ZORBAS: the HPC cluster for biological analysis in IMBBC, HCMR

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Availability: http://hpc.hcmr.gr/
Keywords: HPC, HTS, NGS, workflows, environmental -omics, non-model organisms
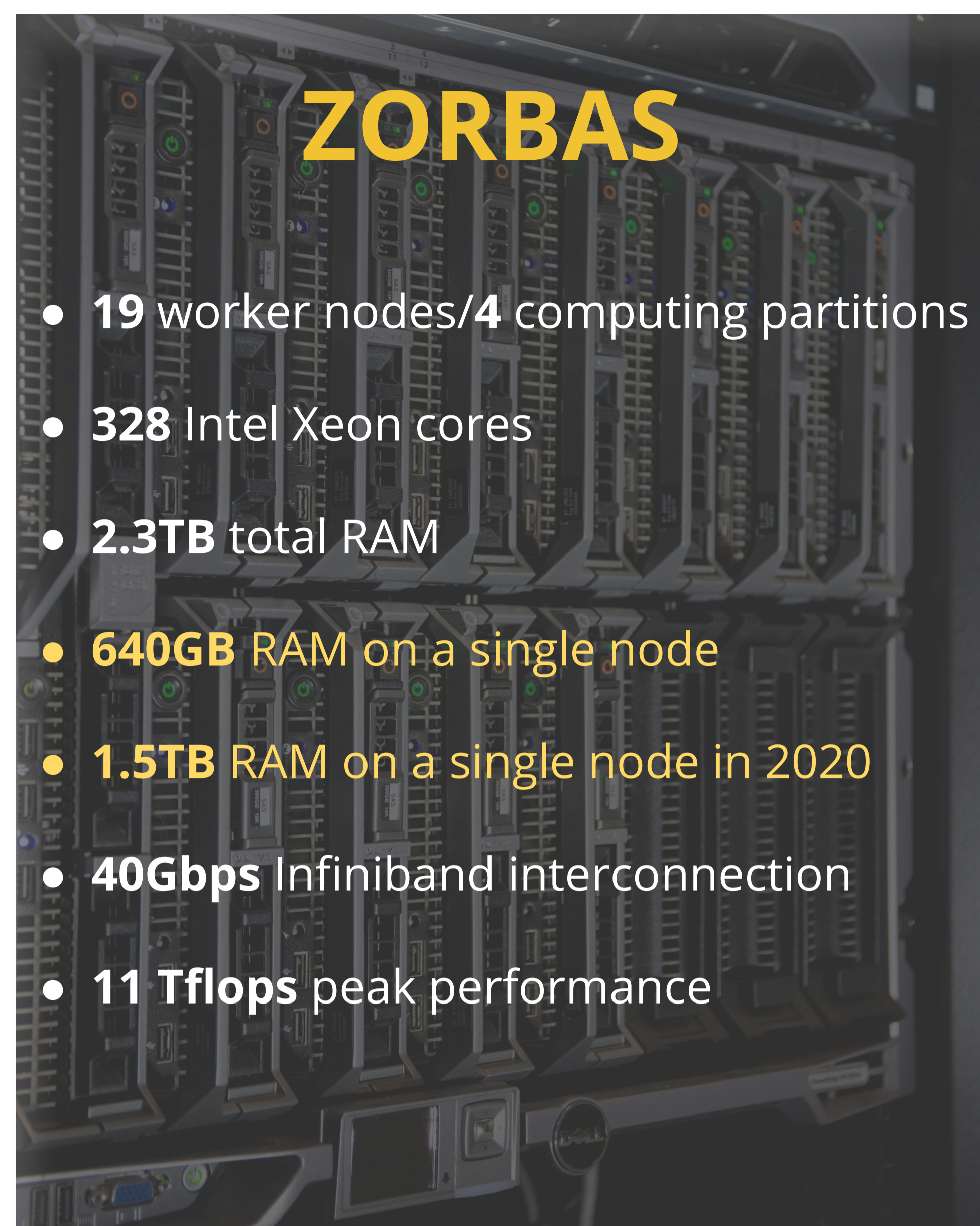
Website   Access

Contact: helpdesk-hpc@hcmr.gr

Description

Zorbas is a High Performance Computing (HPC) system, dedicated to bioinformatics applications for non-model species and ecological data analysis

Software

- More than 200 state-of-the-art software suites support on-model organism next-generation sequencing data, environmental -omics, large-scale ecology, as well as biodiversity data analyses.
- Emphasis on pipeline parallelization and containerization (mainly Singularity-based).

