Building pipelines to support African bioinformatics

The H3ABioNet Pipelines Project

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on behalf of the
H3A Bioinformatics Network Consortium

H3ABioNet
Pan African Bioinformatics Network for H3Africa

SDIMB
SYDNEY BRENNER INSTITUTE FOR MOLECULAR BIOSCIENCE

AWI-Gen
AfricaWits-INDEPTHPartnership

H3A: Human Heredity and Health in Africa

Initiative of ASHG, NIH and Wellcome Trust

- need to build capacity
- Africa's genetic diversity
- rapid epidemiological transition
- health challenges: infectious disease and NCDs
- under-researched

10th Consortium Meeting, Gaborone, Botswana
May 2017

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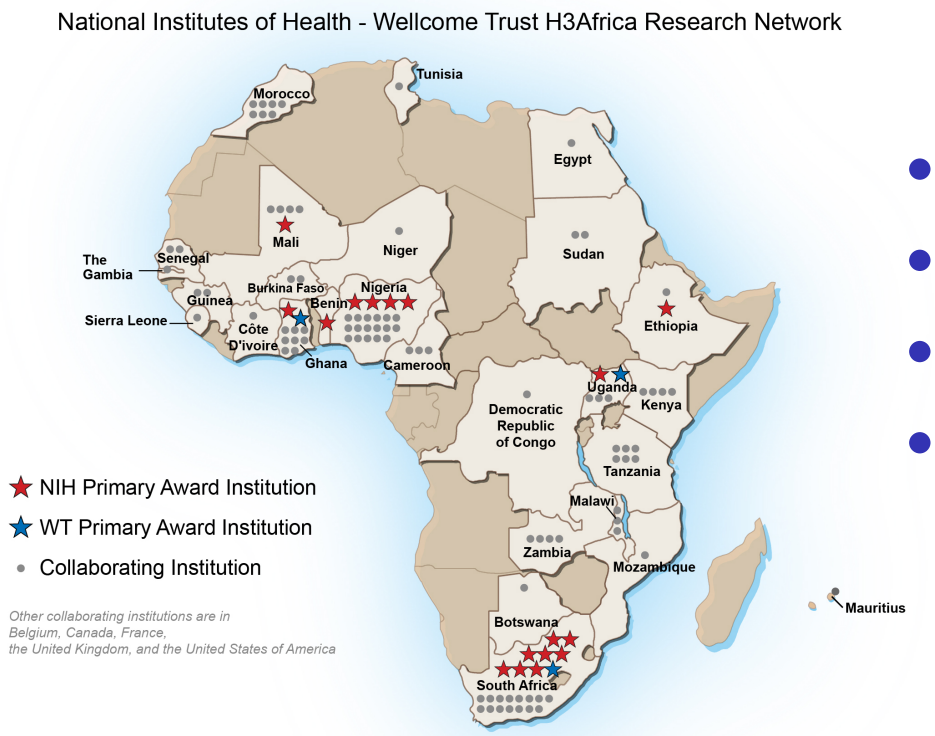

- 8 collaborative centres
- 13 research projects
- Biorepositories
- Pan-African Bioinformatics Network for H3Africa

