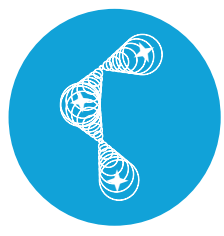


# Reproducible Quantitative Transcriptome Analysis with Oqtans

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**oqtans**  
online  
quantitative  
transcriptome  
analysis



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An open-source workbench integrated in the Galaxy framework that enables researchers to set up a computational pipeline for quantitative transcriptome analysis.

## Accessibility

Oqtans enables users without programming experience to easily specify parameters and run tools and workflows through Galaxy.

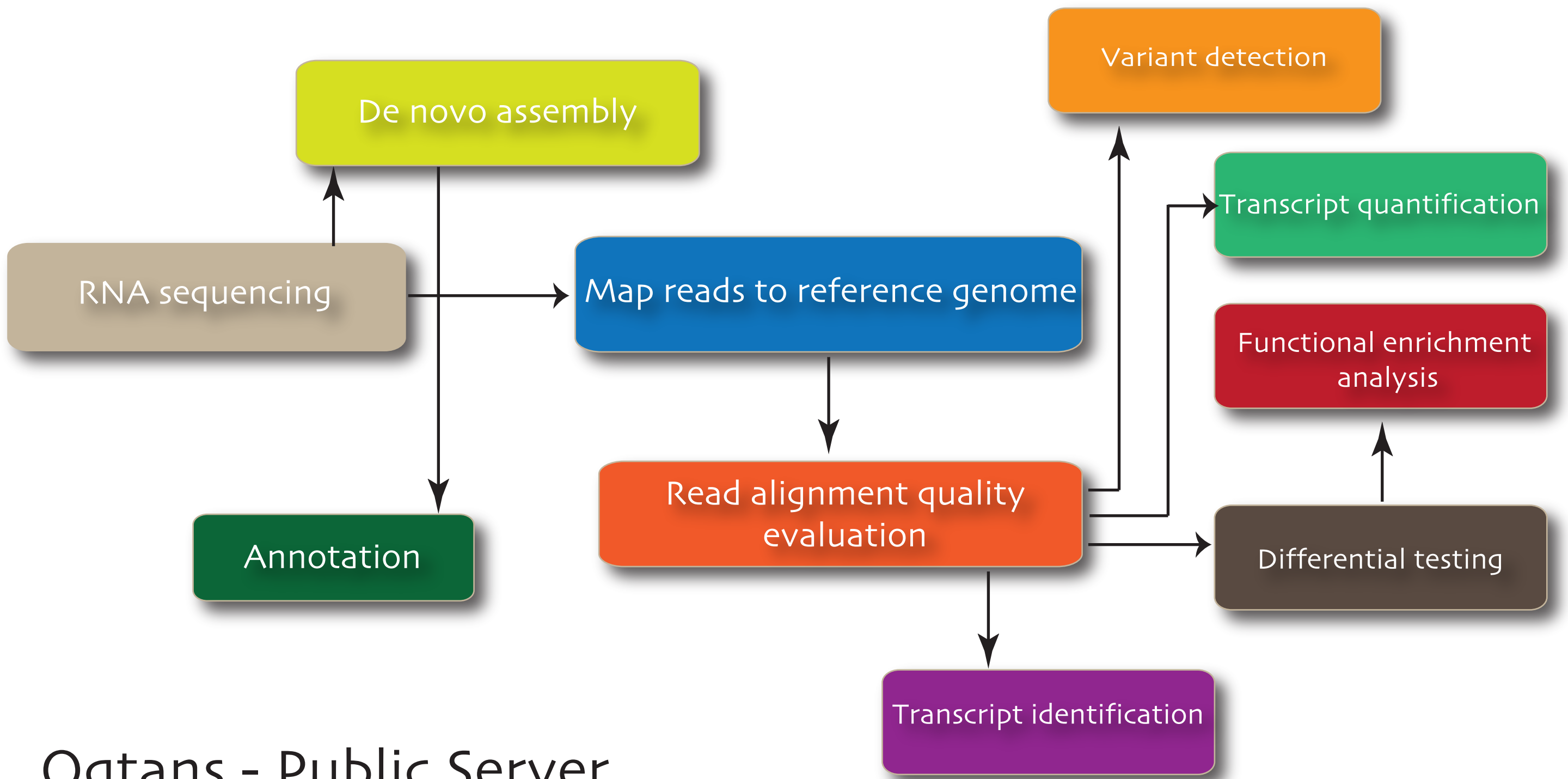
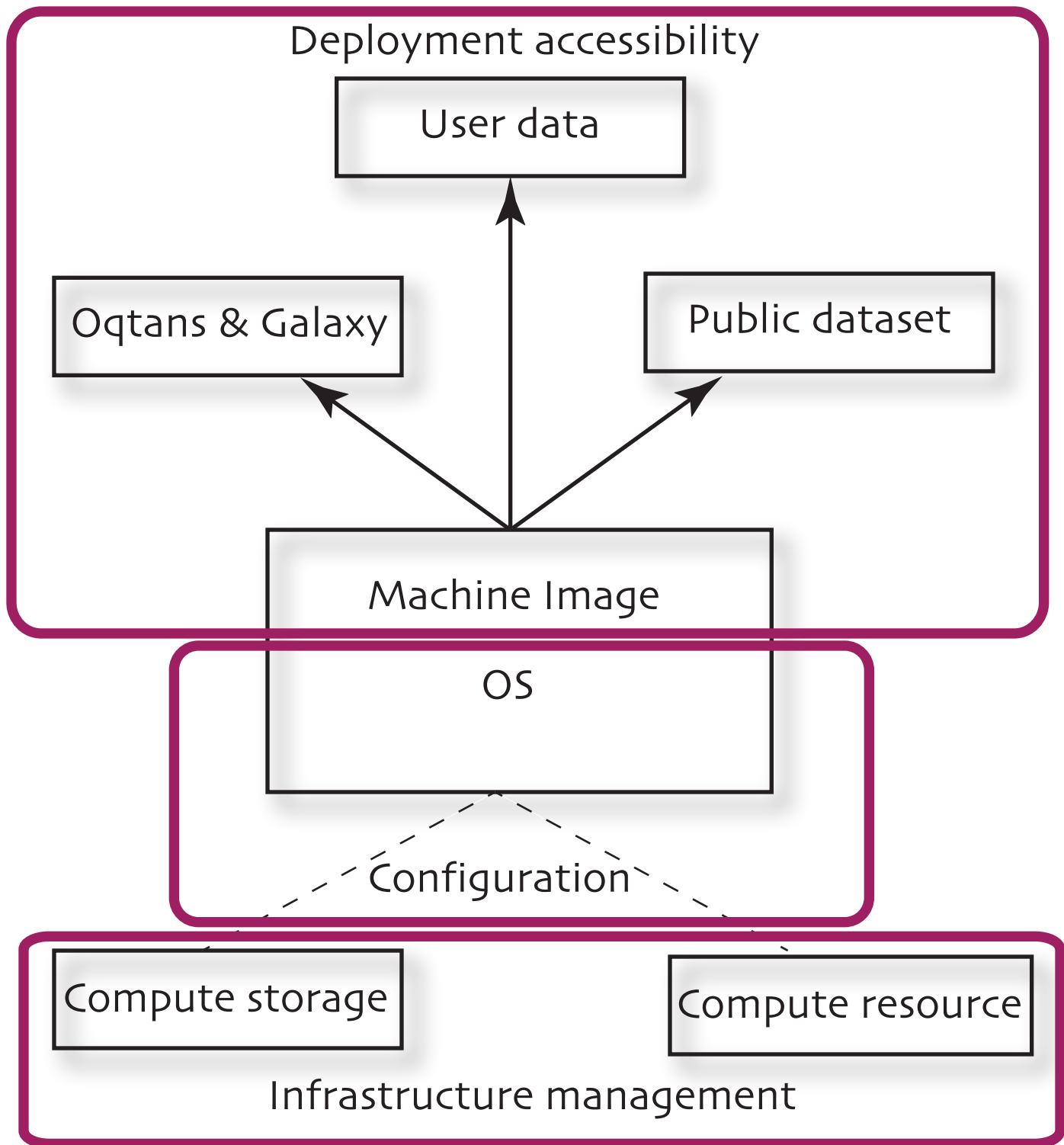
## Reproducibility