ZORBAS

- **19** worker nodes/**4** computing partitions
- **328** Intel Xeon cores
- **2.3TB** total RAM
- **640GB** RAM on a single node
- **1.5TB** RAM on a single node in 2020
- **40Gbps** Infiniband interconnection
- **11 Tflops** peak performance
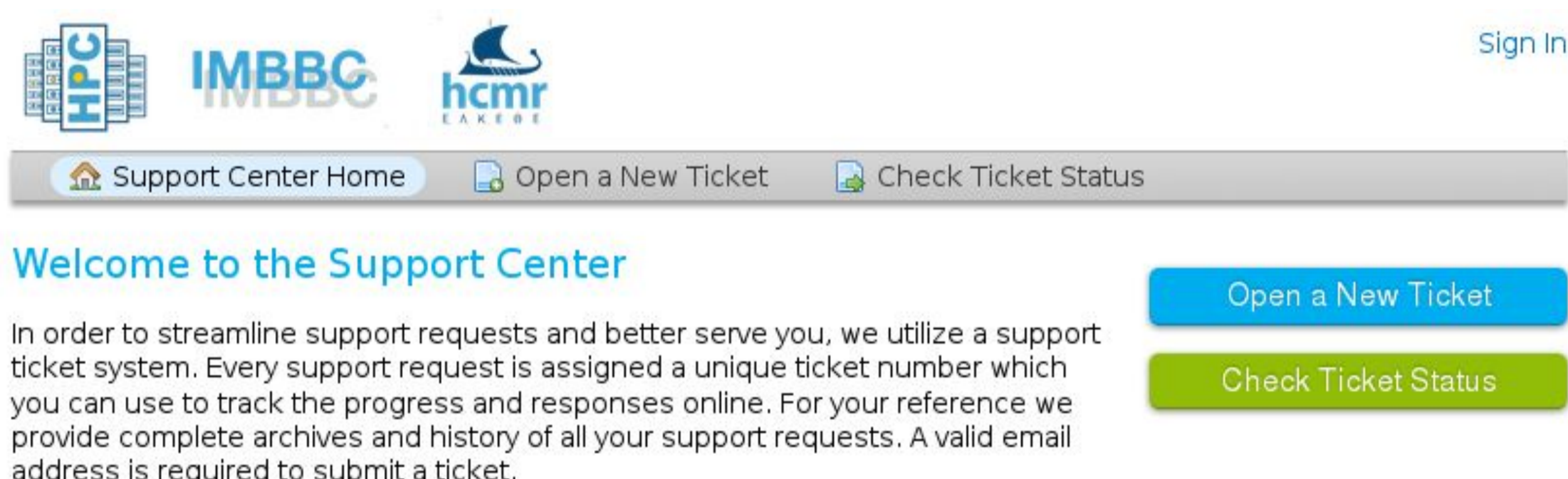
Applications/Analyses

- Read pre-preprocessing
- De novo assembly
- Gene annotation
- Variant discovery
- Mapping
- Differential expression
- Orthology analysis
- Phylogenomics
- Population genomics
- Metabarcoding
- Biodiversity index calculation
- Ecological data analysis

