

Laboratório  
Nacional de  
Computação  
Científica

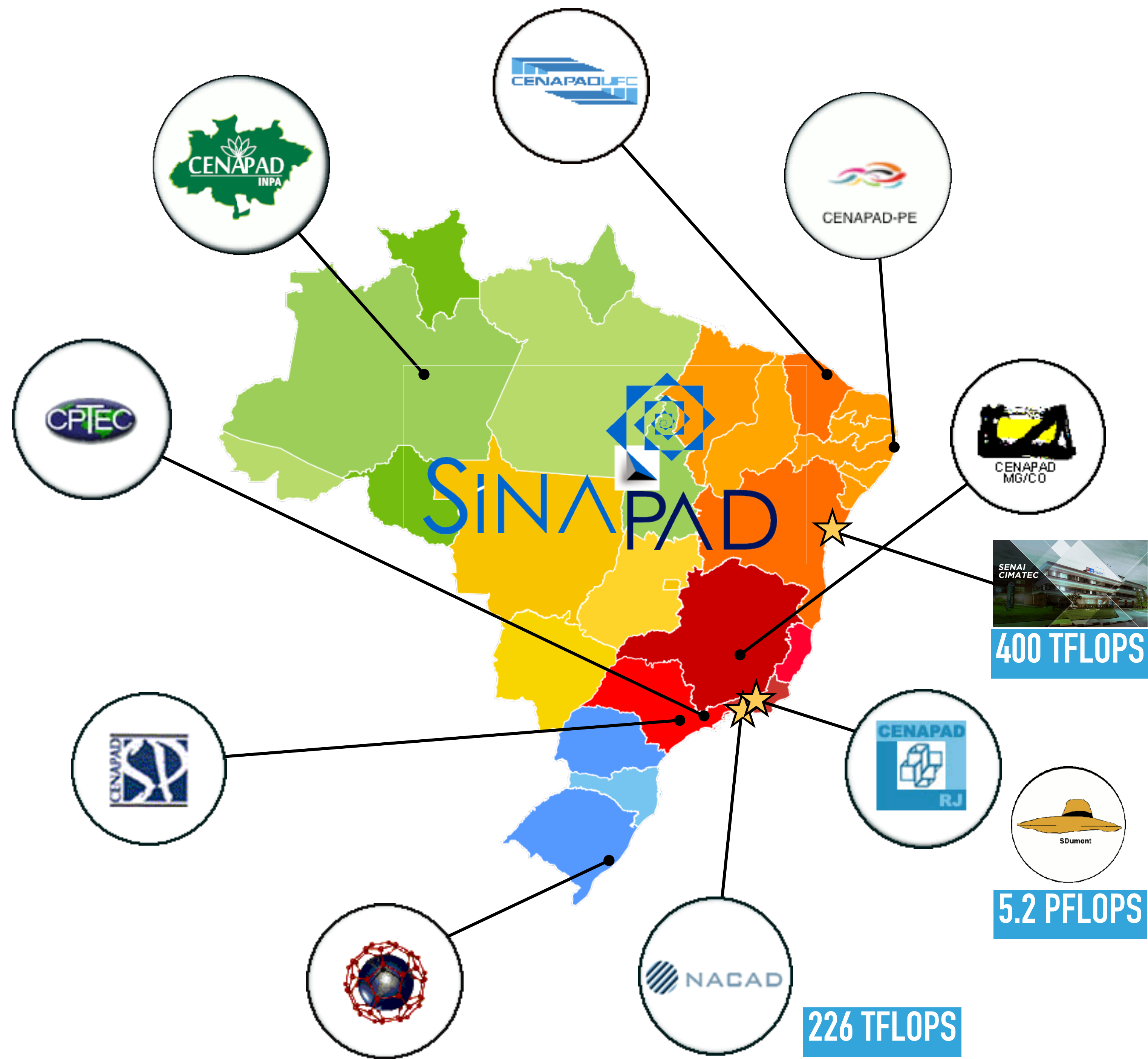
ANTÔNIO TADEU AZEVEDO GOMES — LNCC/MCTI

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**SUPERCOMPUTADOR SDUMONT: VISÕES DE QUEM  
USA (, DE QUEM PROGRAMA) E DE QUEM OPERA**

# O SUPERCOMPUTADOR SANTOS DUMONT

- SERVICE PROVISIONING
- DEVELOPMENT (E.G. SCIENCE GATEWAYS)
- TRAINING



The screenshot shows the DockThor website. The header includes the DockThor logo and navigation links: Home, Docking, References, About, Support, and Login. A main banner reads "Welcome to DockThor" and "A Free Web Server for Protein-ligand Docking". Below the banner is a visual representation of protein-ligand docking: a protein structure (blue and grey) plus a ligand (red and blue) equals a docked complex (blue and grey).

The screenshot shows the Bioinfo-Portal website. The header features the Bioinfo-Portal logo and a button to "Access the Bioinfo-Portal". A statistics box indicates "The portal was accessed 3405 times. 804 applications were executed." Below this is a navigation menu with links for RNBio, Main, Bioinfo, Main, Applications, Team, Publications, Tutorial, and Contact. The main content area is titled "The Brazilian Bioinformatics Network" and contains a detailed description of the network's mission and structure.

The screenshot shows the Rotational Profiler website. The header features the Rotational Profiler logo and a navigation menu with links for Rotational Profiler, Main, Applications, Team, Publications, Tutorial, and Contact. The main content area is titled "Rotational Profiler Intro" and contains a detailed description of the tool's purpose and usage. Below the text is a form with input fields for "Choose Reference Profile" and "Choose Force Field Profile", both with "Browse" buttons, and an "Upload Files" button. At the bottom, there is a mathematical equation for the torsional potential function.

### Rotational Profiler Intro

There is a very fundamental difference in the use of torsional potential functions as compared to bond length and angle potentials. Only a small subset of the full potential energy domain, around the minimum, is realized in the parabolic-like bond length and angle potentials. Therefore the emphasis in fitting these potentials is to reproduce potential near the minimum, with not so much concern about the functional form, or parameterization, or large excursions from equilibrium because they are energetically disallowed.

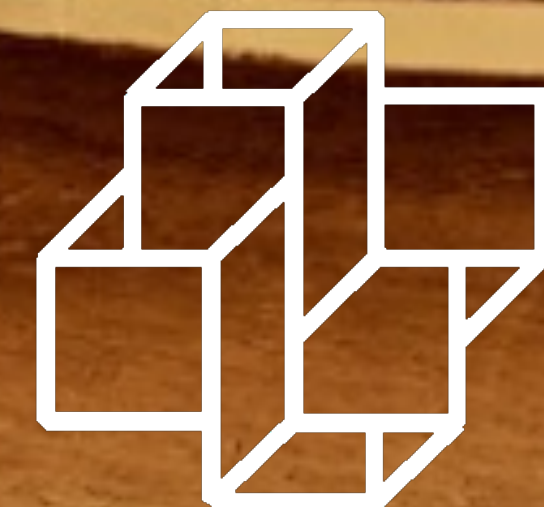
On the other hand, torsional potentials are evaluated over the full 360° of rotation around a bond. Therefore, the torsional parameters must be valid for full torsional rotation. Thus, the precision of fit about individual torsional minima is partially sacrificed for overall fit. The goal, then becomes to reproduce all extrema with less concern about the well shape about minima.

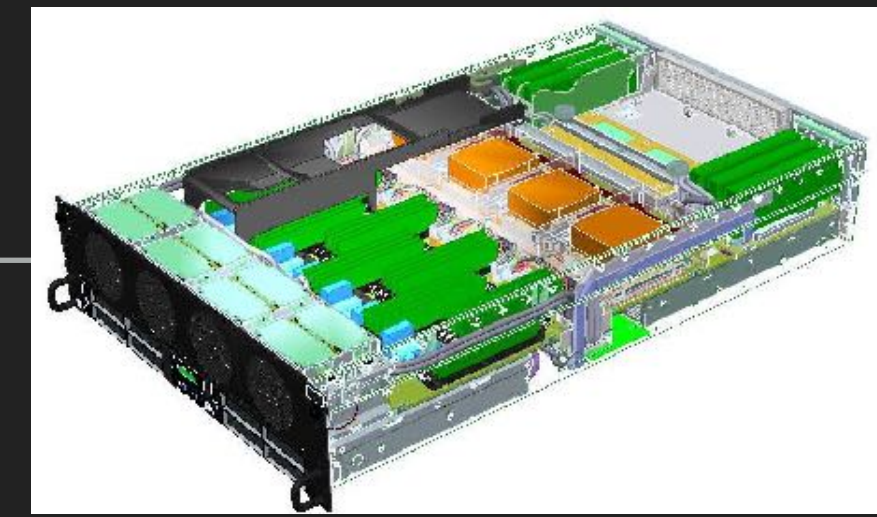
The Rotational Profiler attempts to facilitate the task of performing this overall fit. The functional torsional form used in the code is

$$V_{\text{torsion}}(\phi_{ijkl}) = k_{\phi} [1 + \cos(n\phi - \phi_{\text{offset}})]$$

where  $k_{\phi}$  is the force constant  $n$  is the multiplicity  $\phi$  is the phase shift or offset and  $\phi_{\text{offset}}$  is the torsional angle between the  $i, j, k, l$  particles.

