

# NDGF approach to serve the **non-LHC** **communities needs**: Material Science VO

Ivan Degtyarenko, D.Sc. (Tech)

NDGF

CSC – IT Center for Scientific Computing  
Espoo, Finland



## Because of LHC

the **European Grid** exists because of **LHC**, it has been designed in order to serve **LHC needs**

NDGF: BIO and CO2 CPU time consumption < 1%

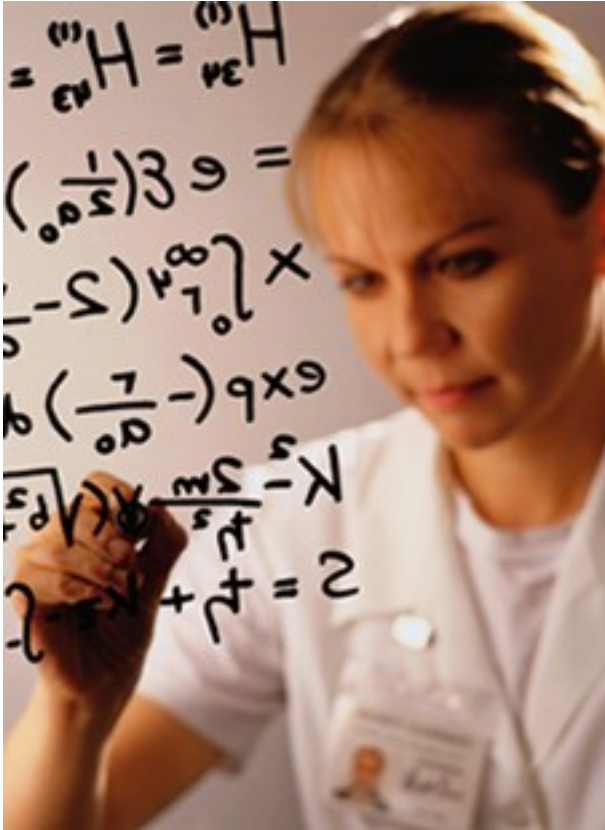
EGEE: of 190 active VOs, 42 are HEP and consume over 90% of the CPU and storage resources

a lot of **data** and short time **serial jobs**

Source: NDGF 2009 Quaterly reports, EGEE accounting portal



# Non-LHC communities



Who are they? What are they running? Where? What are their CPU and storage resource needs?

Why the vast majority of them do not care about grid interfaces?



# Material Science VO

The joint project **between NDGF and CSC** on **extending** the Finnish **Material Science VO** to a **Nordic countries level**.

- support of the **non-LHC** communities
- **not limited** to any particular field of science
- become a strong actor at the **European scale**



## Initial project goals

extend the VO resources, user experience and collaboration by **attracting new** computer centers and labs within Nordics

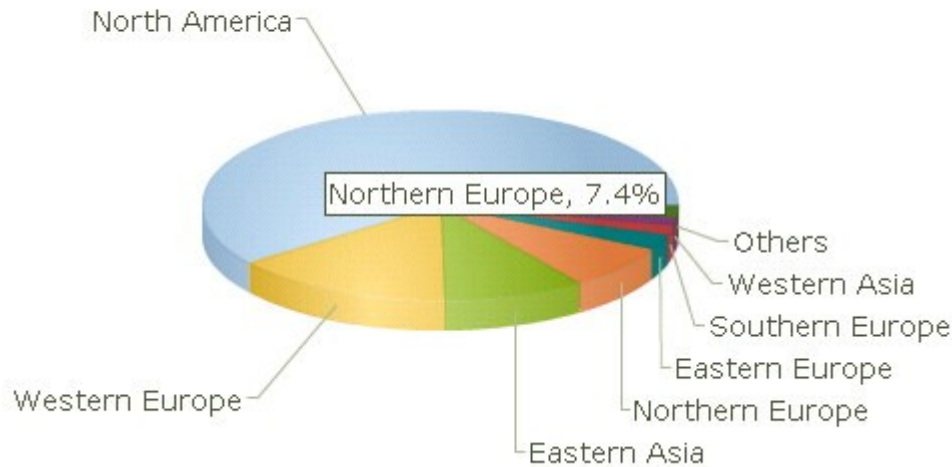
easily **expandable / shrinkable** system based on the **solid statistical numbers** and users preferences

- a number of **popular applications support** over all sites
- **MPI support** and impact on ARC development towards MPI environment support

