UK CYVERSE™

CyVerse UK: widening the scope to the UK and beyond

- Bringing CyVerse to the UK
- UK CyberInfrastructure
- Collaborations

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Decoding Living Systems

UK CYVERSE™

CyVerse UK is the first European instance of CyVerse

Funded by the BBSRC funding agency as a pilot project in 2015

The project hardware and devops staff are hosted at the Earlham Institute

BBSRC bioscience for the future

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UK CYVERSE™

Main purposes of the project are:

- give research groups access to life science cyberinfrastructure in the UK
- allow the analysis of data on UK-provisioned research HPC
- ensure reproducibility of analysis through application versioning / containerisation
- support data sharing
- distribute documentation and code as open source

CyVerse UK aims to give UK and EU users a geographical advantage, though it is available to users worldwide.

BBSRC
bioscience for the future

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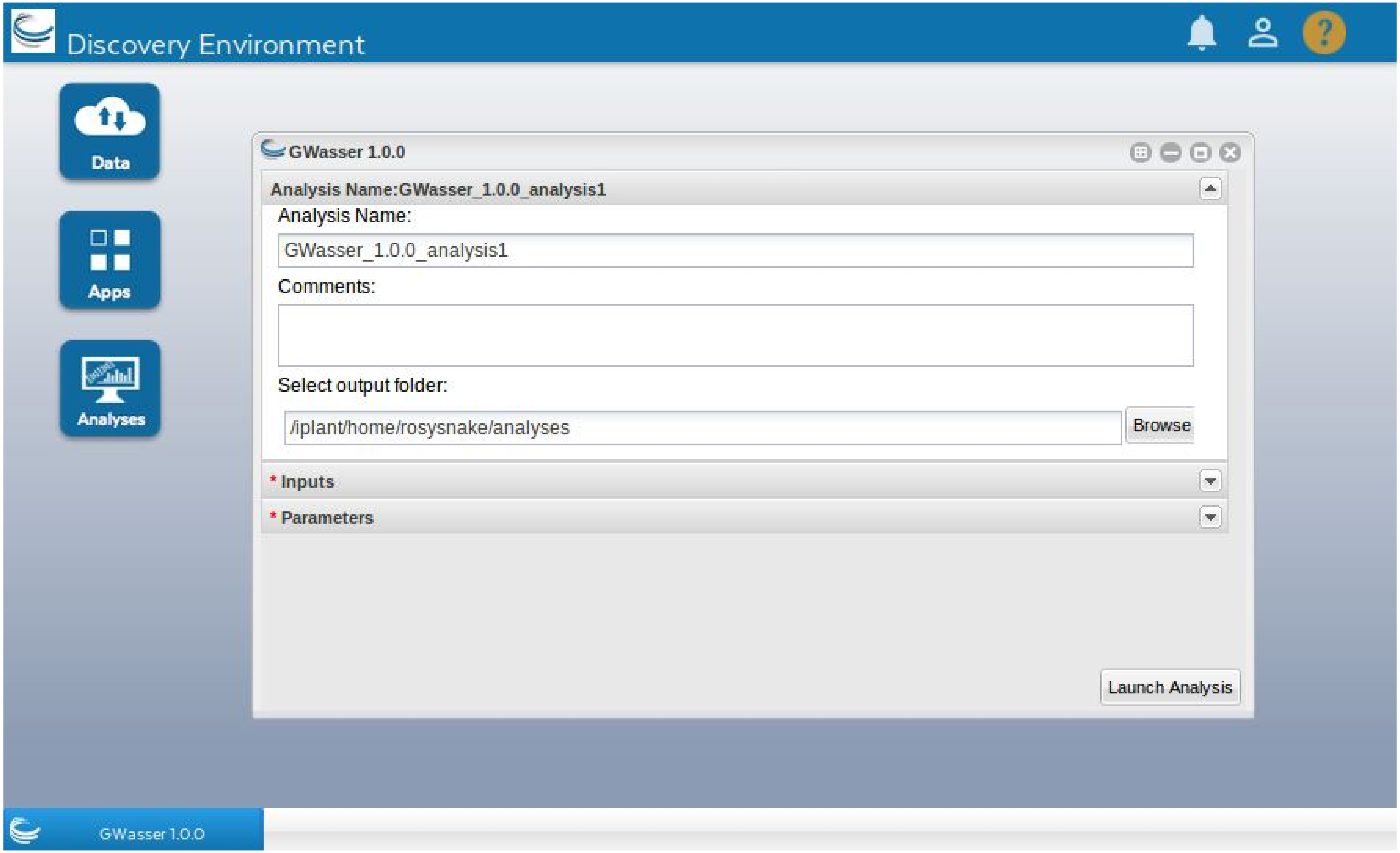
CyVerseUK Apps

- BAM to Fastq
- Beast 2.4.3 (with Beagle) on CyverseUK
- Blastn
- Blastp
- Bowtie2
- Btrim 0.3.0
- Concatenate multiple files
- CoverageBED
- Create Blast Database
- Cuffdiff up to 16 conditions
- Cufflinks
- Cuffmerge
- Cut columns
- Cutadapt SE
- GWasser-1.0.0
- Index BAM and get stats
- Index BAM file
- Index FASTA file (faidx)
- Kallisto v0.43.0
- MUSCLE
- Mikado-1.0.0
- MikadoCompare-1.0.0
- MikadoUtil-1.0.0
- MrBayes 3.2.6 (parallel) on CyverseUK
- Ontologizer 2.1
- Portcullis-1.0.0
- RAxML on CyverseUK
- Retrieve-Brassica-Phenotypes
- SAM to sorted BAM
- Sickle PE
- Sickle SE
- Sort BAM
- TopHat2 PE
- TopHat2 SE
- Tuxedo suite PE up to 4 conditions
- Uncompress files with gunzip

BUT… applications need to be duplicated to be run both in the US and in the UK.