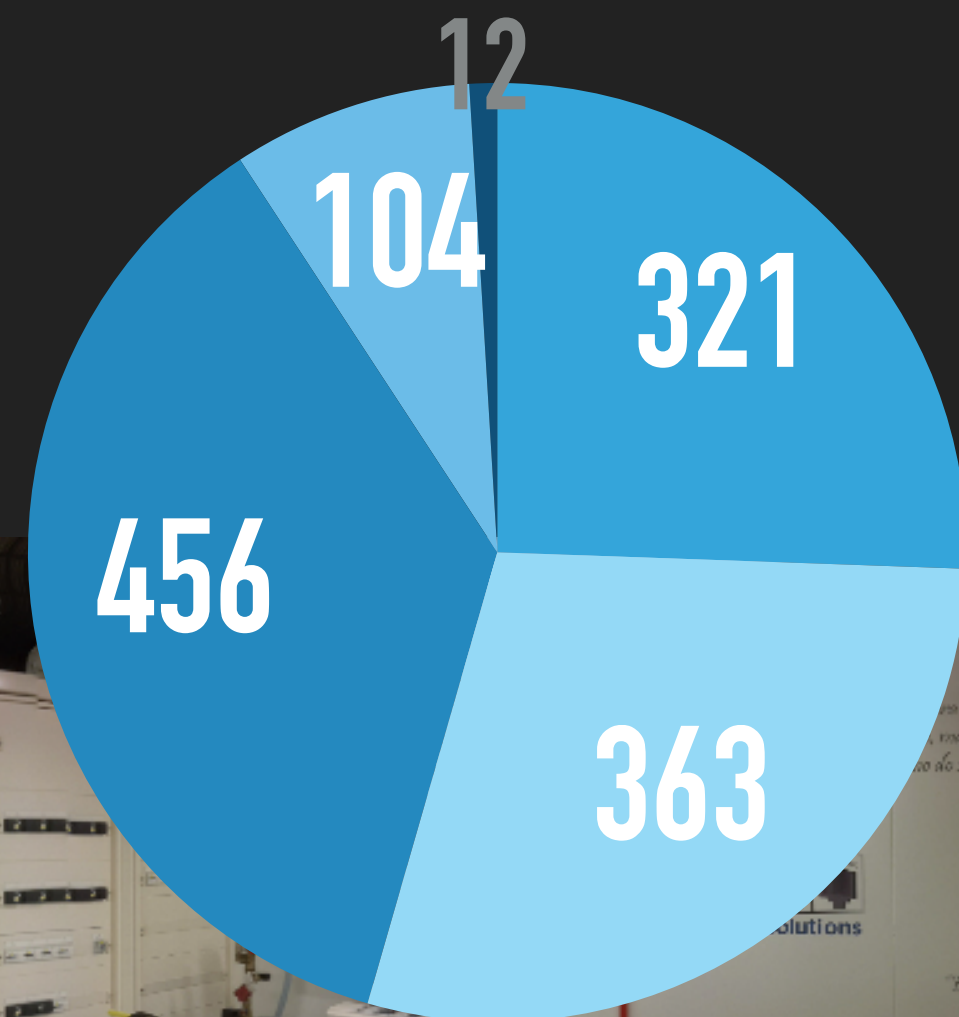
# LNCC



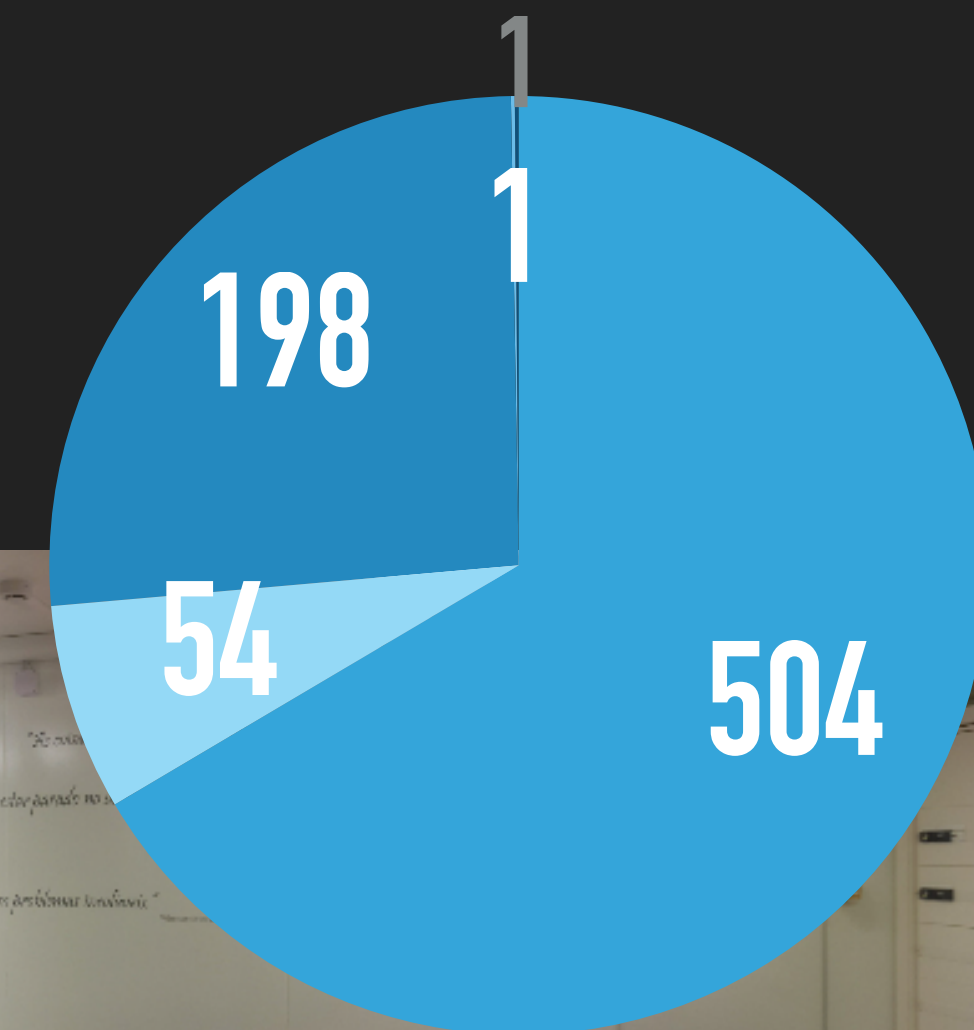


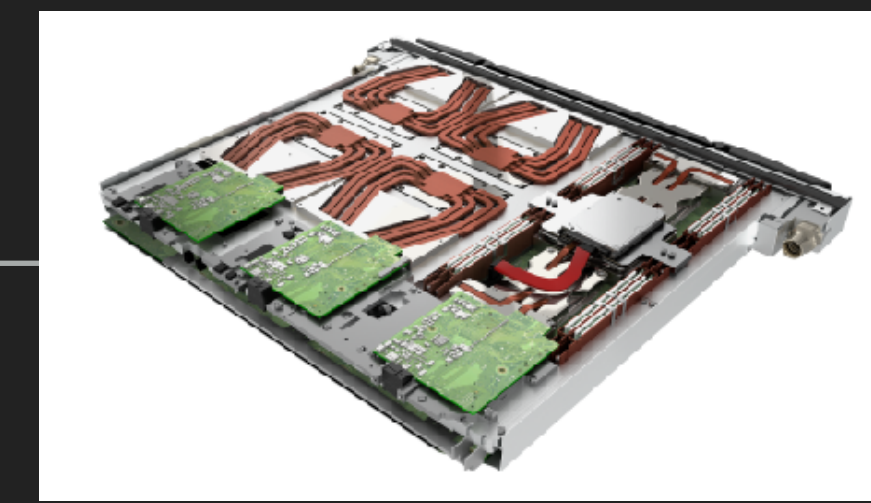
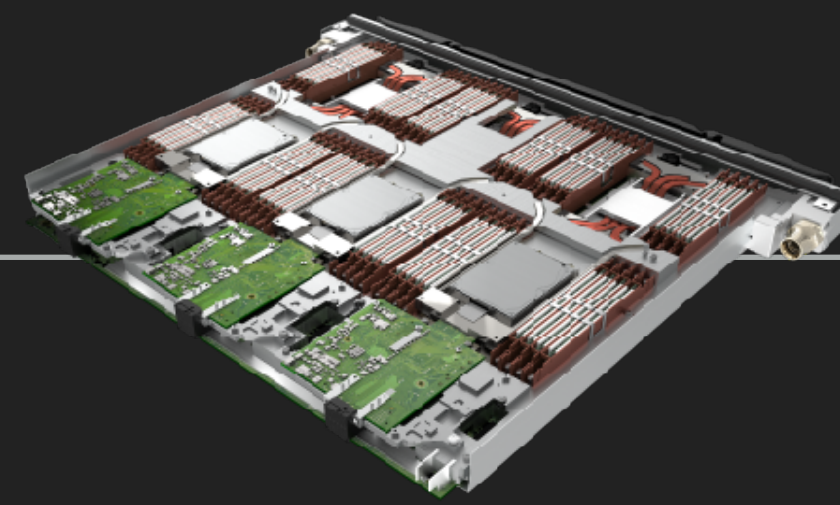
# CONFIGURATION (BULLX)

- ▶ ~1.2 PFlops computing capability
- ▶ 758 nodes: B710 Ivy Bridge, B715 Ivy Bridge + K40 (2 pn), B715 Ivy Bridge + Phi KC (2 pn) 64 Gb, S6030 Ivy Mesca2 6 Tb, DGX-1 V100 (8 pn)
- ▶ ~1.7 Pb Lustre storage; Infiniband interconnection (FDR)



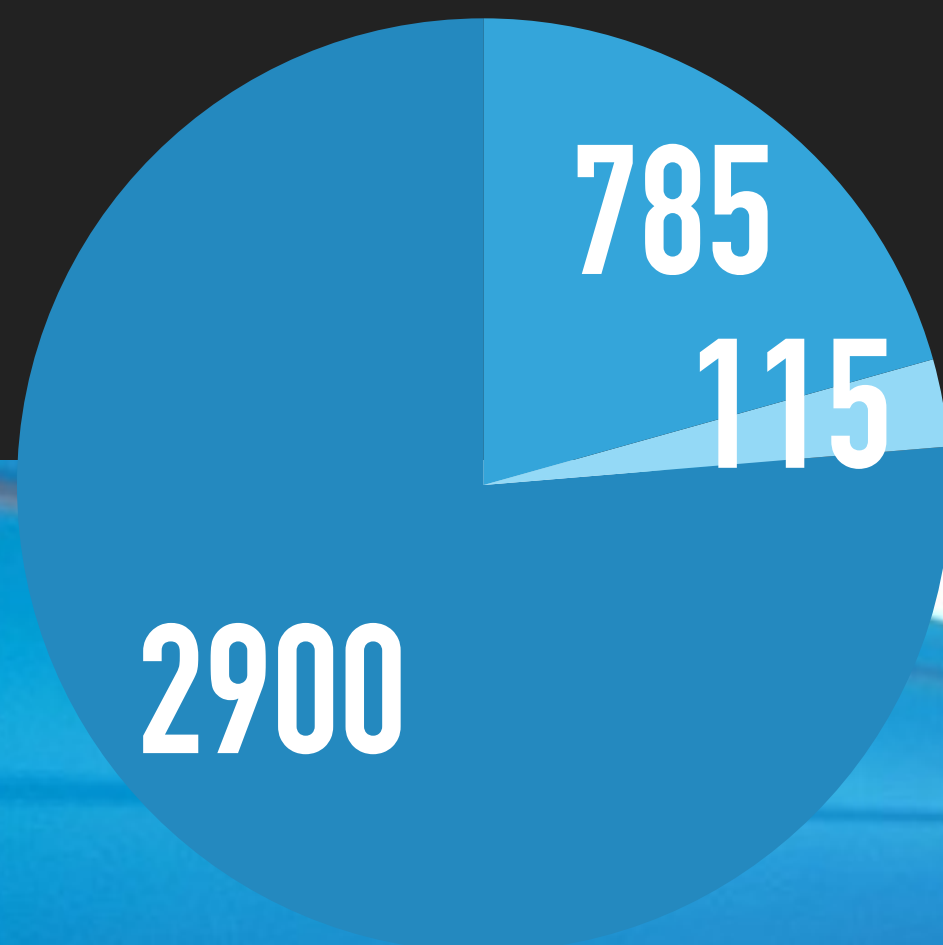
- B710
- B715 K40
- S6030
- B715 PHI
- DGX-1



