ] [ ] [ ] [ ] )

```

```
cat << EOF > input_full.json
{
  "input": "s3://$${yourbucket}/nfcore-scrnaseq/samplesheet_2.0_full.csv",
  "protocol": "10XV2",
  "aligner": "star",
  "fasta": "s3://aws-genomics-static-${region}/workflow_migration_workshop/nfcore-scrnaseq-
v2.3.0/GRCm38.p6.genome.chr19.fa",
  "gtf": "s3://aws-genomics-static-${region}/workflow_migration_workshop/nfcore-scrnaseq-
v2.3.0/gencode.vM19.annotation.chr19.gtf",
  "skip_emptydrops": true
}
EOF
```

## Policy ??

## Prepare IAM service role to run AWS HealthOmics workflow

your-bucket-name, your-account-id, your-region             .

omics\_workflow\_policy.json

```
cat << EOF > omics_workflow_policy.json
{
  "Version": "2012-10-17",
  "Statement": [
    {
      "Effect": "Allow",
      "Action": [
```

```
        "s3:GetObject"
    ],
    "Resource": [
        "arn:aws:s3:::${yourbucket}/*",
        "arn:aws:s3:::aws-genomics-static-${region}/workflow_migration_workshop/nfcore-scrnaseq-v2.3.0/*"
    ]
},
{
    "Effect": "Allow",
    "Action": [
        "s3:ListBucket"
    ],
    "Resource": [
        "arn:aws:s3:::${yourbucket}",
        "arn:aws:s3:::aws-genomics-static-${region}/workflow_migration_workshop/nfcore-scrnaseq-v2.3.0",
        "arn:aws:s3:::aws-genomics-static-${region}/workflow_migration_workshop/nfcore-scrnaseq-v2.3.0/*"
    ]
},
{
    "Effect": "Allow",
    "Action": [
        "s3:PutObject"
    ],
    "Resource": [
        "arn:aws:s3:::${yourbucket}/*"
    ]
},
{
    "Effect": "Allow",
    "Action": [
        "logs:DescribeLogStreams",
        "logs:CreateLogStream",
        "logs:PutLogEvents"
    ],
    "Resource": [
        "arn:aws:logs:${region}:${your_account_id}:log-group:/aws/omics/WorkflowLog:log-stream:*"
    ]
},
{
    "Effect": "Allow",
```

```

    "Action": [
        "logs:CreateLogGroup"
    ],
    "Resource": [
        "arn:aws:logs:${region}:${your_account_id}:log-group:/aws/omics/WorkflowLog:*"
    ]
},
{
    "Effect": "Allow",
    "Action": [
        "ecr:BatchGetImage",
        "ecr:GetDownloadUrlForLayer",
        "ecr:BatchCheckLayerAvailability"
    ],
    "Resource": [
        "arn:aws:ecr:${region}:${your_account_id}:repository/*"
    ]
}
]
}
EOF

```

```
echo "omics_workflow_policy.json" > omics_workflow_policy.json
```

```
trust_policy.json
```

```

cat << EOF > trust_policy.json
{
    "Version": "2012-10-17",
    "Statement": [
        {
            "Effect": "Allow",
            "Principal": {
                "Service": "omics.amazonaws.com"
            },
            "Action": "sts:AssumeRole",
            "Condition": {
                "StringEquals": {
                    "aws:SourceAccount": "${your_account_id}"
                }
            }
        }
    ]
}
EOF

```

```

    "ArnLike": {
        "aws:SourceArn": "arn:aws:omics:${region}:${your_account_id}:run/*"
    }
}
}
]
}
EOF

```

```
echo "trust_policy.json" | cat /dev/null
```

## IAM Role ??

```
aws iam create-role --role-name ${omics_role_name} --assume-role-policy-document file://trust_policy.json
```

Policy document

```
aws iam put-role-policy --role-name ${omics_role_name} --policy-name OmicsWorkflowV1 --policy-document
file://omics_workflow_policy.json
```

## ????? ??

```

input.json, input_full.json

```

```

aws omics start-run \
  --name scrnaseq_workshop_test_run_1 \
  --role-arn arn:aws:iam::${your_account_id}:role/${omics_role_name} \
  --workflow-id ${workflow_id} \
  --parameters file://input.json \
  --output-uri s3://${yourbucket}/output/

```

Revision #29

Created 22 July 2024 11:45:23 by Hyunmin Kim

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