User interfaces



Analysis Name:GWasser_1.0.0_analysis1

Analysis Name: GWasser_1.0.0_analysis1

Comments:

Select output folder: /iplant/home/rosysnake/analyses

* Inputs

* Parameters

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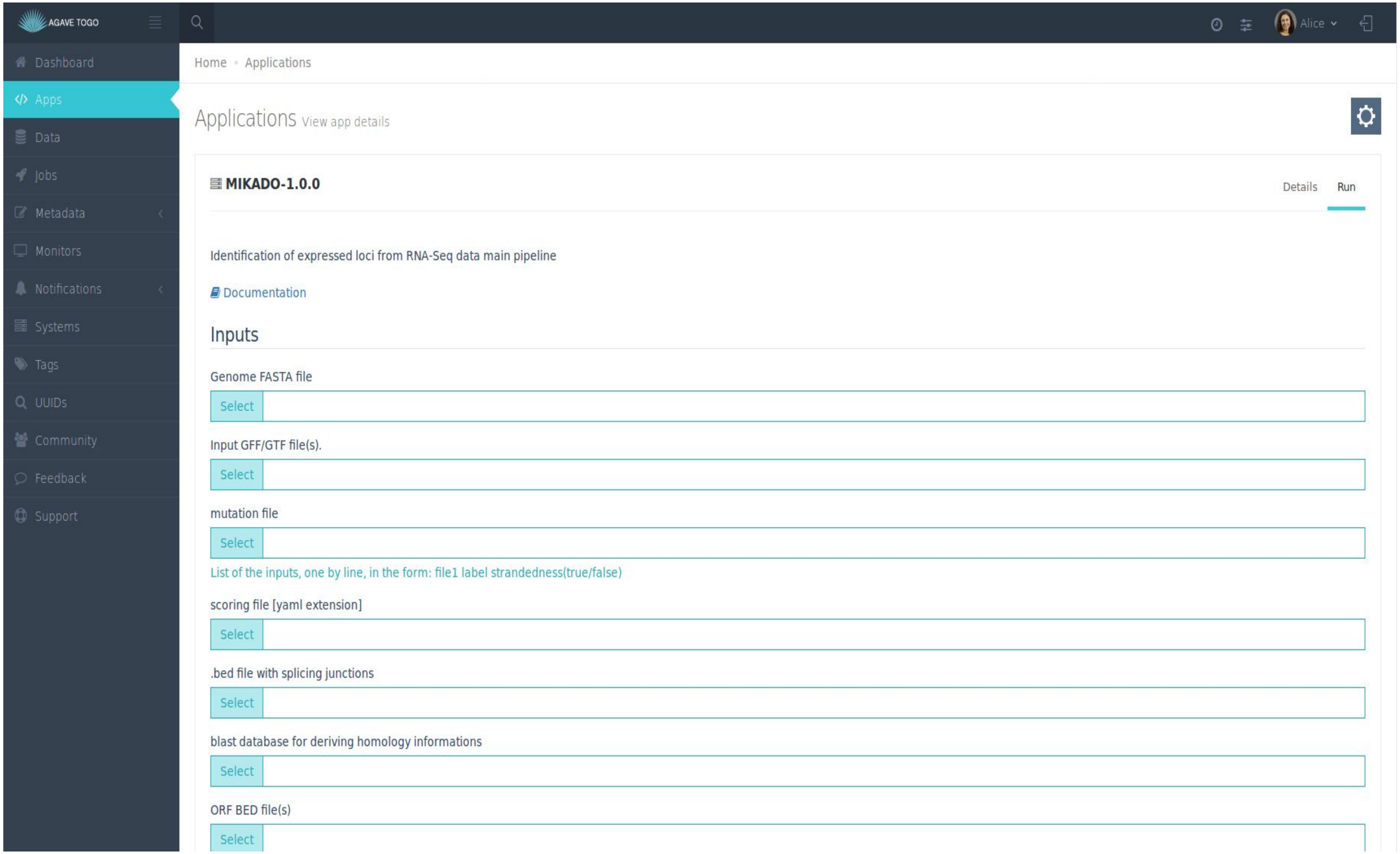
User interfaces



Applications View app details

MIKADO-1.0.0

Identification of expressed loci from RNA-Seq data main pipeline

Documentation

Inputs

Genome FASTA file

Select

Input GFF/GTF file(s).

Select

mutation file

Select

List of the inputs, one by line, in the form: file1 label strandedness(true/false)

scoring file [yaml extension]