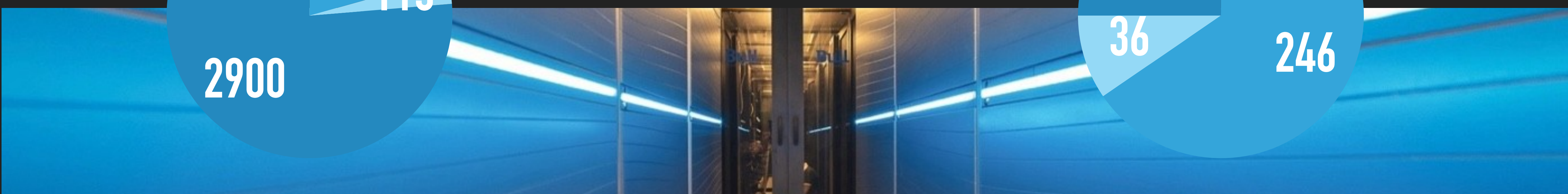
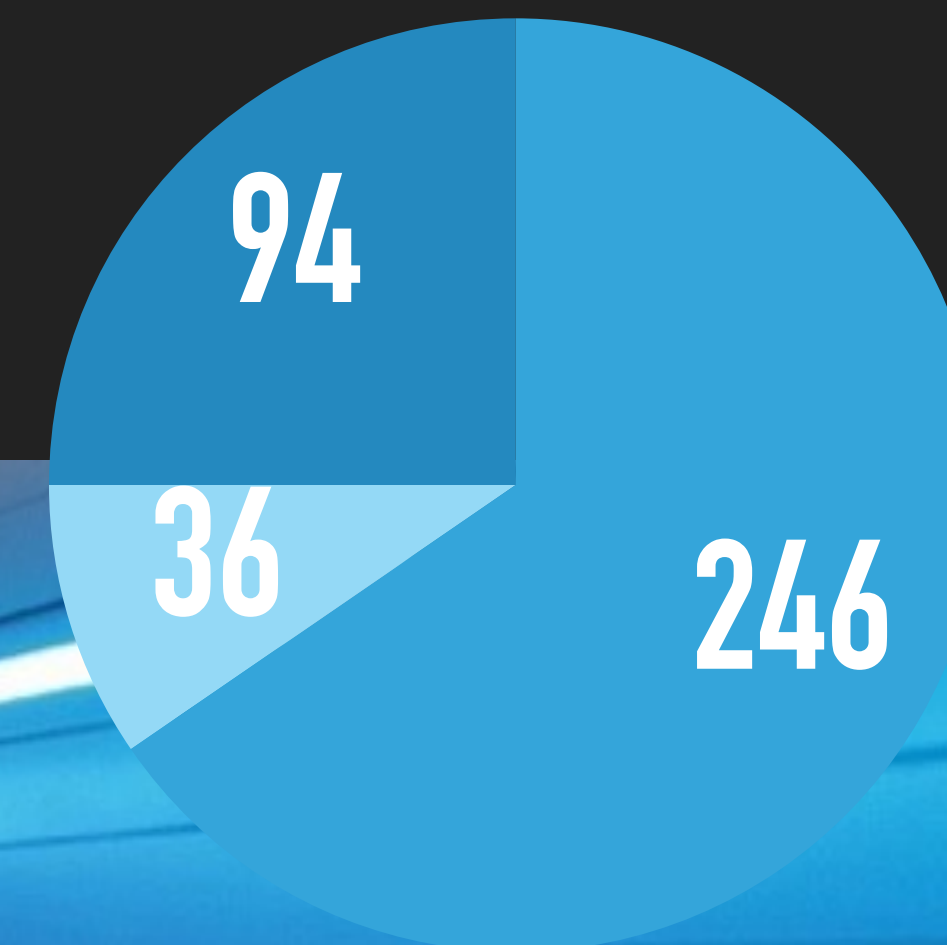


## CONFIGURATION (SEQUANA)

- ▶ + ~4.0 PFlops computing capability
- ▶ 376 nodes with 3 configurations: X1120 CascadeLake 384 & 768 Gb, X1125 Volta V100 (4 pn)
- ▶ + ~1 Pb Lustre storage; Infiniband interconnection (EDR)



- X1120 CL 384G
- X1120 CL 768G
- X1125 CL+V100



**SOBRE QUEM USA**

# 5 OPEN CALLS

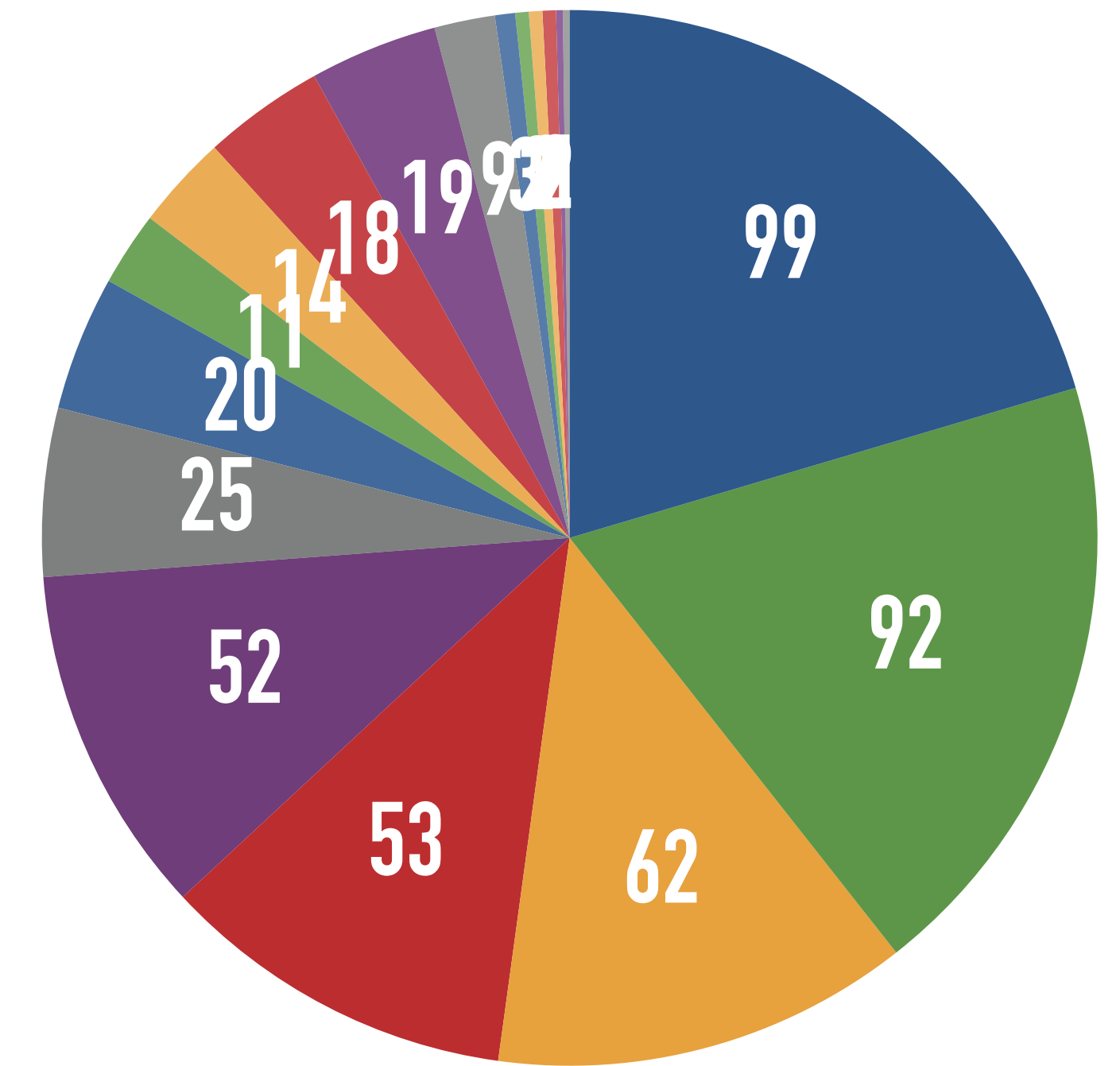
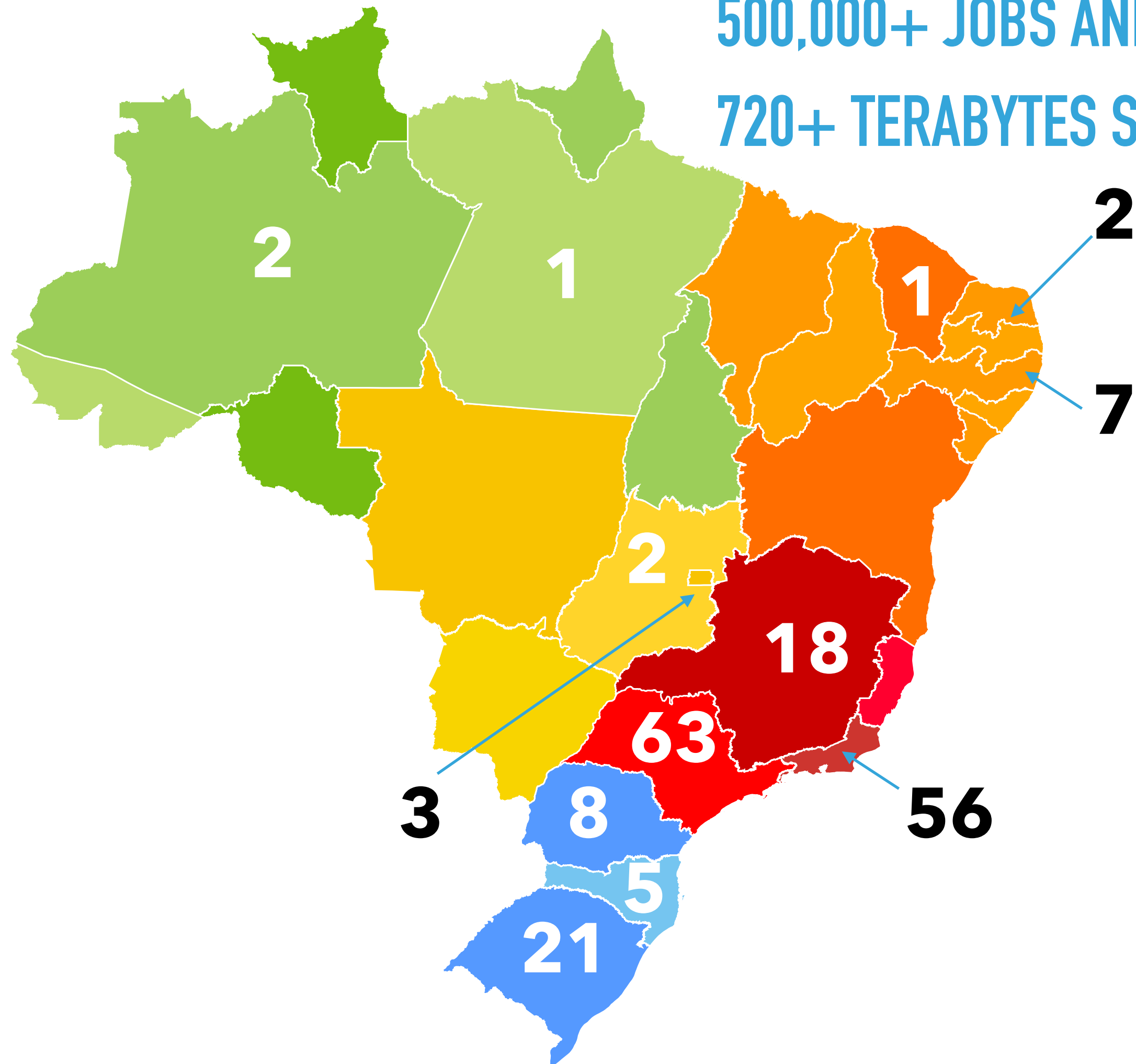
(PROJECTS FROM 1ST CALL ENDED IN 2018; FROM 5TH CALL BEGINNING THIS YEAR)