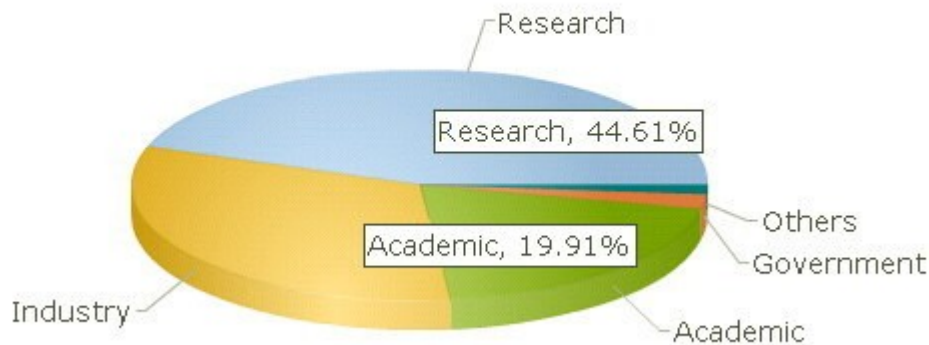


# Who?

Geographical Region / Performance  
November 2009



Segments / Performance  
November 2009



## Who are them?

computational scientists at universities, polytechnics and research institutions

by fields of science: bio-sciences (including drug design and structural analyzes), physics and chemistry (and corresponding nanosciences), astrophysics, fluid dynamics, economics, medical, environmental, social and earth sciences, mathematics and computer science, language research ... others where scientific computing has influenced



# What?

## NUMBER of JOBS

total	6213569
<b>serial</b>	4753250 ( <b>76.50%</b> )
parallel	1460319 (23.50%)
lam	56640 (3.88% of pe jobs)
mpich	888456 (60.84%)
mpich2	51152 (3.50%)
openmpi	349598 (23.94%)
mvapich	79519 (5.45%)
threaded	31385 (2.15%)

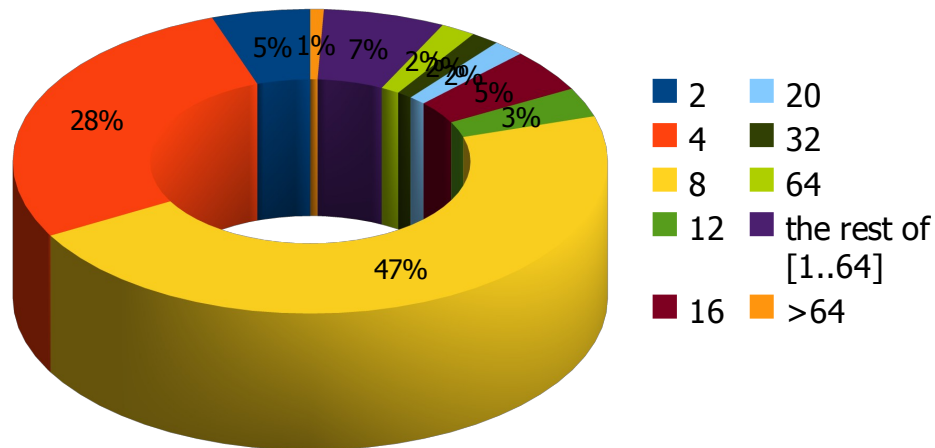
## WALLTIME (hours)

total	48920078
serial	9535418 (19.49%)
<b>parallel</b>	39384660 ( <b>80.51%</b> )
lam	2616030 (6.64% of pe jobs)
mpich	11557678 (29.35%)
mpich2	889372 (2.26%)
openmpi	11481871 (29.15%)
mvapich	12234506 (31.06%)
threaded	100057 (0.25%)