Select

.bed file with splicing junctions

Select

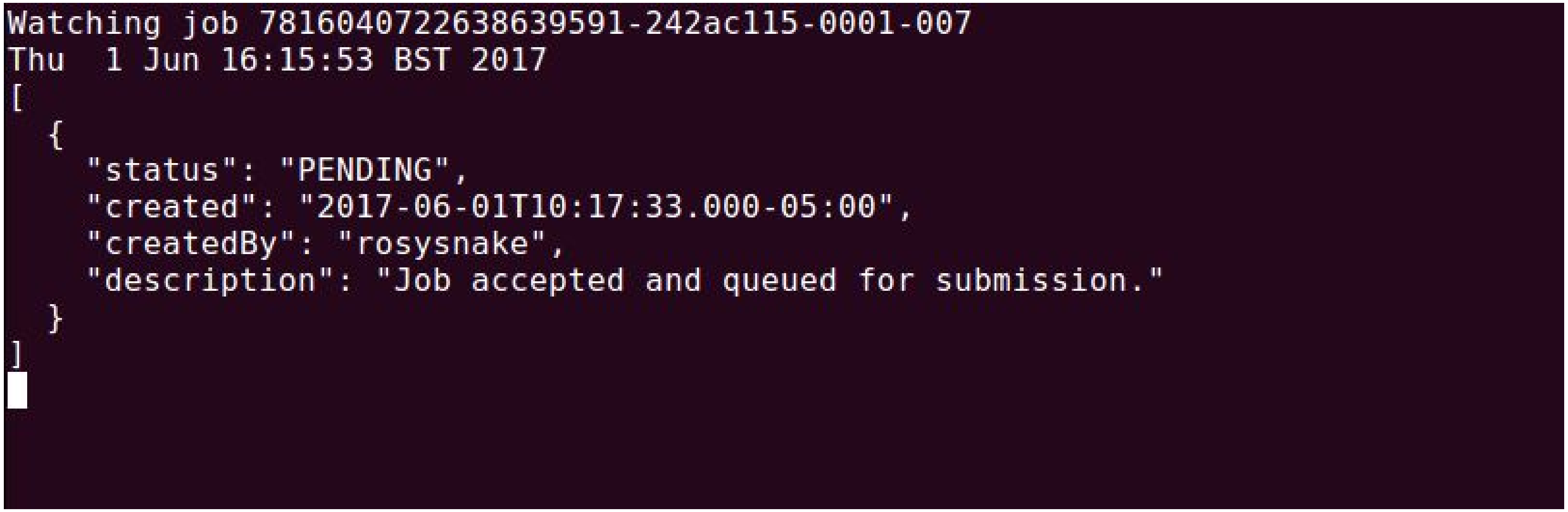
blast database for deriving homology informations

Select

ORF BED file(s)

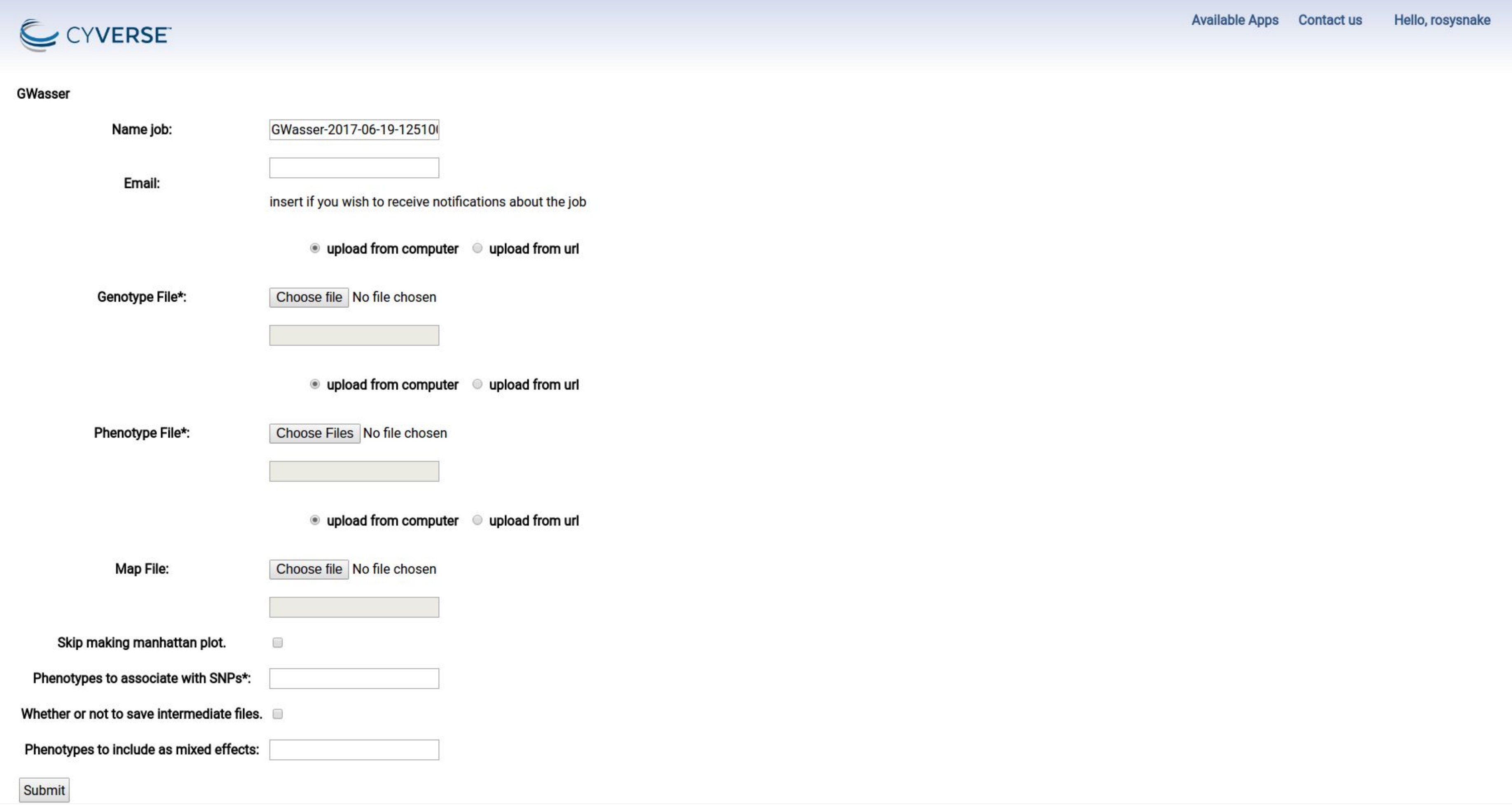
Select

User interfaces



```
Watching job 7816040722638639591-242ac115-0001-007
Thu  1 Jun 16:15:53 BST 2017
[
  {
    "status": "PENDING",
    "created": "2017-06-01T10:17:33.000-05:00",
    "createdBy": "rosysnake",
    "description": "Job accepted and queued for submission."
  }
]
```