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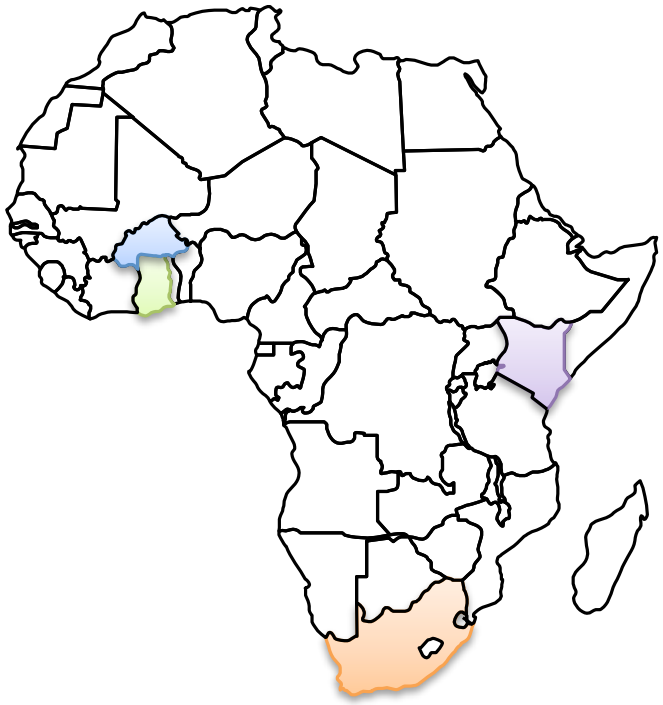
Example project: AWI-Gen

Genetic & environmental factors in cardio-metabolic disorders in African populations – hub at Wits

- Soweto, Johannesburg
- Wits Agincourt Research Unit
- Dikgale HDSS, University of Limpopo
- APHRC, Nairobi, Kenya
- Navrongo Health Research Centre, Ghana
- CRUN, Nanoro, Burkina Faso



Data to be collected

12000 participants in all – data collected at site

- Extensive personal histories
- Measured, weighed, scanned, blood, urine samples
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Genome-wide association test: relating genotype data to the phenotype data

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- needs to be reproducible
- needs to be portable
- under tight deadlines

Other projects – ditto

AWI-Gen just one project

- Similar needs – range of different workflows

Pan-African Bioinformatics Network for H3Africa

H3ABionet created by NIH in 2012 to complement H3Africa research projects:

- bioinformatics key for the projects
- bioinformatics capacity in Africa sparse

Goals:

- Support H3A projects
- Build capacity in bioinformatics

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- Central node at UCT – Overall PI, Nicola Mulder
- $>$ 30 nodes in 15 African countries; US and UK partners

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Overall goal: improve capacity through training and infrastructure development

Working groups

- Education & Training
- Research
- Infrastructure
- User Support
- Accreditation

H3A Bionet Pipelines Project

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2. Bionet partners at the University of Illinois/NCSA involvement in NIH"s Big Data to Knowledge (BD2K) initiative & the *Knowledge Engine for Genomics*.

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1. Strategic decision by Bionet to explore
   - "cloud computing"
   - build skills in pipelines
2. Bionet partners at the University of Illinois/NCSA involvement in NIH"s Big Data to Knowledge (BD2K) initiative & the *Knowledge Engine for Genomics*.
3. Some prior work (Lerato Magosi and Rob Clucas)

Overview of project

- Decision to start at H3A Consortium meeting in Dakar in May 2016.
- Involves about 30 people from over 10 institutions, led by Sumir Panji.
- Identified key people, planning starts
- Ran 5-day "Cloud Hackathon" at the University of Pretoria in August 2016
- Sept– pipelines being completed
- January – pipelines published, paper written

Goals

1. Develop production-quality pipelines for key workflows
    - Direct support for stated needs
    - Position Bionet strategically
2. Develop human capacity for building pipelines
3. Explore different technologies

Constraints

1. Must be highly portable, scalable
   - Ideally laptop to CHPC
   - Support cloud environments
   - Container support essential
2. Must have skills within the network : both workflow and technology
3. Limited resources : start with focus and explore other technologies and workflows later

Identified four workflows, two workflow technologies

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CWL		
Nextflow		

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CWL	NGS data	16S metagenomics
Nextflow	GWAS	Imputation

Nextflow

Developed by the Comparative Bioinformatics group at the Barcelona Center for Genomic Regulation (CRG)

- General purpose workflow system
- DSL based on Groovy
- Portable
- Scalable
- Very easy to install
- Container support
- Supports a range of scheduling systems, cloud

Common Workflow Language

Language specification rather than a tool – several tools support it.