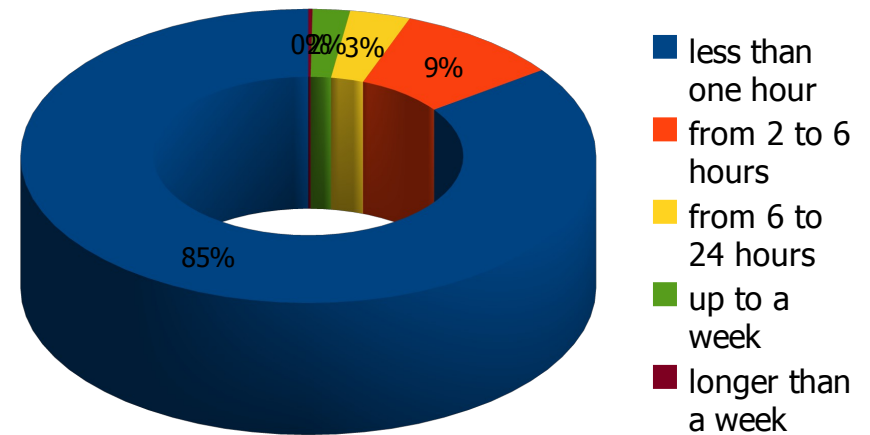


# Statistics: Finnish M-grid clusters

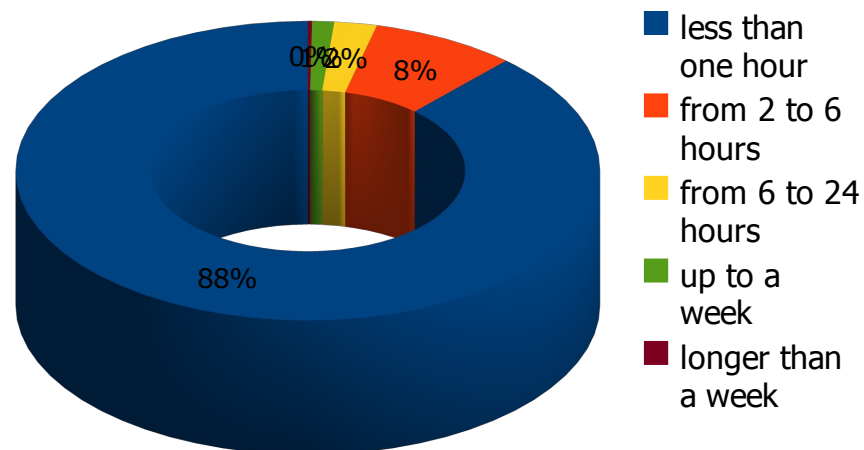
Use of CPU cores in parallel



Walltime distribution for parallel jobs



Walltime distribution for serial jobs

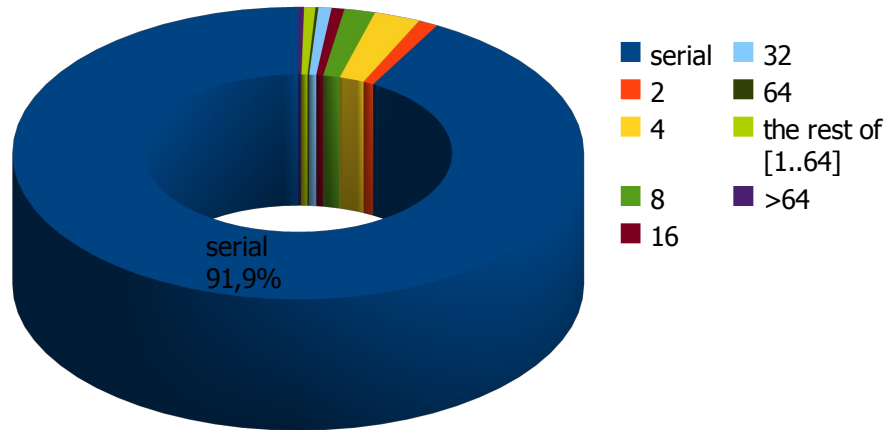




# Statistics: cluster at CSC

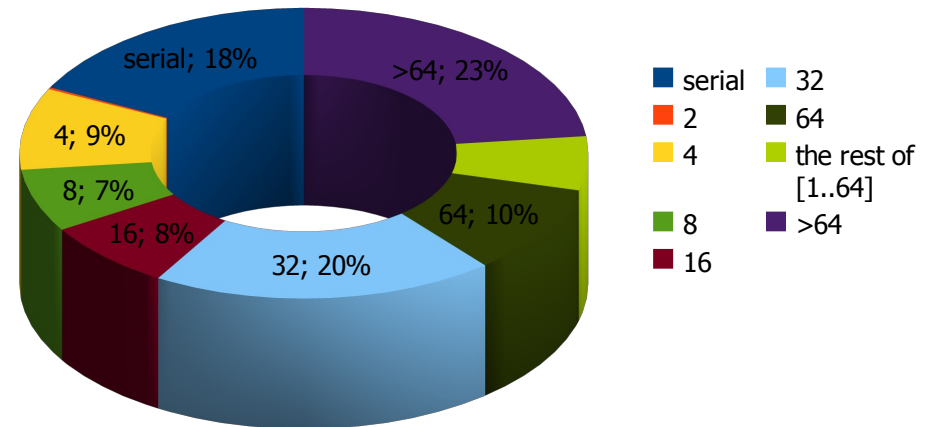
## Number of jobs distribution

total jobs number run on 1, 2, 4 ... 512 CPU cores



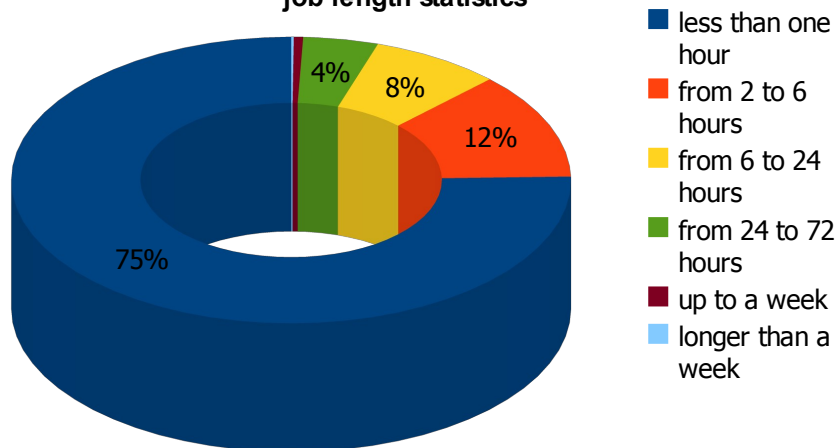
## CPU time consumption distribution

total CPU time consumed by 1, 2, 4 ... 512 CPU core jobs



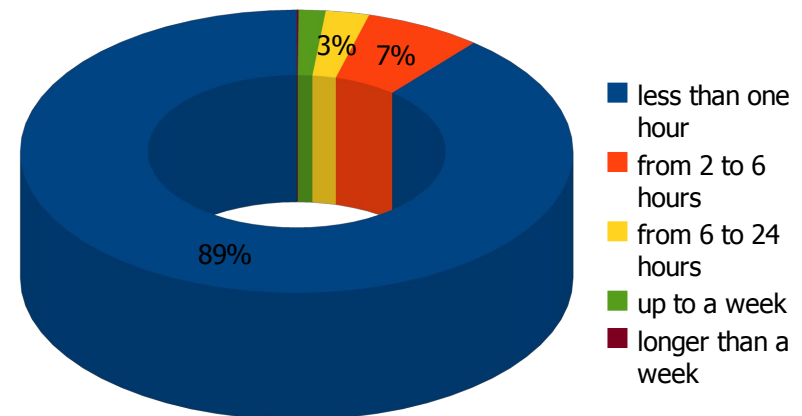
## parallel jobs walltime distribution

job length statistics



## serial jobs walltime distribution

job length statistics



## Runtime needs summary

majority of the jobs are:

no longer than **24 hours**

**serial** (in terms of job number)

**parallel** (in terms of CPU time)



## Type of applications

**a.out** (70%, another 30% are pre-installed apps)

Top list of pre-installed apps (Finland): GPAW, NAMD, Gromacs, TURBOMOLE, Gaussian, CPMD, ADF, BLAST, Elmer, Molpro, Dmol, NWChem

(Norway): WRF, VASP, ROMS, CCSM, EnKF, Dalton, Gaussian, ADF

Others?