User interfaces



GWasser

Name job:	GWasser-2017-06-19-12510(
Email:	insert if you wish to receive notifications about the job
	● upload from computer ○ upload from url
Genotype File*:	Choose file No file chosen
	● upload from computer ○ upload from url
Phenotype File*:	Choose Files No file chosen
	● upload from computer ○ upload from url
Map File:	Choose file No file chosen
Skip making manhattan plot.	☐
Phenotypes to associate with SNPs*:	
Whether or not to save intermediate files.	☐
Phenotypes to include as mixed effects:	

The infrastructure

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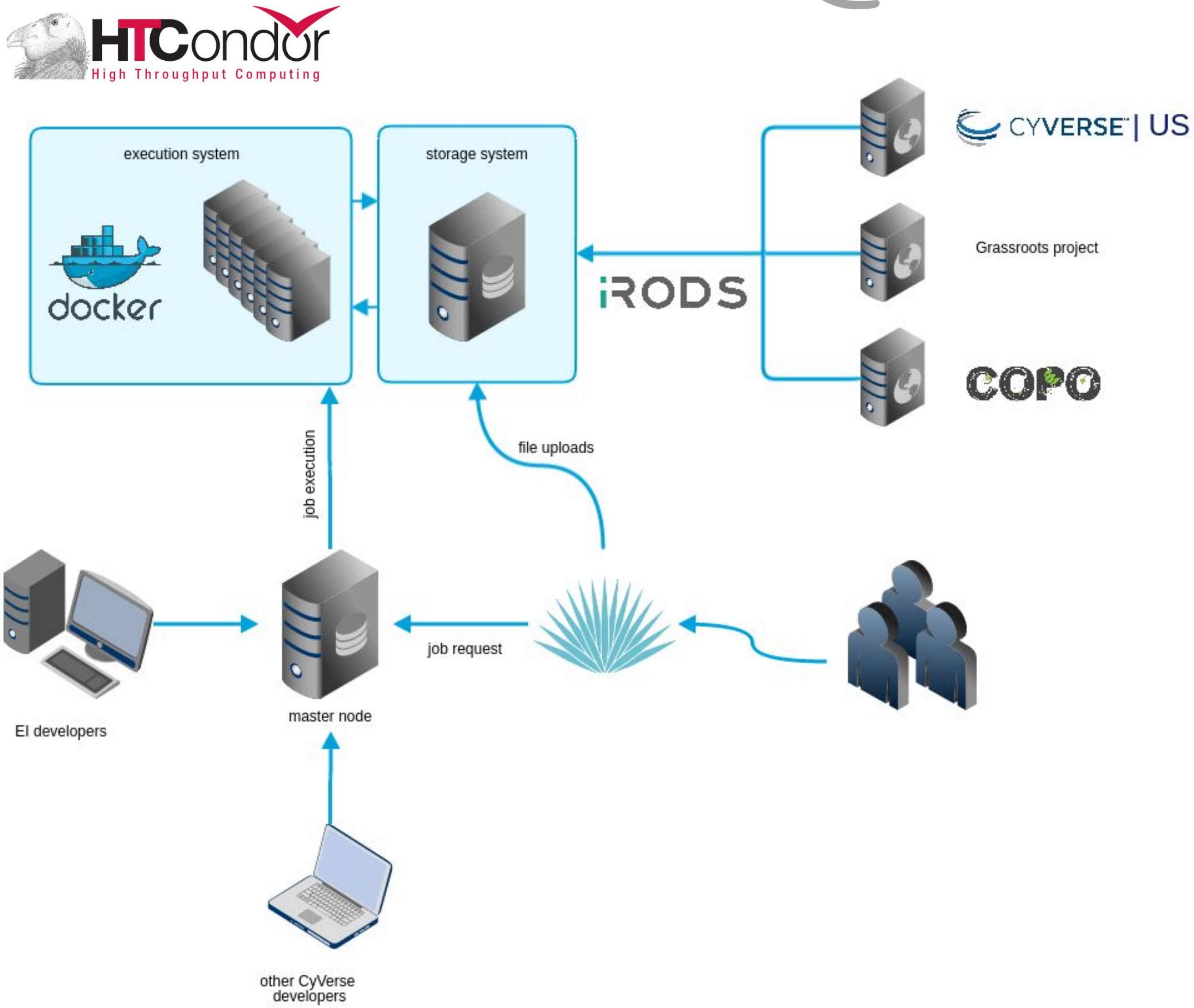