- Community-driven, Multi-vendor
- Supports Docker, parallelism
- Language based on YAML
- Extensible

Came out of the bioinformatics community (BOSC) but general purposes

- has buy in from major players

Bionet has good collaborators with CWL experience

```
class commandLineTool
inputs:
  fastqFile:
    type: File
    inputBinding:
      position: 1
baseCommand: [ fastqc, "--outdir", "res" , "--extract" ]
outputs:
  zippedFile:
    type: File
    outputBinding:
      glob: "*.zip"
  report:
    type: Directory
    outputBinding:
      glob: "res"
```

```
process fastQC {
  input:
     file fastqFile
  output:
     set file("*.zip"), file(res) into output_ch
  script:
    "fastqc $fastqFile --outdir res --extract"
}
```

Pros & Cons

Differences in syntax, semantics, capabilities, performance in tools

- Community & standards based language
- Small group driving architecture and system

For whom?

- Biologists with bioinformatics expertise
- Bioinformaticists
- Specialist pipeline builders

Pipeline building process

Building capacity an important goal

- Team distributed across 4 continents, many countries, timezones
- Variable quality internet

Make heavy use of electronic communication

- mconf
- Slack
- Trello
- GitHub

But personal interaction key

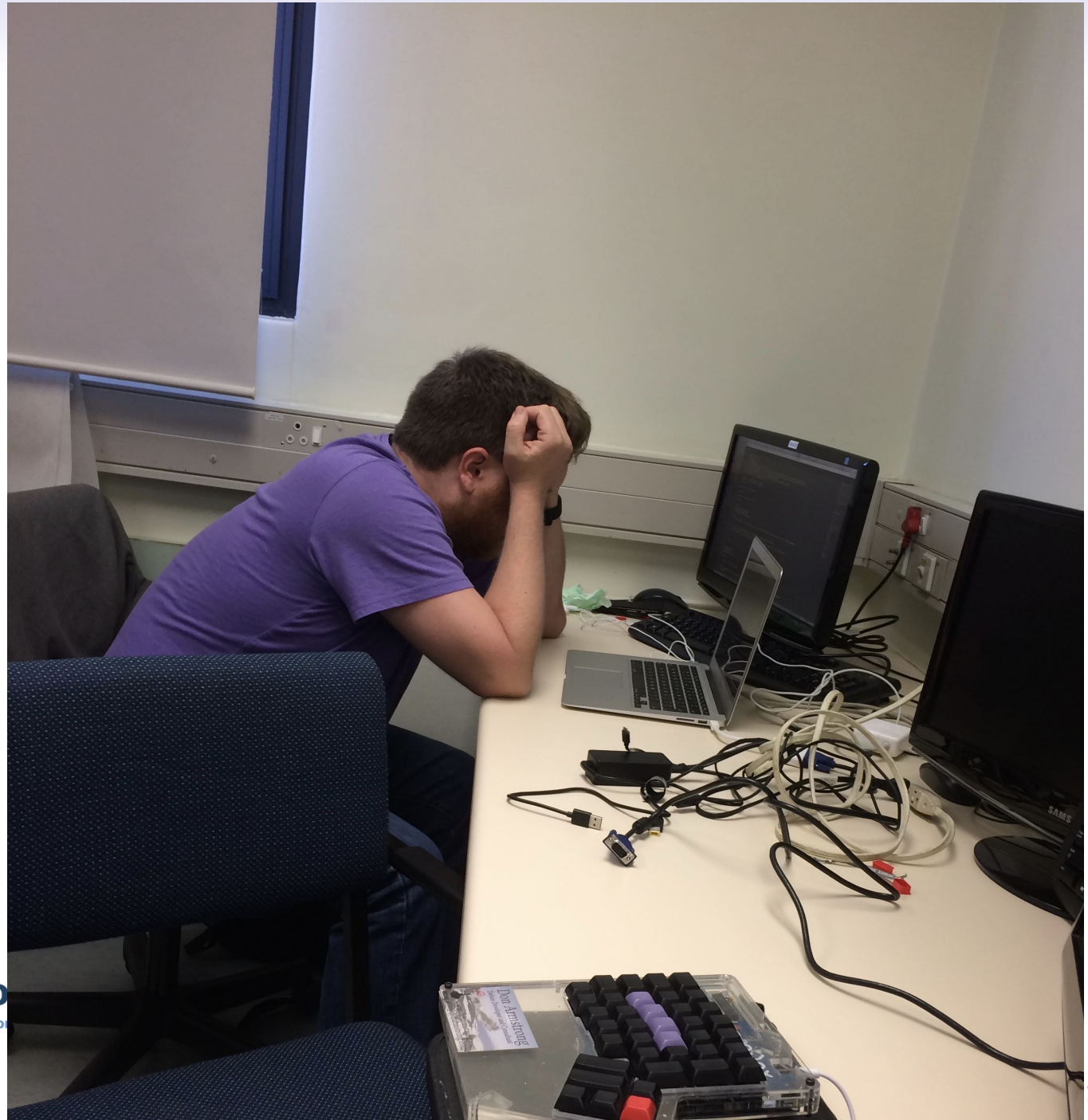
Bionet Cloud Hacakthon

Planning crucial for production meeting

- Identified key participants but also advertised widely – selection process
- Pre-workshop preparation
- 5-days concentrated work – some participation remotely
- Some training, a few talks but mainly work

2014 HPC-ISC
STUDENT CLUSTER COMPETITION

SAMSUNG



H3ABio
Pan African Bioinfo

Status of project

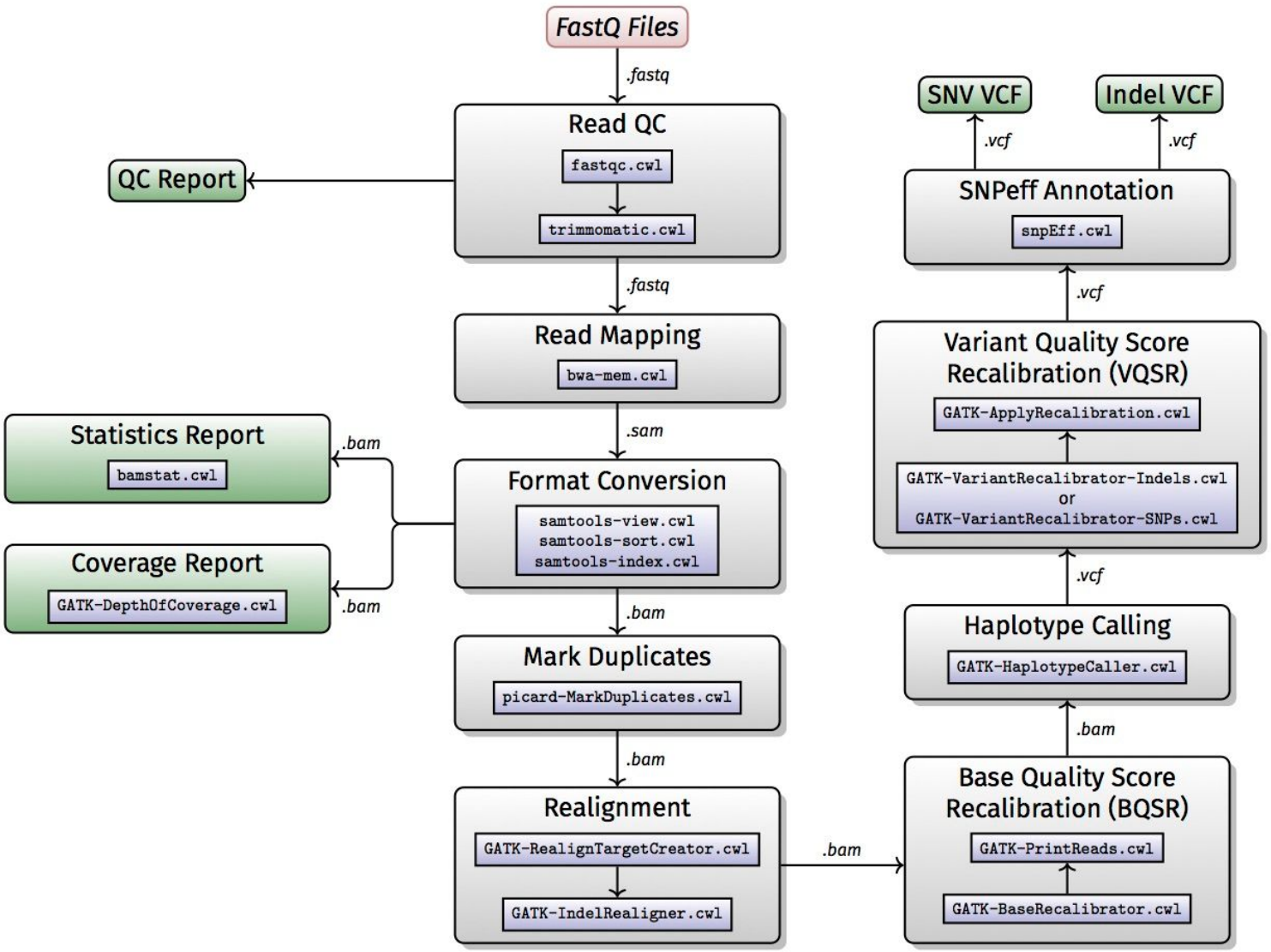
- Developed skills in pipeline creation
- Almost done!
  - `github.com/h3abionet/h3agtk`
  - `github.com/h3abionet/h3abionet16s`
  - `github.com/h3abionet/h3agwas`
  - `github.com/h3abionet/chipimputation`

