Keep moving forward

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Our starting point:

- pipelines for standard tasks:
  - not all ChIP-seq experiments are the same, but share a common part: QC + Mapping + peak calling + ...
  - same applies to other experiments: RNA-seq, Exome-seq, etc.
  - many options: bash, make, bpipe, snakemake, Galaxy, HTCondor
- infrastructure: workstations, servers, clusters, cloud
Context

Nice idea, let's think further

**Challenges:**

- making analysis reproducible over time
- changing versions
- new standards: Tophat + Cufflinks vs. Star + edgeR, Bowtie vs. BWA, ...
- being able to reuse pipelines: new projects, new infrastructure
- scalability: +samples → +cores

**[one possible] Solution:**

containerizing software stacks
What's this talk about?

How to painlessly run all this
(painless to run, painful to set up)

- Analyzing a new project, as easy as copy & paste
- Getting the same results
Containers wrap up a piece of software in a complete filesystem that contains everything it needs to run: code, runtime, system tools, system libraries – anything you can install on a server. This guarantees that it will always run the same, regardless of the environment it is running in.

source: www.wikipedia.org
Containers

Benefits:

✔ lightweight VM
✔ image portability → pack once, run
✔ everywhere: workstation, server, cloud
✔ software stack exportable to tar.gz: pack with data
✔ control versions/dependencies of packaged software
✔ collaborate/branch/merge

Docker specific:

✔ build facility
✔ App containers: PaaS oriented single process container
✔ storage separated via layers
Containers

Downsides:

✗ security concern: need special group permissions. Possible solutions:
  • grant permissions: works on some configs. OK
  • up at boot time, add a listener. Complex, not cluster friendly

✗ complex integration with the batch scheduler. Partial solutions:
  • run the full stack as a single task, with max resources allocated. 
    Cons: no fine grained management of the resources
  • containerize tools (samtools, bwa, R), not workflows/pipelines/stacks. 
    Cons: more complex bundle/share/deploy

2 paradigms:

• pack single apps → friendly with LSF

✓ pack full software stacks → friendly with the data and the concept of PaaS
Working with docker containers

- **Create a docker container: Dockerfile**
  
  ```
  FROM debian:stable
  ENTRYPOINT ["/opt/bpipe/default/bin/bpipe","run"]

  ## install samtools
  COPY ./deps/samtools-1.2 /usr/local/src/samtools-1.2
  WORKDIR /usr/local/src/samtools-1.2
  RUN     make && \
            make install prefix=/opt/samtools/1.2 && \
            rm -rf /usr/local/src/samtools-1.2 && \
            echo "export PATH=/opt/samtools/1.2/bin:\$PATH" > \
                /opt/samtools/1.2/env.sh && \
            chmod ugo+rx /opt/samtools/1.2/env.sh

  ## install pipelines and wrappers
  COPY ./deps/imb-forge /opt/imb-forge
  ```

- **Build:**
  
  `$ docker build -t imbforge/chipseq:v1 .`

- **Push to the docker hub:**
  
  `$ docker push imbforge/chipseq:v1`

- **Run a container:**
  
  `$ docker run --rm -v {WORKDIR}:${WORKDIR} -w {WORKDIR} -t imbforge/chipseq:v1\n  -n {MAX_PAR_PROCS} {WORKDIR}/chipseq_v1.2.txt {WORKDIR}/rawdata/*.fastq.gz`

- **Run an interactive shell:**
  
  `$ docker run --entrypoint=/bin/bash -ti imbforge/chipseq:v1 -s`
Working with docker containers
Containers in a workstation

Pull & play:

- pull the container image from the repo
  
  $ docker pull imbforge/rnaseq

- run with bind mount the local volume
  
  $ export WORKDIR=/project/rna-seq
  $ docker run --rm -v ${WORKDIR}:${WORKDIR} -w \\    ${WORKDIR} -t imbforge/chipseq:v1 -n ${MAX_PROCS} \\    ${WORKDIR}/chipseq_v1.2.txt ${WORKDIR}/rawdata/*.fq.gz
Containers in a private cluster

Complex setup, many questions open:

✔ SAN/NAS/parallel FS help

✗ security concern: grant permissions or boot up the container with a listener

✗ difficult to fine-grain resource allocation

• possible solution (unexplored): the pipeline splits in batches and dynamically boots up containers
  
  ✔ complex setup of the pipeline

✔ suitable for large scale projects
Containers in a (semi)public cluster

- 555 nodes, 35,520 cores, 89TB RAM, 1110TB storage

✗ even worse, strict security policy!

✗ no root-like for us

- Partial solution: chroot jails + special queues for the pipelines that automatically decompress a tarball with the software stack. **Downsides:**
  - ✗ no fine-grained resource allocation
  - ✗ CPU intensive (.tar.gz ~2Gb)
  - ✗ complex setup

source: www.wikipedia.org
Horizon: Containers in the cloud

- PaaS: allow customers to develop, run, and manage applications without the complexity of building and maintaining the infrastructure

- load and boot the software stacks as containers

- easy/transparent to scale-up/down hardware, AWS

- better management of the resources (although not ideal)
Conclusions

✔ Containers are a neat way to deploy full application stacks
✔ Can be packed with the data to ensure reproducibility
✗ Not trivial to attach them to a batch scheduler
✔ The cloud paradigm may help to leverage the use of resources
Thanks!