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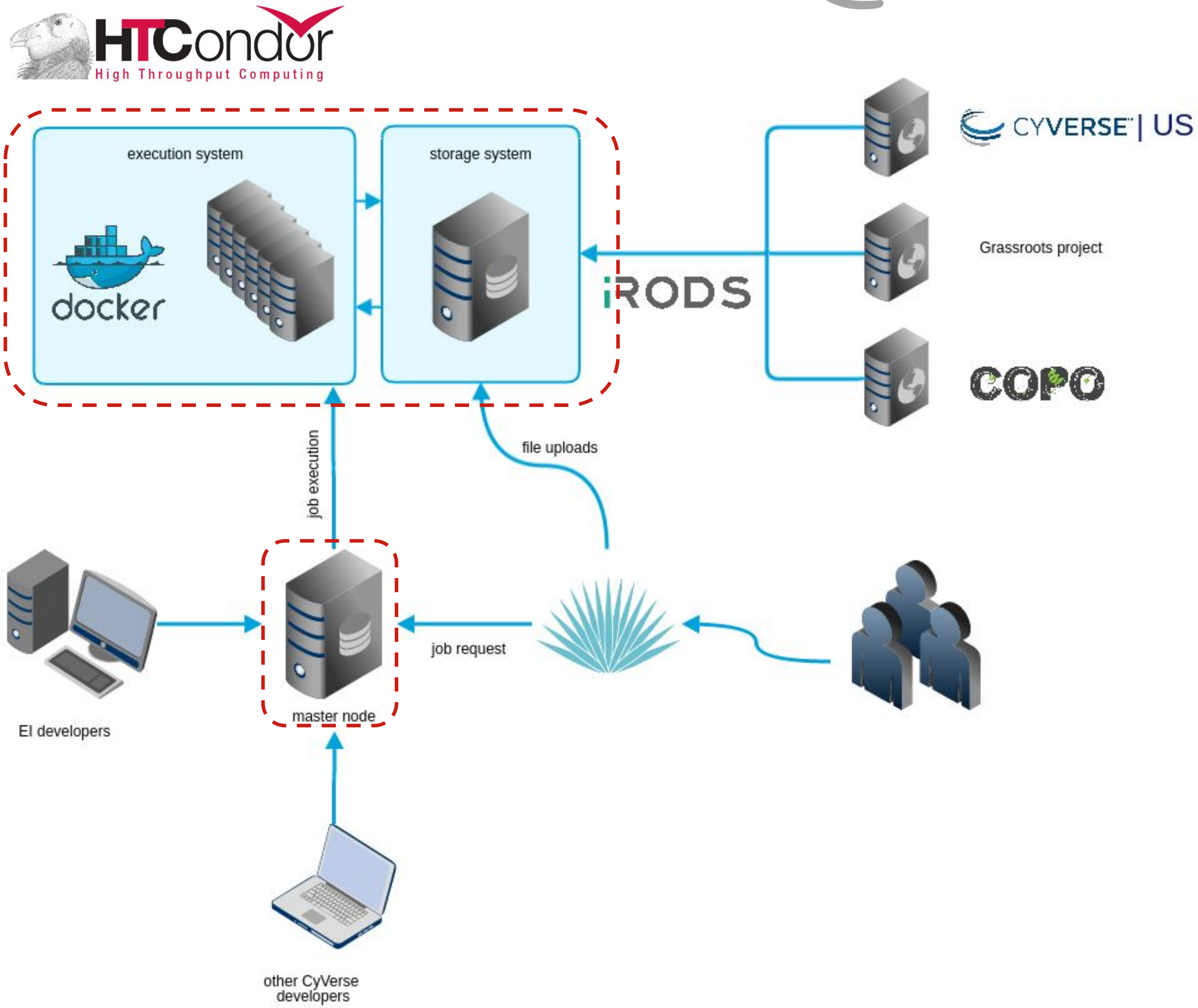

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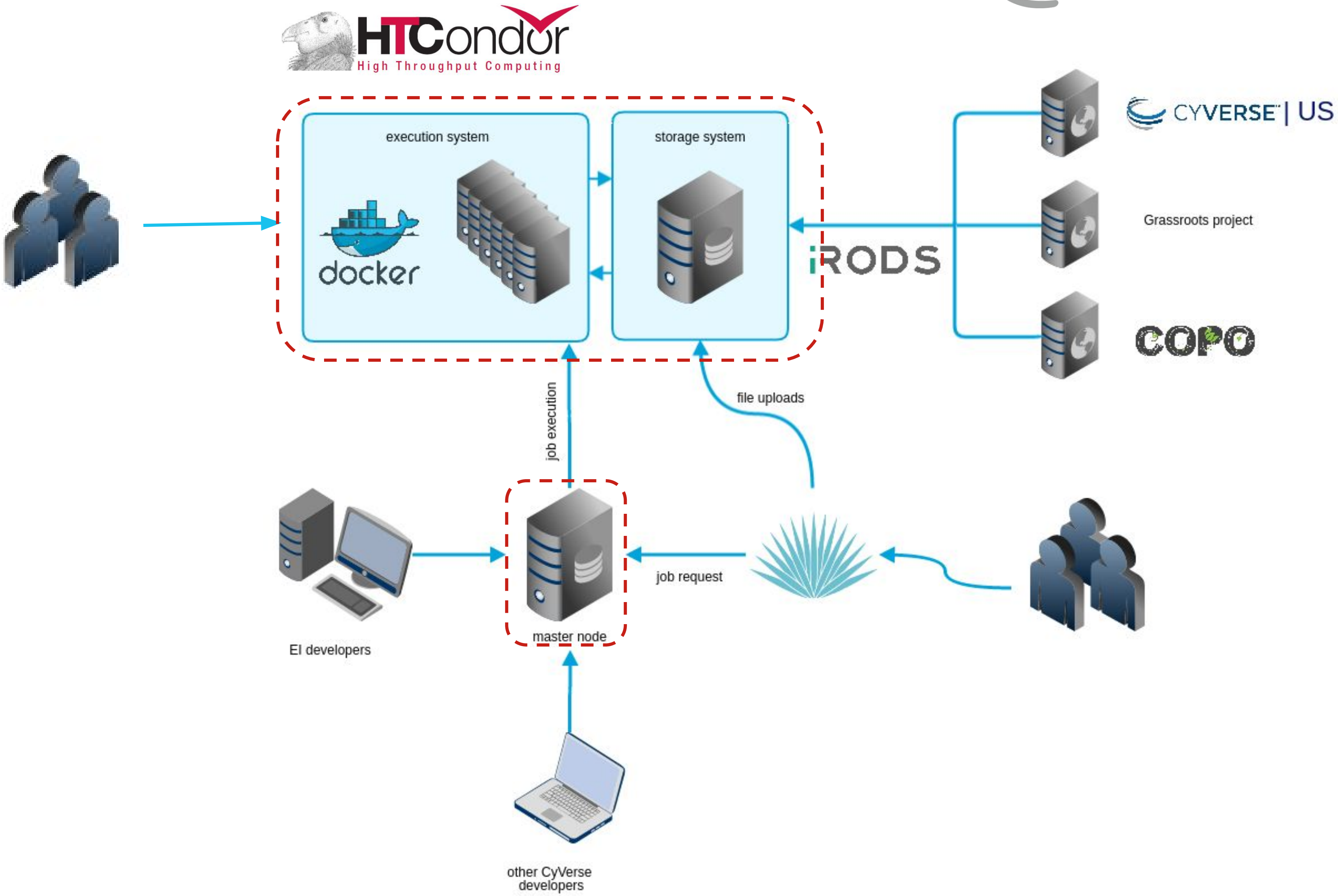