230+ PROJECTS IMPLEMENTED (PEER-REVIEWED)

1,200+ ACTIVE USERS

500,000+ JOBS AND 530,000,000+ SERVICE UNITS SINCE AUG/2016

720+ TERABYTES STORED



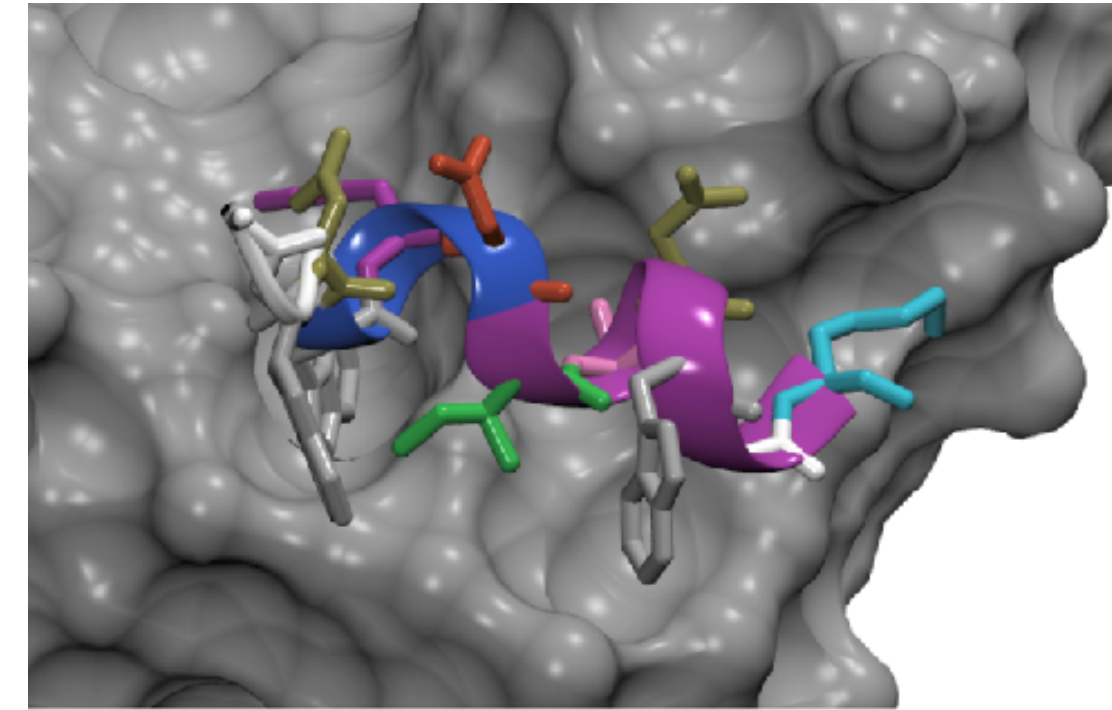
- Chemistry
- Biological sciences
- Geosciences
- Maths
- Pharmacy
- Agricultural sciences
- Physics
- Computer science
- Weather/climate
- Material sciences
- Economy
- Social sciences
- Engineering
- Health sciences
- Astronomy
- Biodiversity
- Oceanography
- Linguistics



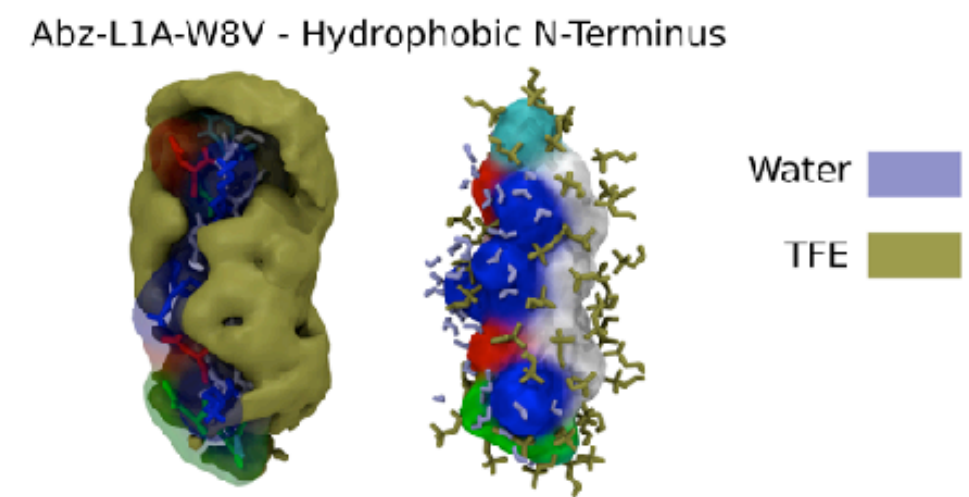
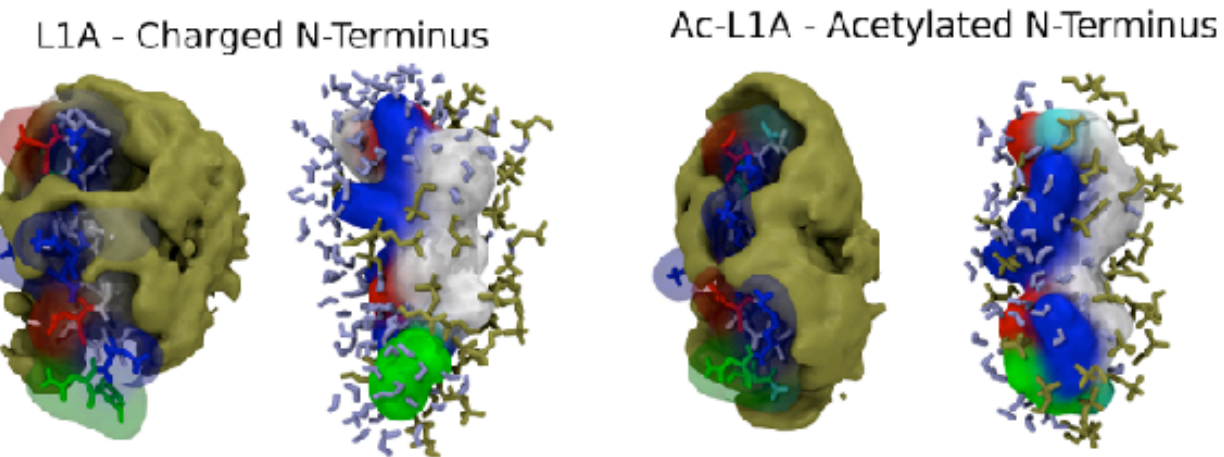


