Bioinformatics Computing on Private Clouds with the CloudBioLinux-CloudMan Framework

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Abstract

Background: Text for this section of the abstract . . .

Results: Text for this section of the abstract . . .

Conclusions: Text for this section of the abstract . . .

Background
Current State of Cloud Computing For Bioinformatics

Here we do a review of applications of cloud computing to bioinformatics. Everything from CloudMan, Galaxy, CloVR, Qiime, CBL etc.

Open-Source Cloud Computing PlatForms and Private Clouds
Eucalyptus

Ntino and Alex. Describe the Eucalyptus architecture and components (Walrus, EBS etc) that it provides. Example private cloud installations that use it.

OpenStack

Enis and collaborators. Describe the OpenStack architecture and components (Nova, S3 etc) that it provides. Example private cloud installations that use it.

Results and Discussion
Porting the CloudBioLinux-CloudMan Framework to Private Clouds
The CloudMan Implementation For Scalable Computing on The Cloud

Enis, technical description of CloudMan as it stands for Amazon EC2. For example it uses two data volumes, pulls the code on boot from S3, how does it work with snapshots etc. This will serve as leeway for when describing how we mapped these components to the other platforms, see below.

Porting CloudBioLinux-CloudMan to Eucalyptus

Alex, technical description of changes to the CloudMan EC2 codebase to run on Eucalyptus. How components that CloudMan uses on EC2 where mapped to Eucalyptus. Specific nagging that Eucalyptus does with running CloudMan - i.e. different responses from the API returned when doing calls via boto, and changes in the cloudman codebase in order to take care of these. Also is there something that sysadmins that set up Eucalyptus should pay attention too (in the settings, in order to leverage those applications that create scriptable infrastructures by calling the API)

Porting CloudBioLinux-CloudMan to OpenStack

Enis, technical description of changes to the CloudMan EC2 codebase to run on OpenStack. Changes that have be made to code in order to communicate with the API correctly. What sysadmins that set up OpenStack should pay attention too...

Porting CloudBioLinux-CloudMan to VirtualBox for Desktop Computers

Ntino's adventures in the hacker-land...

Execution and Performance of Bioinformatic Pipelines on Private Clouds
An HMM-BLAST Pipeline for Metagenomic Annotation at JCVI

Ntino... I got the numbers, need to write it.

A Variant Calling Analysis Pipeline at HSPH

Brad... Wanna write about this historic pipeline, or save it for another paper ? Up to use.

Enis Other Example of Pipeline

Enis... Some bioinformatics pipelines run with the other Foster drinkers down under....

Conclusions

We conclude that we are freaking awesome ! ...

Author's contributions

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Acknowledgements

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References

Figures
Figure 1 - Sample figure title

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Figure 2 - Sample figure title

Figure legend text.

Tables
Table 1 - Sample table title

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Additional Files
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Additional file 2 — Sample additional file title

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