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“Docker is the world’s leading software containerisation platform.”

- Wrap a piece of software in a self-contained package
- Contains everything needed to run: code, runtime, system tools, system libraries
- Small portable server
- Software will always run the same, regardless of where it is run

The infrastructure

Work in Progress and Future Developments

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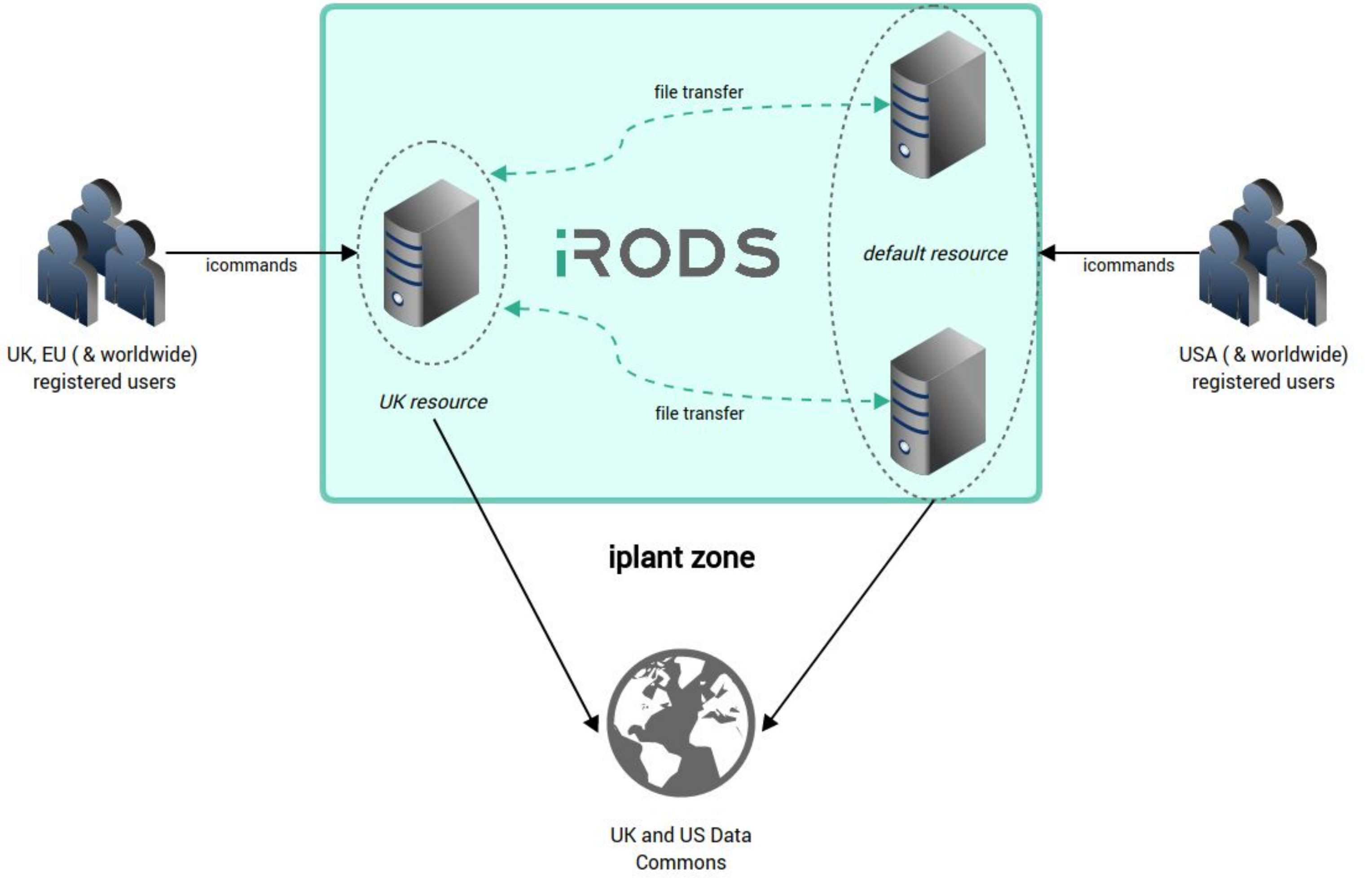
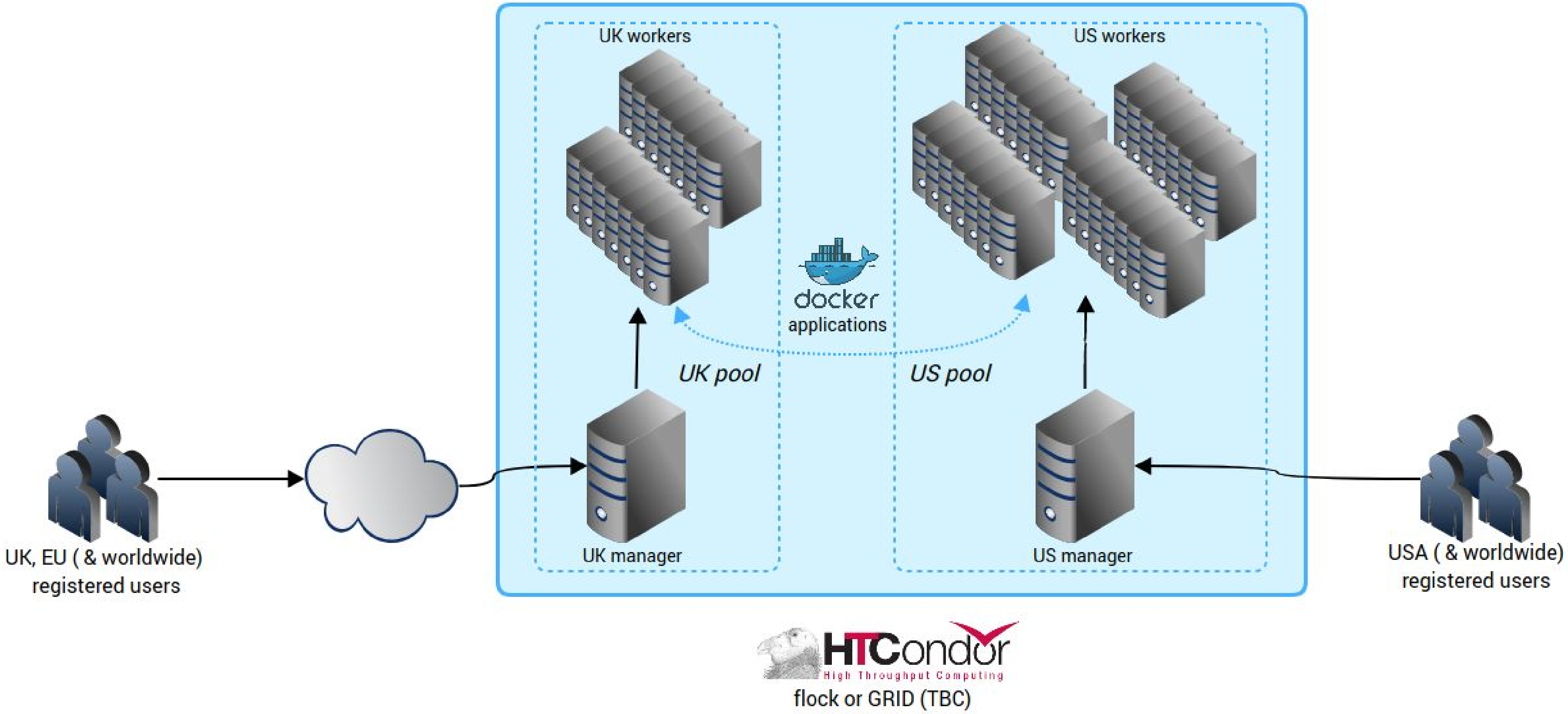
iRODS Storage Federation