# MOLECULAR PRODUCTION

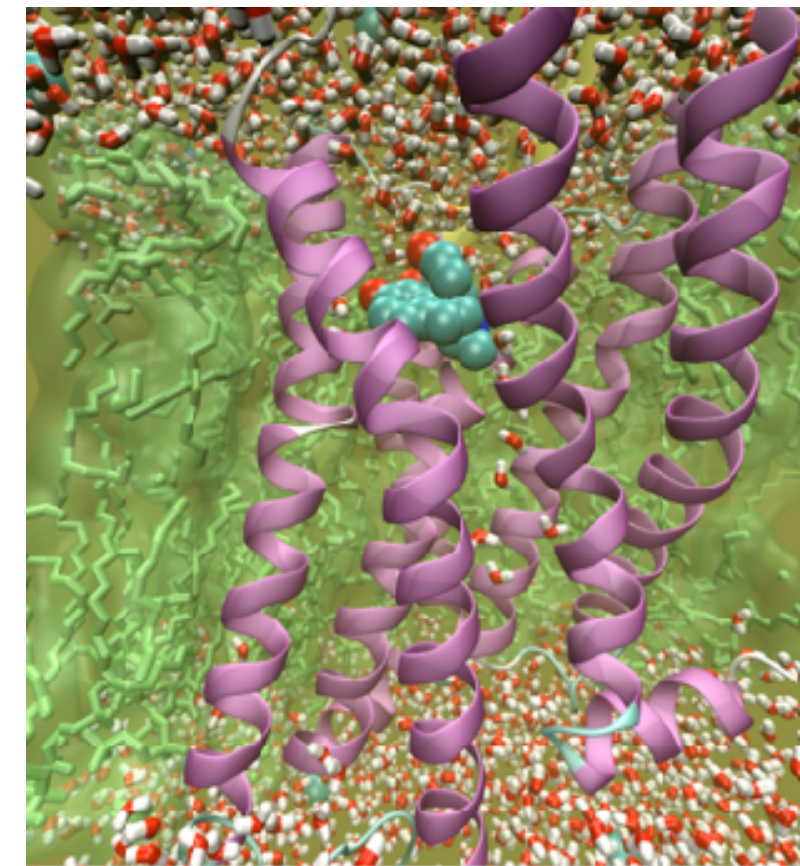
Zika / Dengue



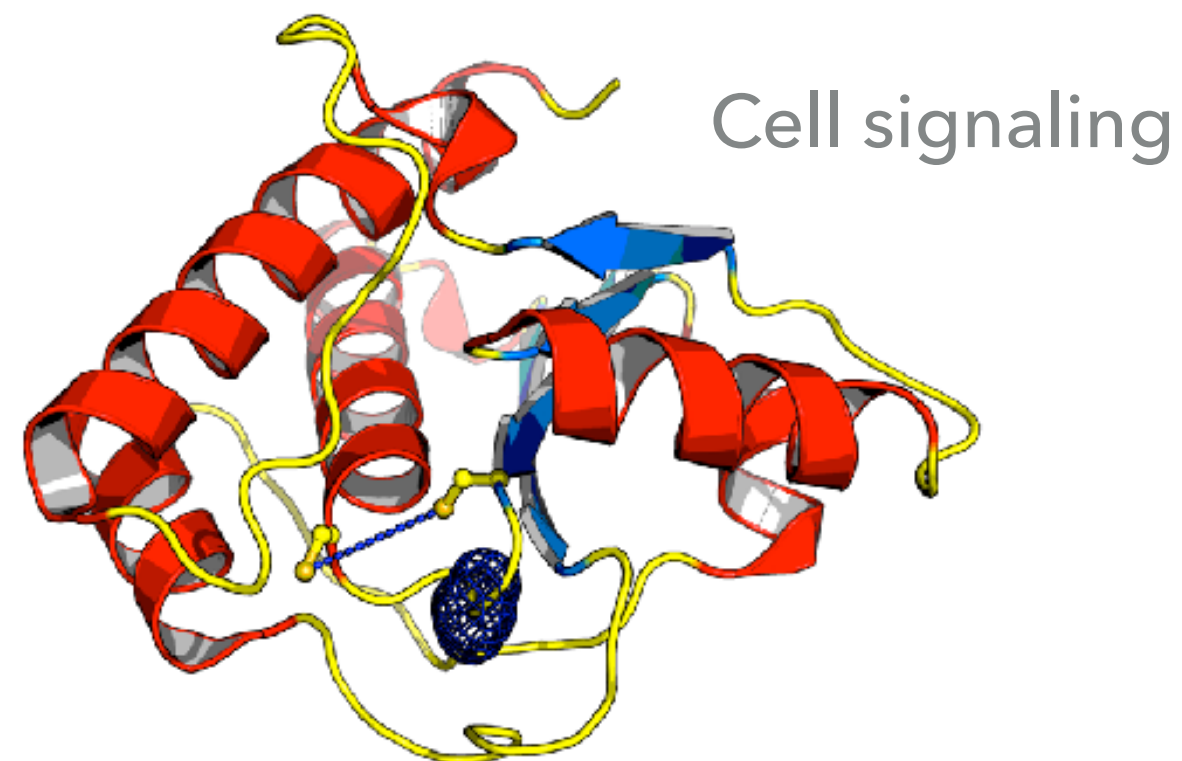
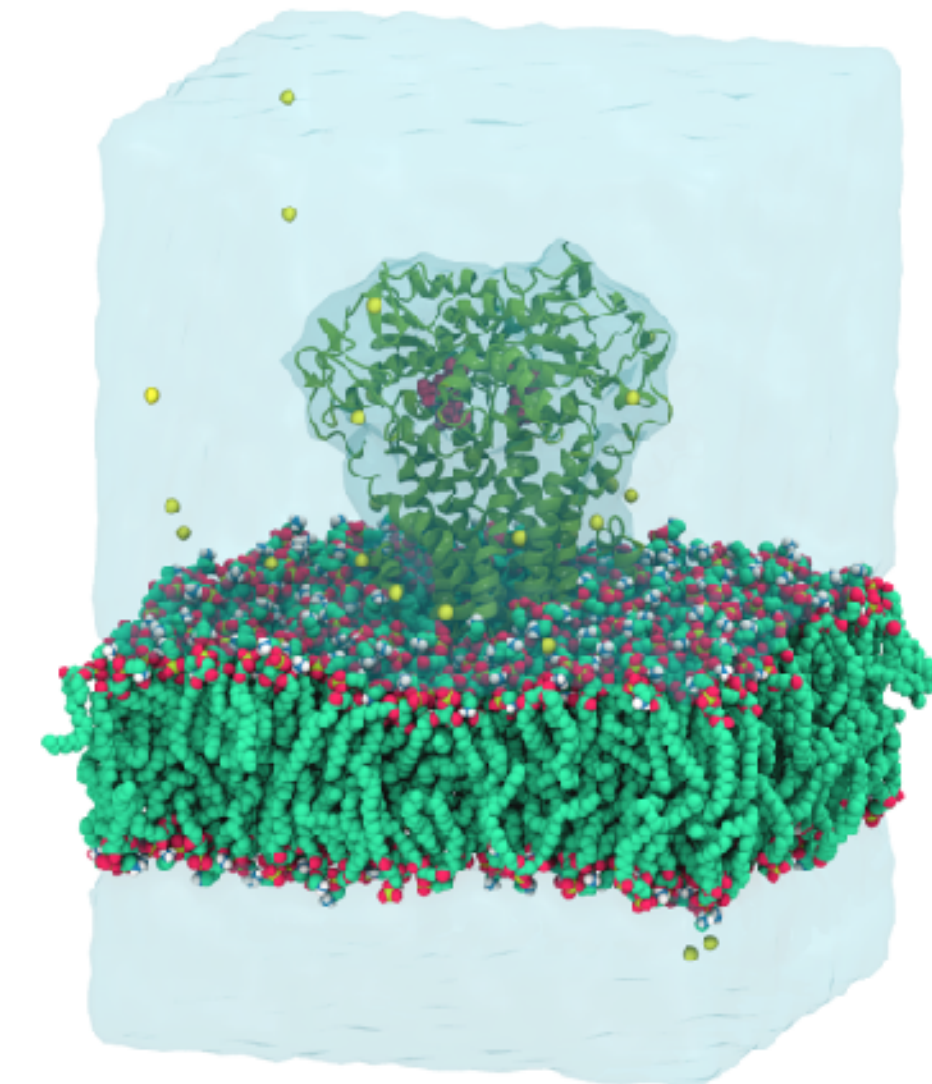
## Antimicrobial peptides