Whole genome/exome analysis

Based on GATK's *Best Practices* SOP – Done in CWL

- sequence adapter trimming
- QC of fastsq files, BAM files
- Indel and SNV annotation

Dockerised (except for GATAnalysisTK.jar)



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16S rRNA Diversity

Done in CWL – want to re-implement in Nextflow
Use key tools

- FastQC
- USEARCH and UPARSE for clustering and more QC
- QIIME for demultiplexing, taxonomic reconstruction, diversity analysis
- Statistical analysis (scripts using R)

Helper scripts to put together

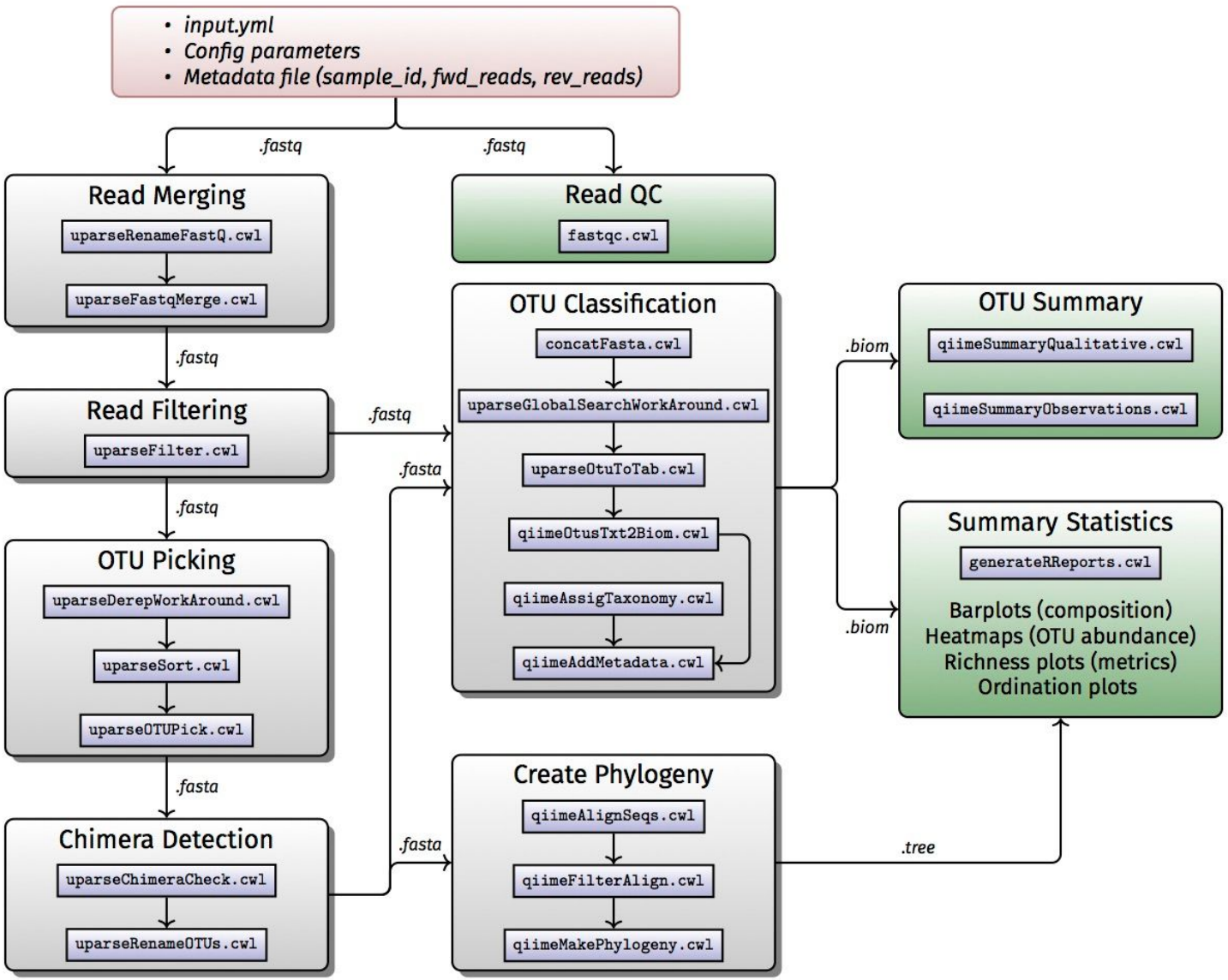


Figure 2 - Workflow B: 16S rRNA Diversity Analysis

GWAS Pipeline

Three separate pipelines – implemented in Nextflow