Galaxy captures all information necessary so that any user can repeat and understand a complete computational analysis.

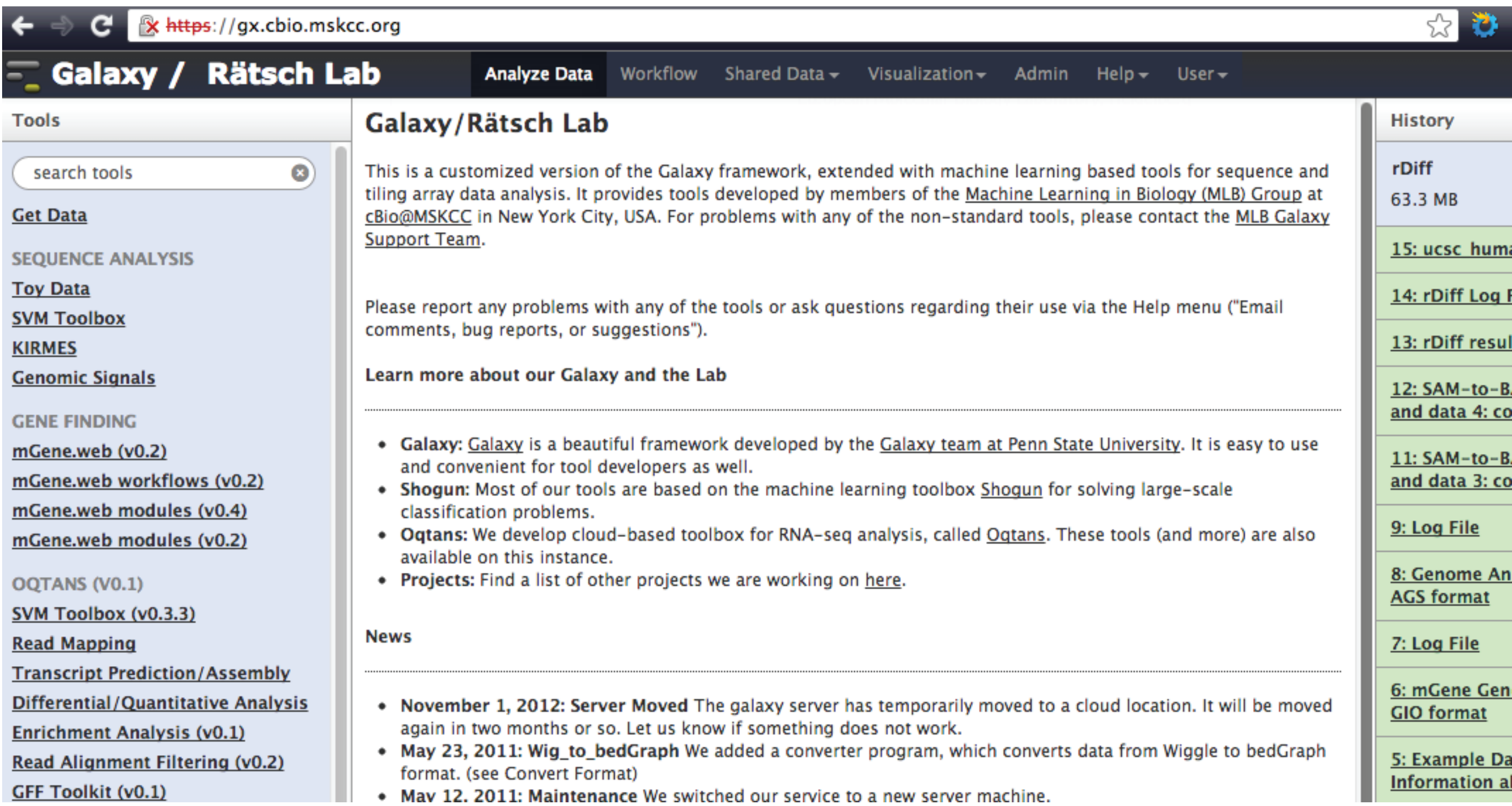
## Transparency

Galaxy enables users to share and publish analyses via the web and create interactive, web-based documents that describe a complete analysis.

## Oqtans Deployment



## Oqtans - Public Server



## Oqtans Instantiation & Availability

### Support

support@oqtans.org  
galaxy@raetschlab.org

### Sharing tools



```
from urllib import urlopen
from fabric.api import *

def get_latest_commit():
    return urlopen('http://commit

@task
def check():
    """check if local changes have
    python fabric script
```

### Useful links

<http://oqtans.org/>  
<https://github.com/ratschlab/>  
<http://galaxy.cbio.mskcc.org/>  
<https://usegalaxy.org/>  
<http://toolshed.g2.bx.psu.edu/>

## References

- [1] Blankenberg, D. et al., Galaxy: a web-based genome analysis tool for experimentalists, Curr Protoc Mol Biol, 2010.  
[2] Schultheiss, S. et.al., Oqtans: a Galaxy-integrated workflow for quantitative transcriptome analysis from NGS Data, BMC Bioinformatics, 2011.

## Cloud computing platforms