## Painkillers

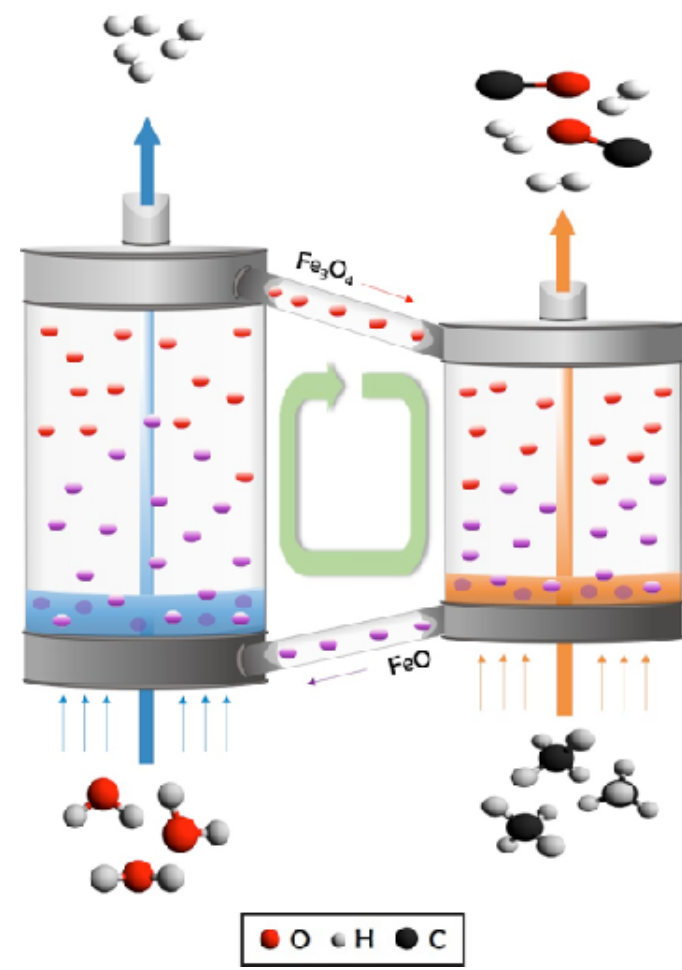


## Inflammatory processes

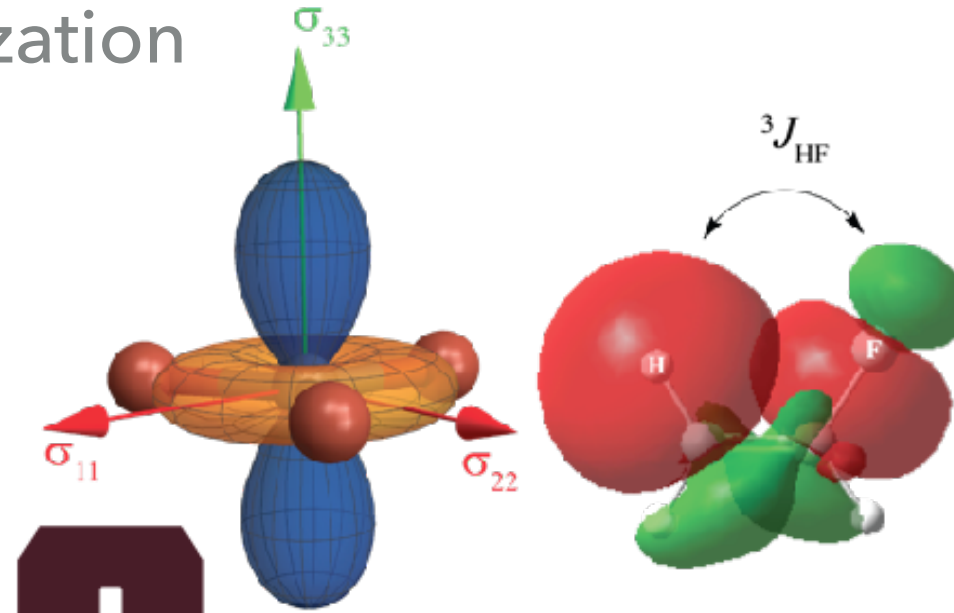




Catalytic hydrogen production

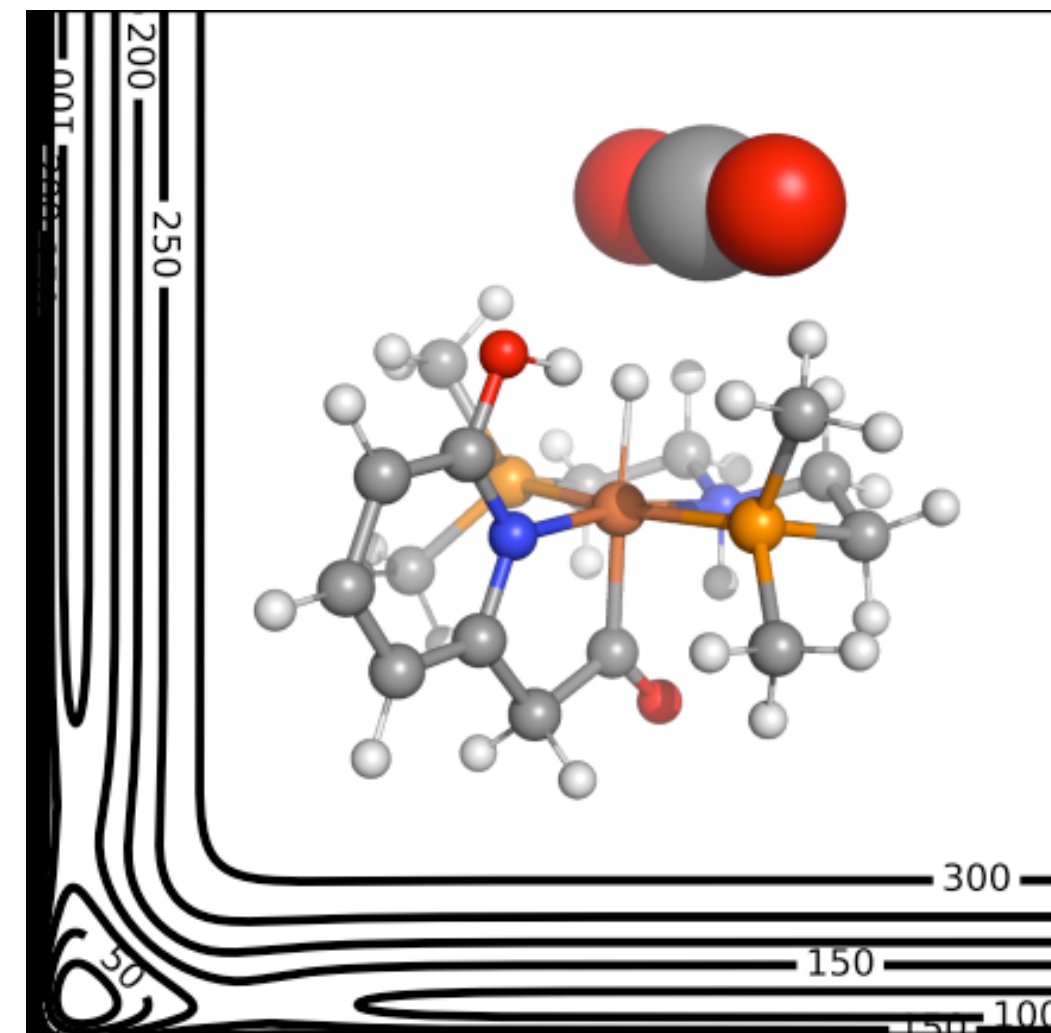


Nuclear magnetic resonance (NMR) parameterization

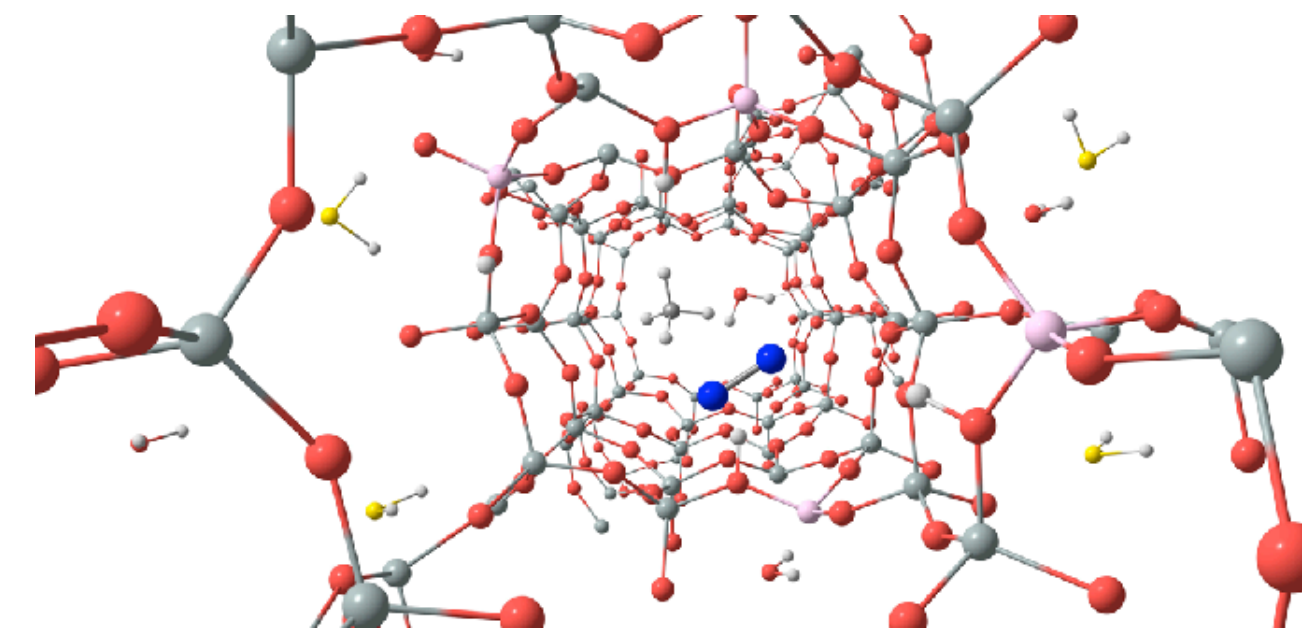


# MATERIALS

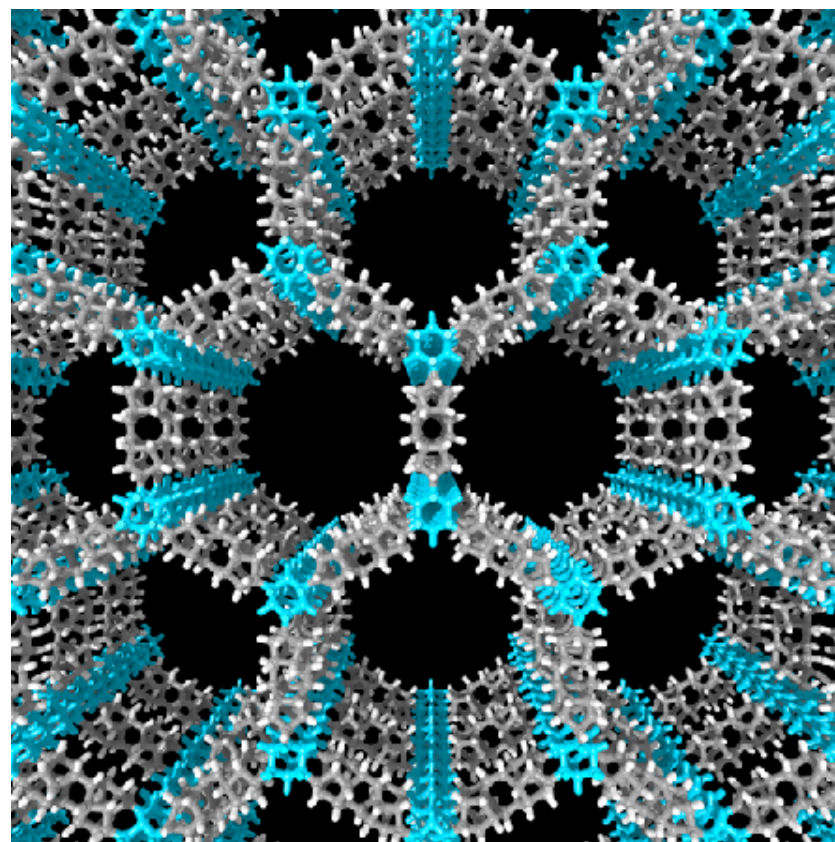