Usage/Services

- **> 50 users** (Greece, Italy, Spain etc)
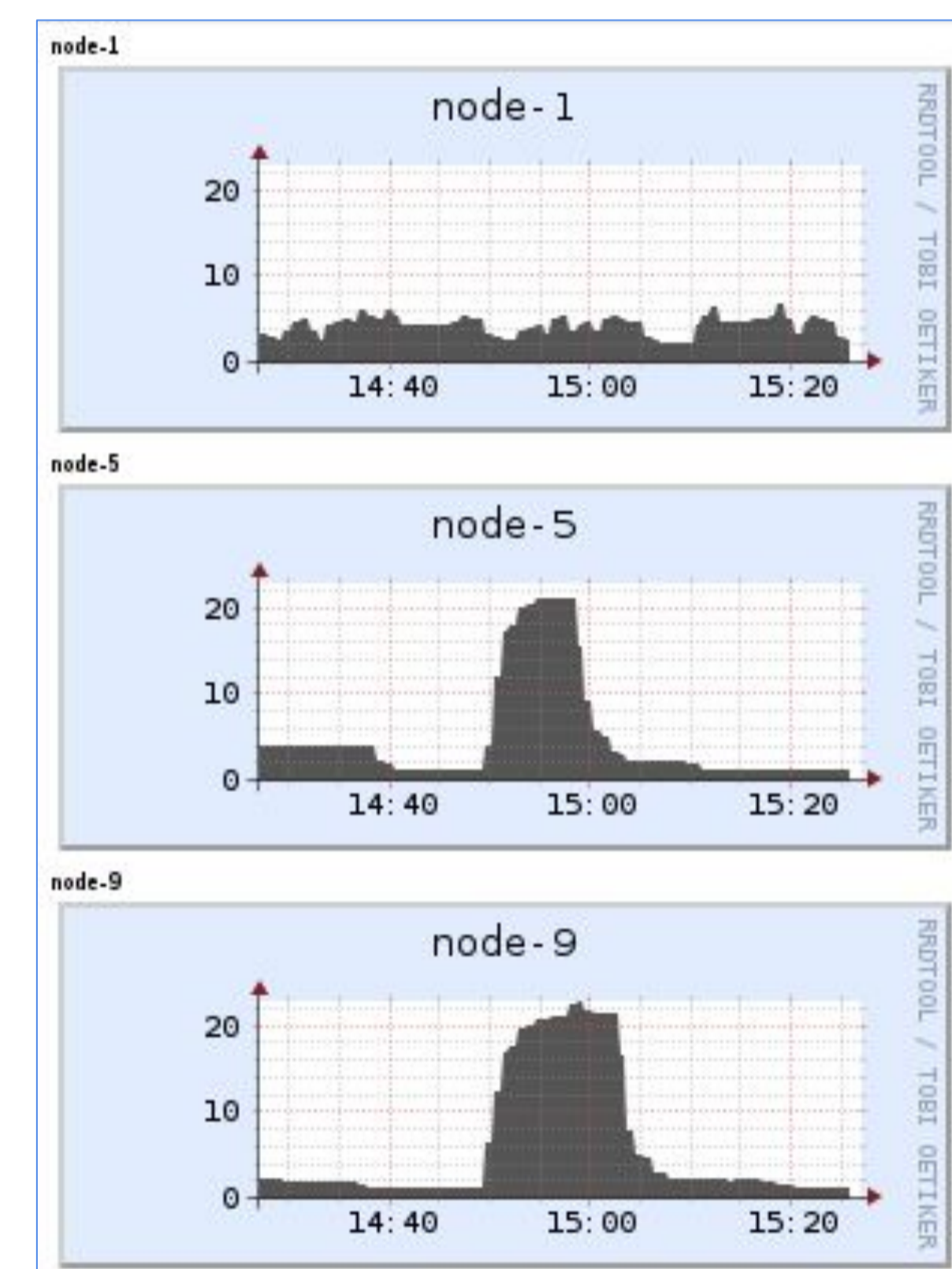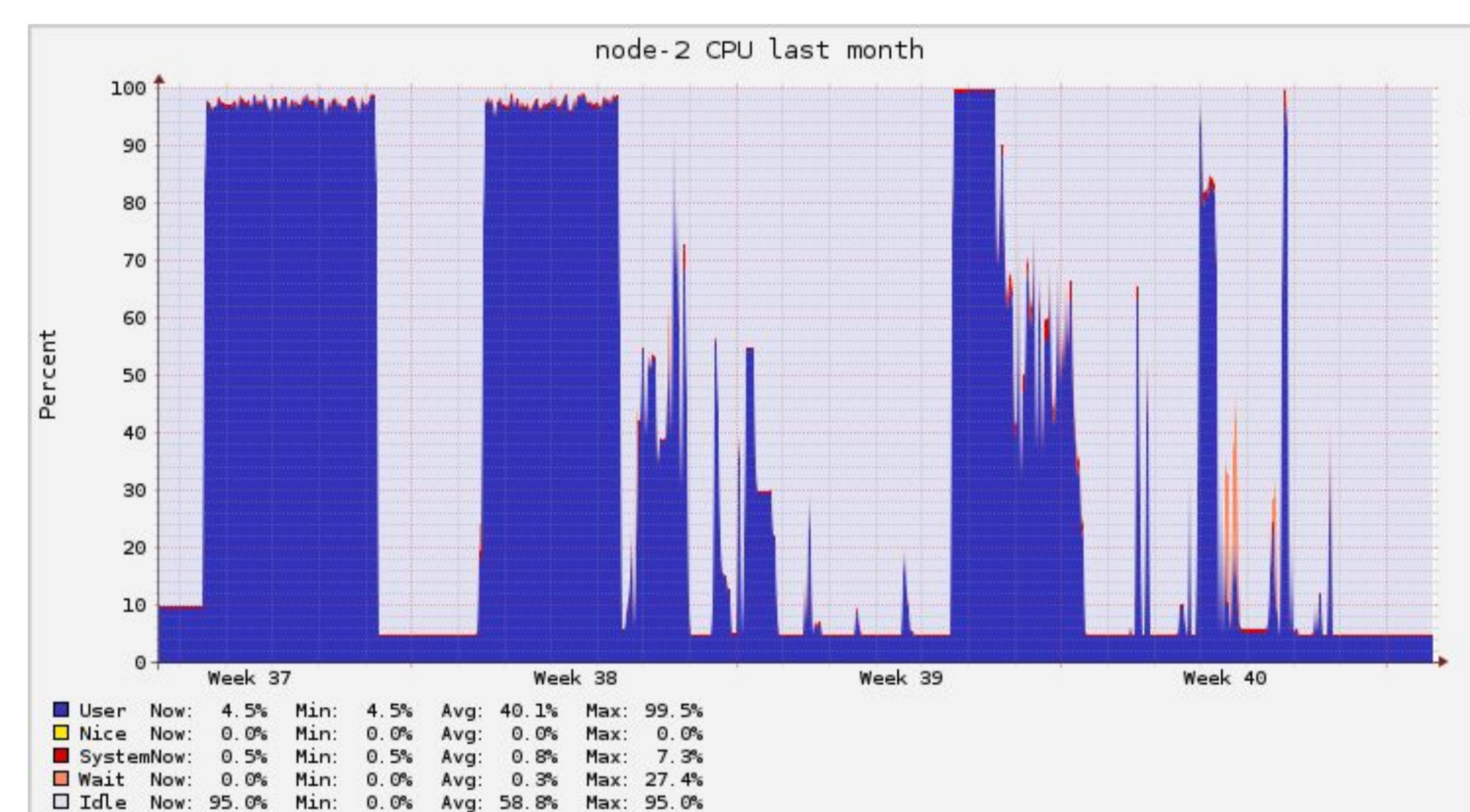- **2** hpc system administrators
- **~20000** submitted jobs in 2019
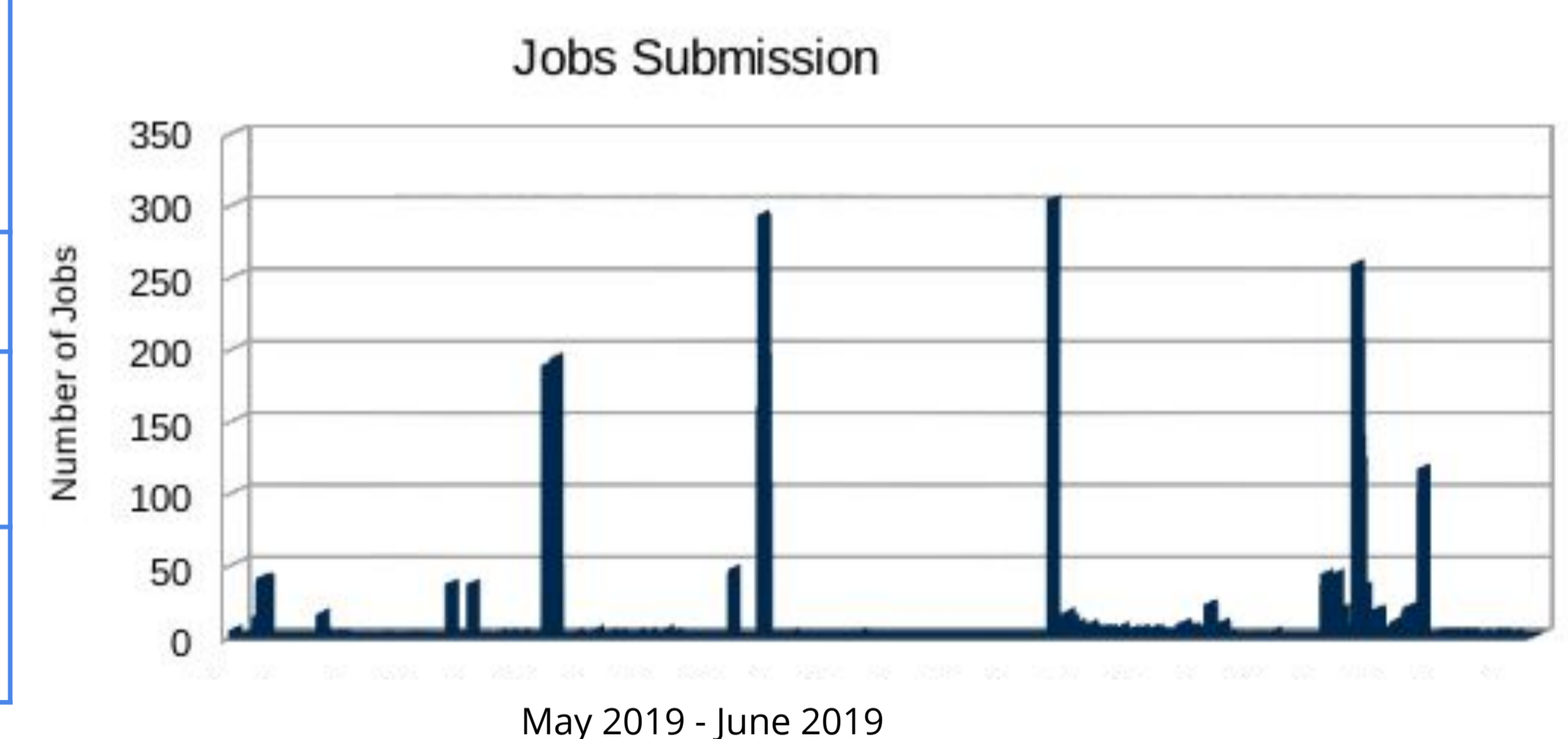
Helpdesk Site

Resources Monitoring Site

2019 Memory Utilization Distribution	Number of Jobs
<20 GB	18330
>=20 GB and <100GB	184
>=100GB and <=640GB	34

Jobs Submission

May 2019 - June 2019

node-2 CPU last month

Ongoing Collaborations

Ongoing collaborations with the LifeWatch ERIC, EMBRC ERIC, and the ELIXIR Research Infrastructures aim at sharing resources and accumulated expertise to the broader pertinent Hellenic and European bioinformatics and biology communities.

Funding

IMBBC
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hcmr ΕΛΚΕΘΕ   MARBIGEN   CMBR   LifeWatch GREECE   NSRF 2014-2020 programme for development   IMBBC HPC