Licensing: an obstacle or opportunity?



## MPI must be taken seriously

ability to run and compile MPI easily

OpenMPI: the default recommended flavor

ability to request the varying number of slots

ability to request logical CPUs within

one physical CPU only, or one WN

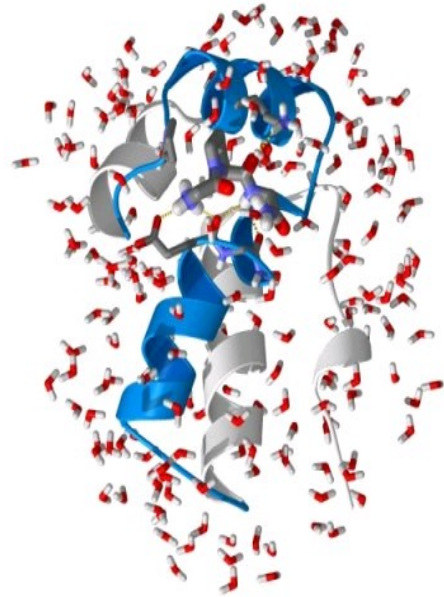
available memory per logical CPU

interconnecting choice

Others (?)



# Canonical use case



## Grid type of job

compile/install app (optional), prepare the application  
 input files, submit the job, fetch the results,  
 analyze&visualize

## canonical use case: Gromacs

description: classical molecular dynamics package,  
 widely used by biophysicists and other bio-scientists

input: a few files, ~megabytes

output: no limits, typically a few gigabytes

execution: may take a few hours or weeks, in serial,  
 parallel (typically), as an array jobs

analyzes&visualization: VMD, PyMol, gOpenMol



## General observations

batch system users are **the target auditory**

**make sure they know** about grid interface  
opportunity

the community of computational scientists must be  
a **driven force**, look for the critical mass

the **concrete user**, and not a user

**HPC** and not HTC