$\text{CO}_2$  catalysis



$\text{CO}_2$  capture



Resistant nanostructures



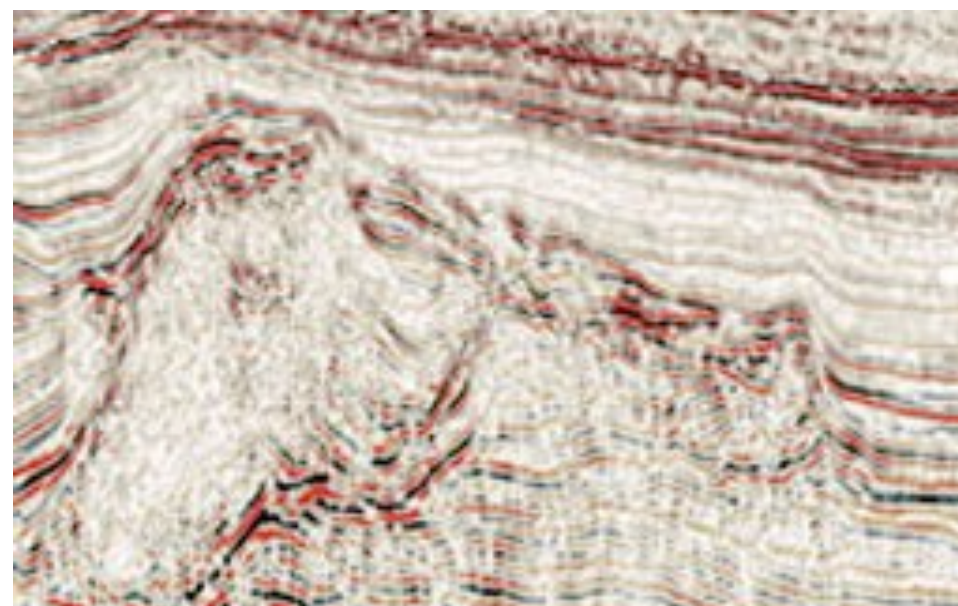


Combustion engines

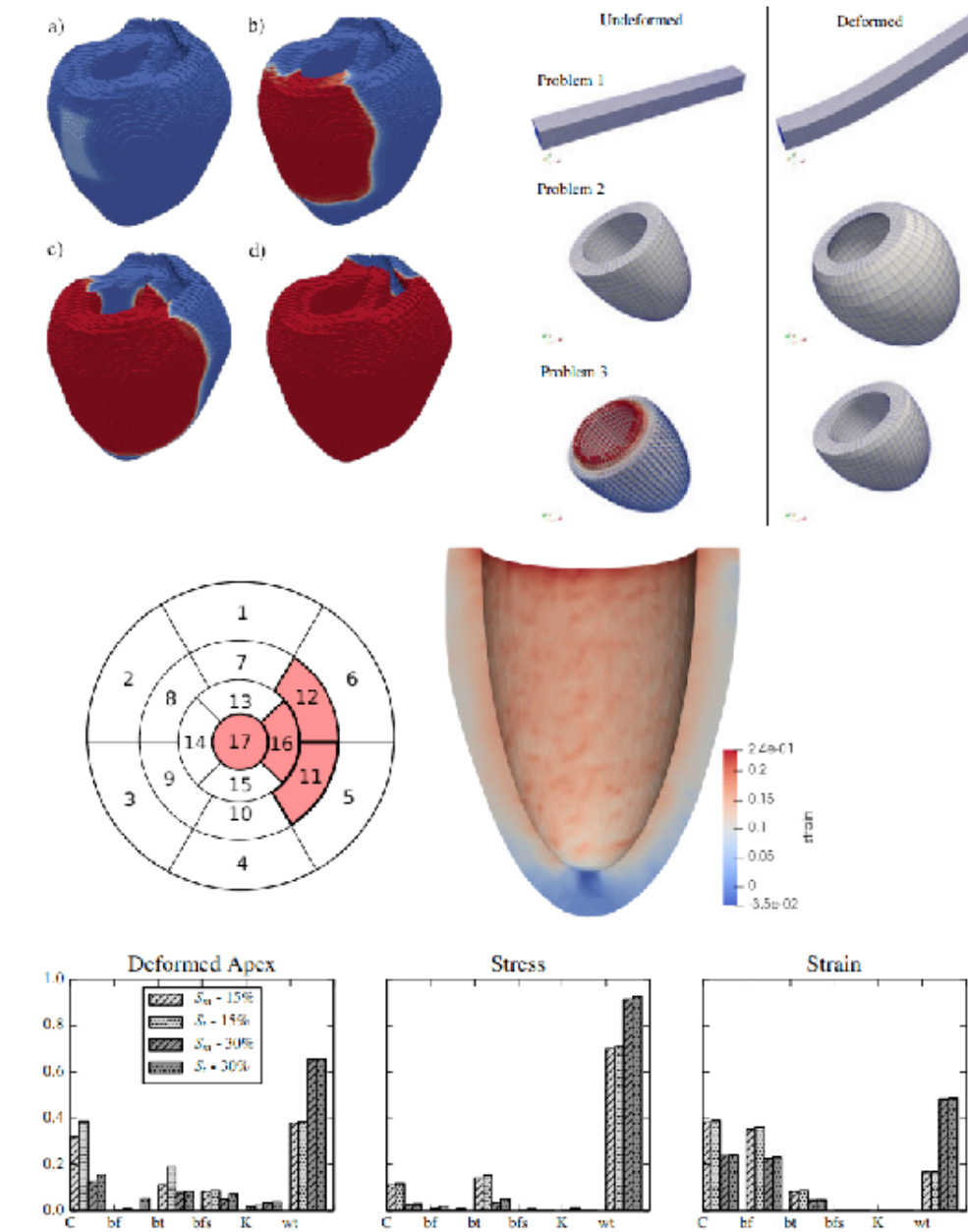


**HIGH-PERFORMANCE**

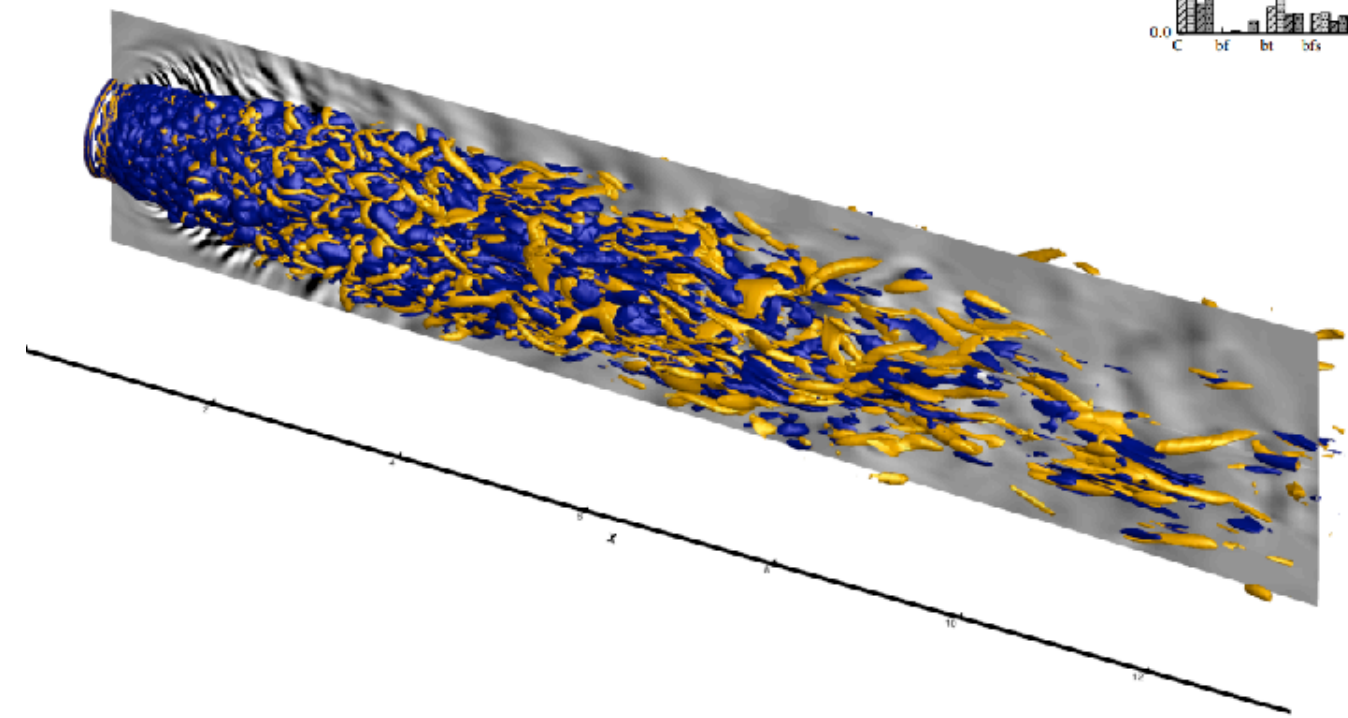
Seismic inversion



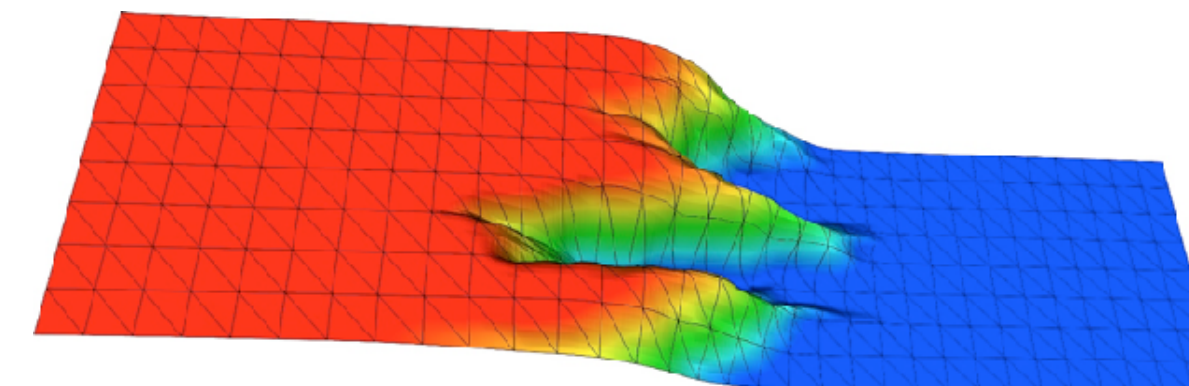