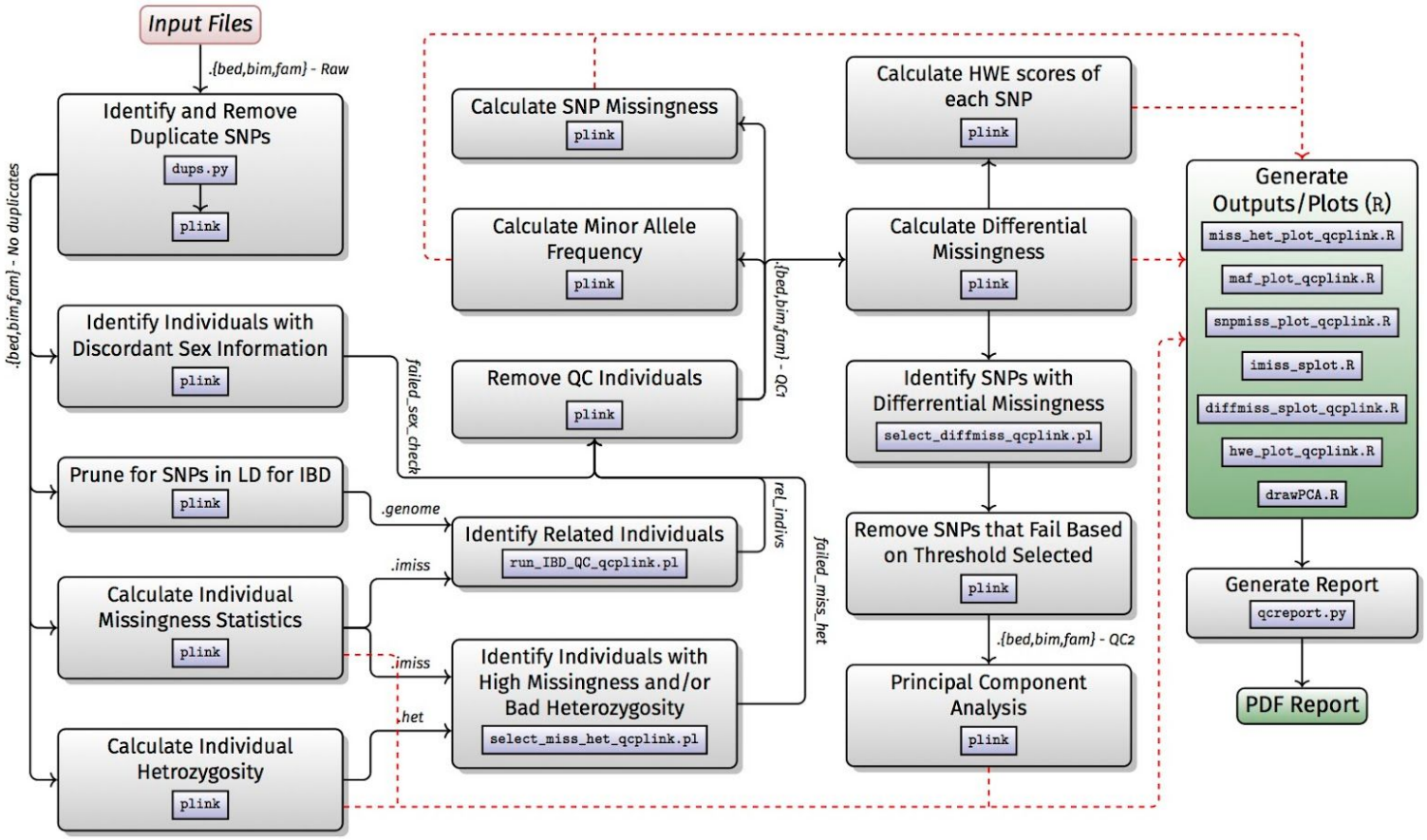
- Convert from Illumina calls to PLINK format
- Quality control: PLINK to PLINK
- GWAS

- SNP, individual missingness
- heterozygosity (individual, SNP)
- relatedness
- case-control differences
- basic PCA

Workflows very portable

Used

- local computer (with or without Docker)
- local cluster (with or without Docker)
- Amazon EC2 AMI
- Docker Swarm
- OpenNebula (NCSA, ARC)



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Imputation

Developed in Nextflow

- Assume genotype data as input
- Converted to Impute format
- Chromosomes split
- Check for correct strandedness
- Pre-phased using Shapeit
- Use IMPUTE2 to do imputation
- Recombine dataa