HTCondor Federation

- Federation between US/UK HTCondor pools
  - Users grouped by location
  - User interface stays the same



- Agave application to become DE Docker application
  - **Enable shared applications between UK and US**

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Collaborations

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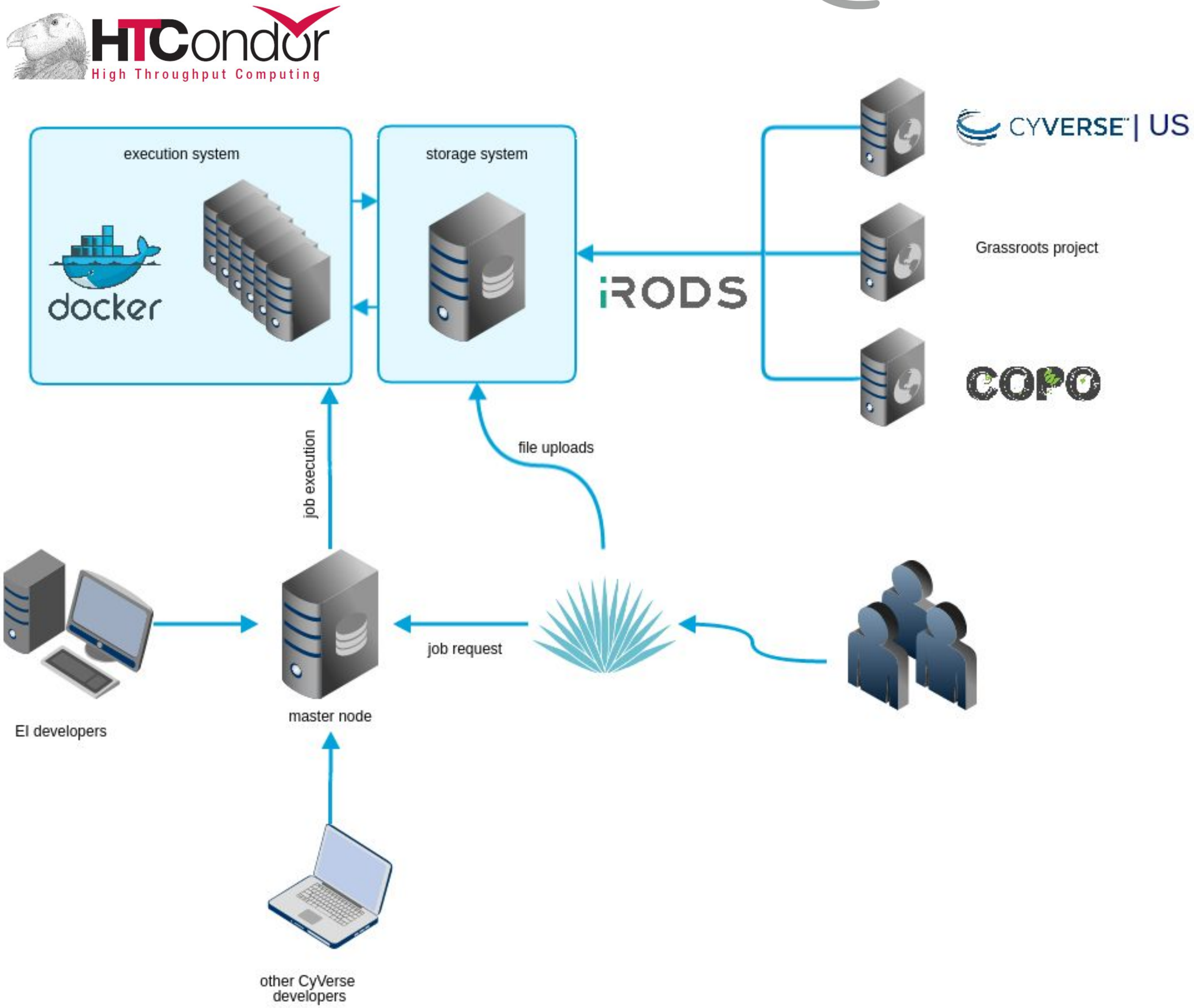

HTCondor
High Throughput Computing

execution system

docker

storage system

iRODS

CYVERSE™ | US

Grassroots project

COPO

job execution

file uploads

EI developers

master node

job request

other CyVerse developers

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Expansion and Community Support

Won a £400k BBSRC 16ALERT grant to expand the compute capacity of CyVerse UK

- Larger core count and RAM
- Better networking and switching
- Project-initiated VM requests to provide specific groups with cloud access
- Planning to include flexible analysis frontends such as the Genomics Virtual Laboratory

?

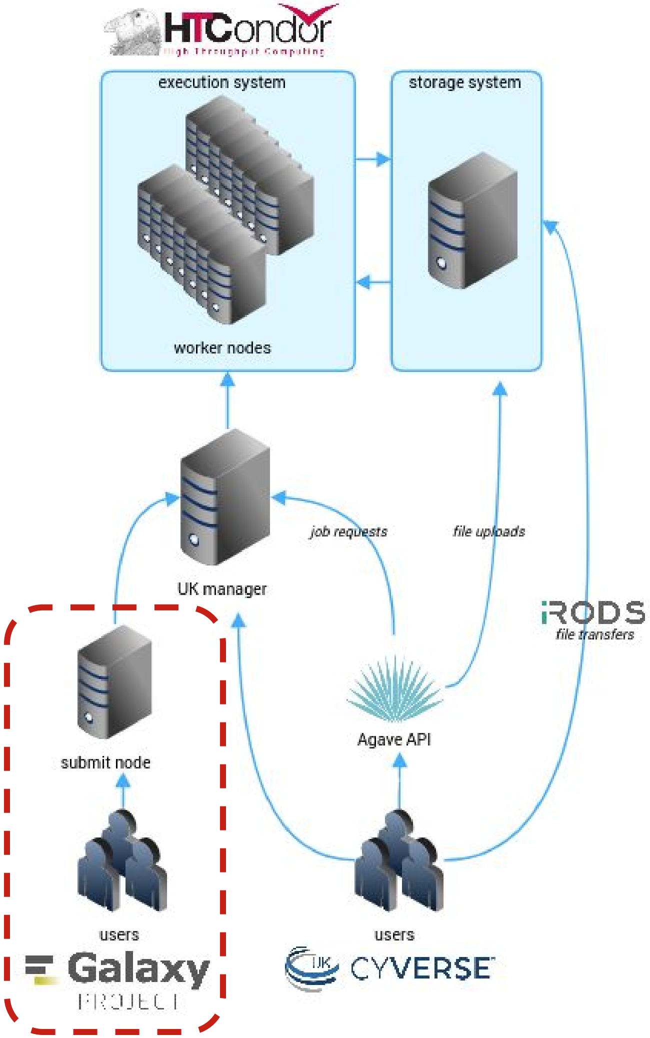
- Now providing webservice VMs to:
    - SignaLink
    - COPO
    - Grassroots

Galaxy Integration

Set up a pilot Galaxy integration project to demonstrate service provision

Users at BecA-ILRI in Nairobi, Kenya can submit Galaxy jobs to the CyVerse UK execution system:

- taking advantage of the CyVerse UK infrastructure
- Researchers can share and analyse data already available in the storage system (upload once)
- Reduces need for hardware on-site, and can promote collaboration
- Helps us understand limitations of intercontinental internet



CYVERSE™

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