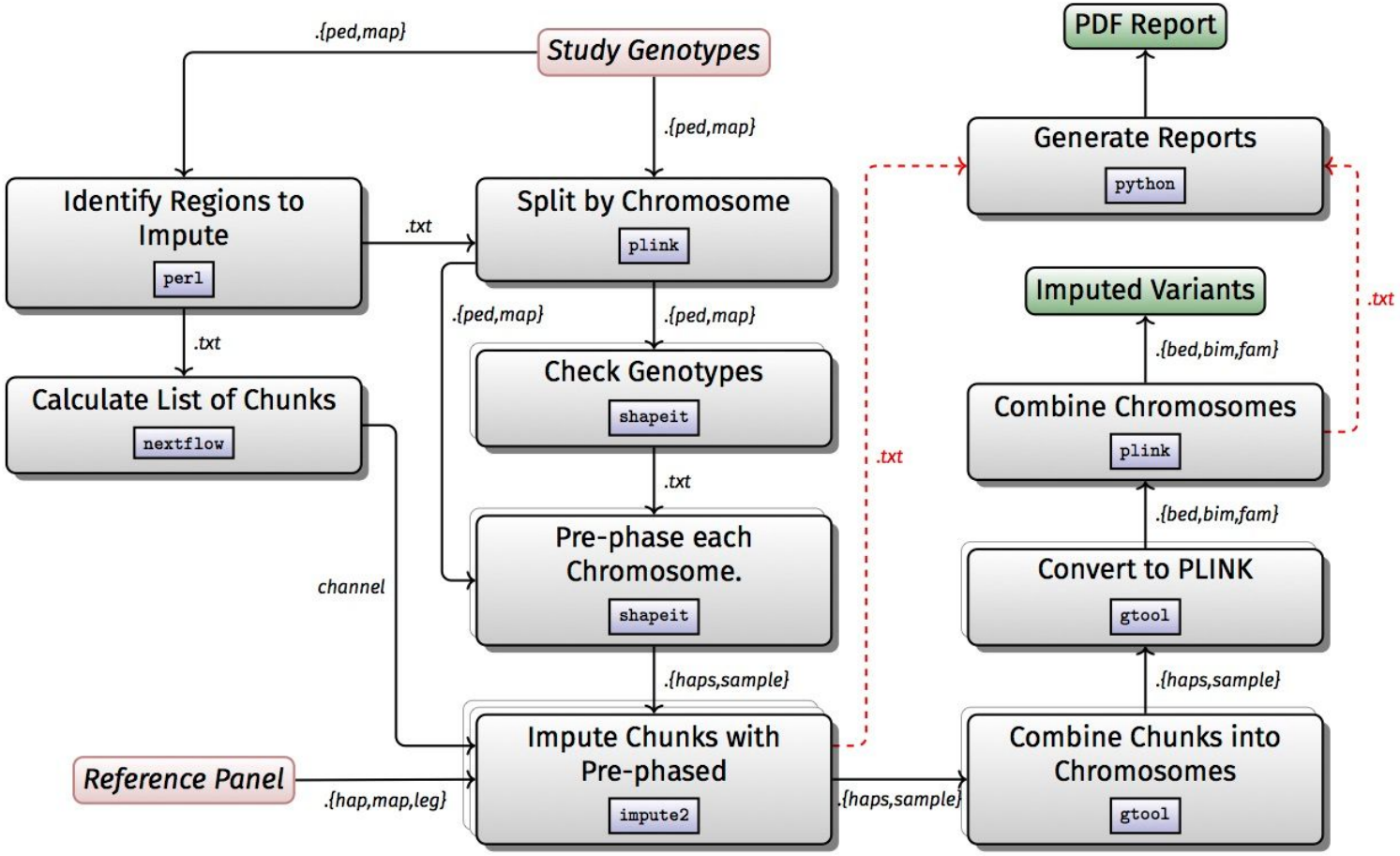

Figure 4 - Workflow D: SNPs Imputation

Experiences

Both Nextflow and CWL worked well

- Both have responsive communities
- ?? Nextflow has an easier learning curve
- ?? When we started Nextlow was maturer
- ?? may be momentum behind CWL.
- ?? CWL may have an advantage in packaging workflows

Future work

1. Extend, maintain existing pipelines
2. Rigorous comparison
3. Develop new pipelines – major set of activities for the next five years
4. Look at other systems, e.g., JMS

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