Heart electric-mechanical processes



Avionics

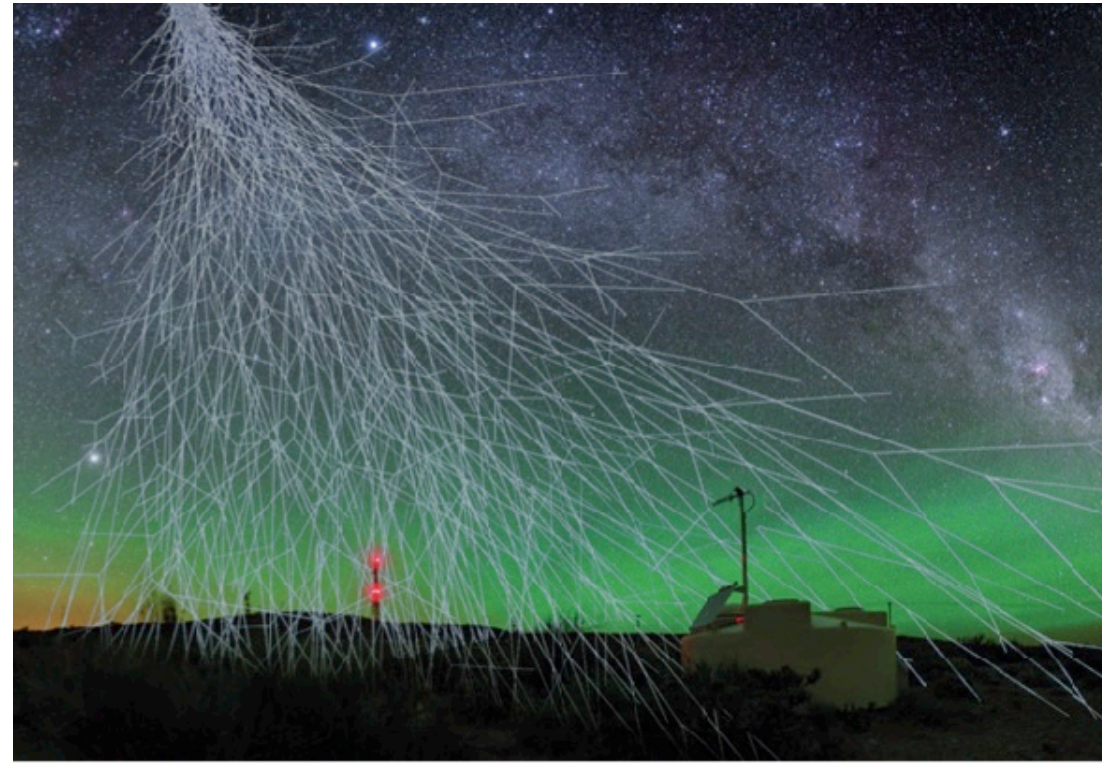


Multiscale porous-media flows

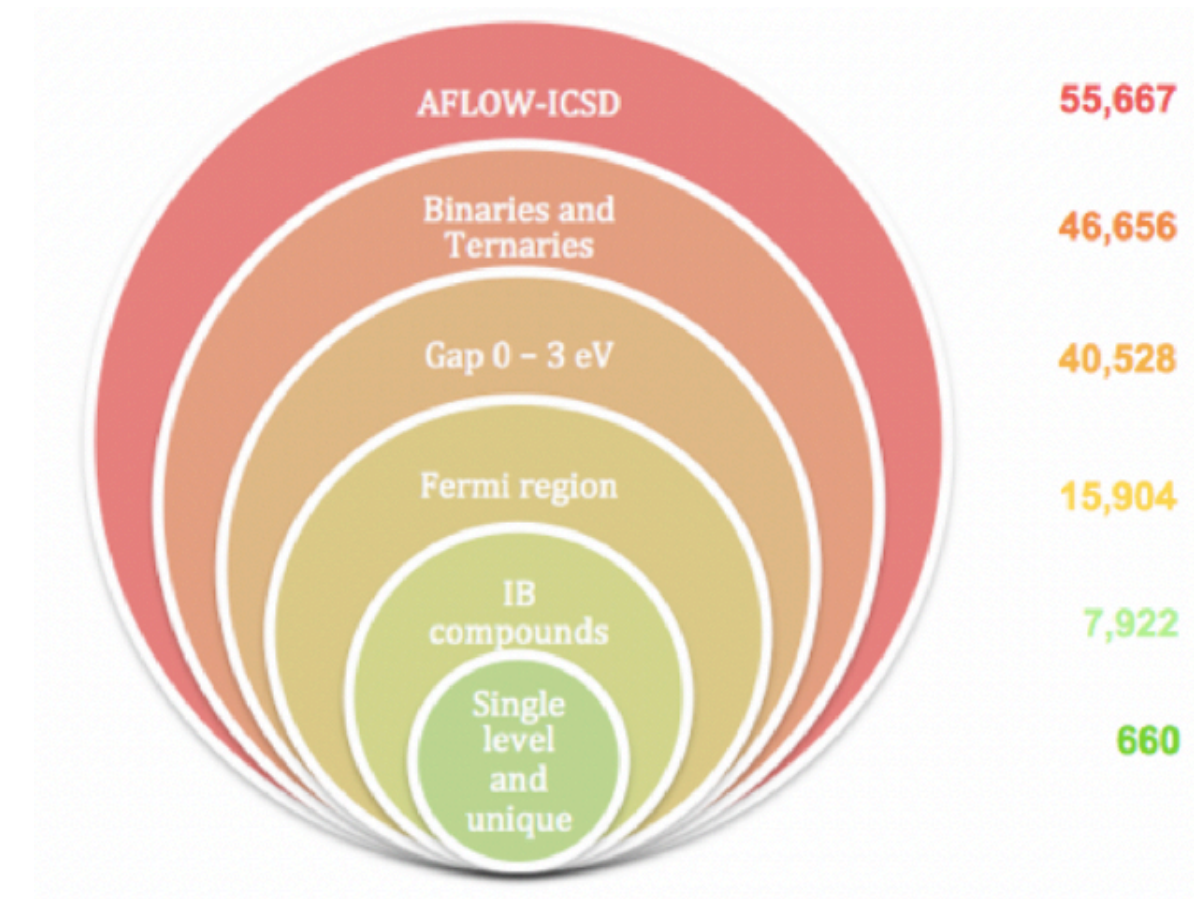




## Cosmic collisions



## Design of photovoltaic cells

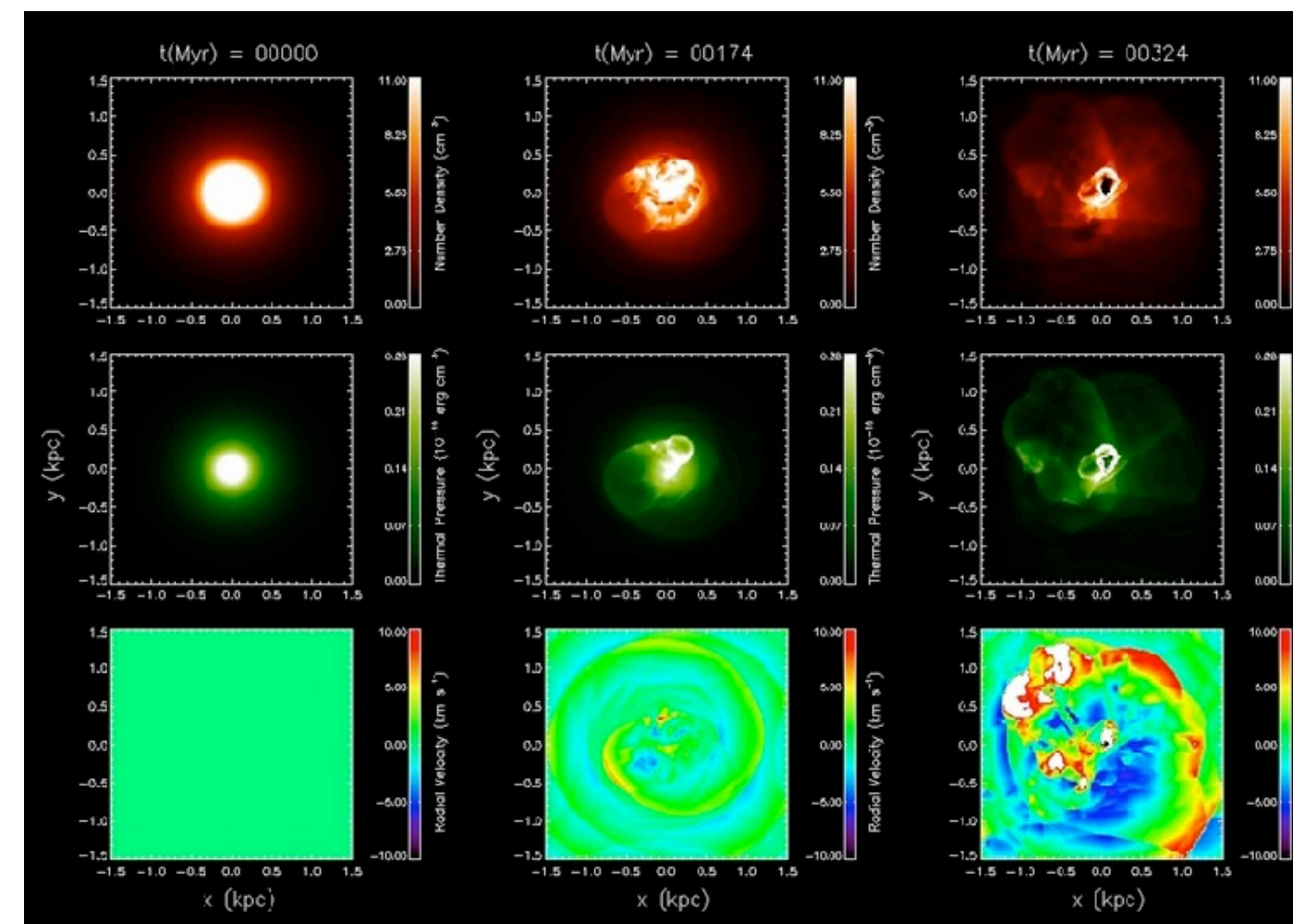


## Hemodynamics



# LARGE-SCALE

## Evolution of dwarf galaxies



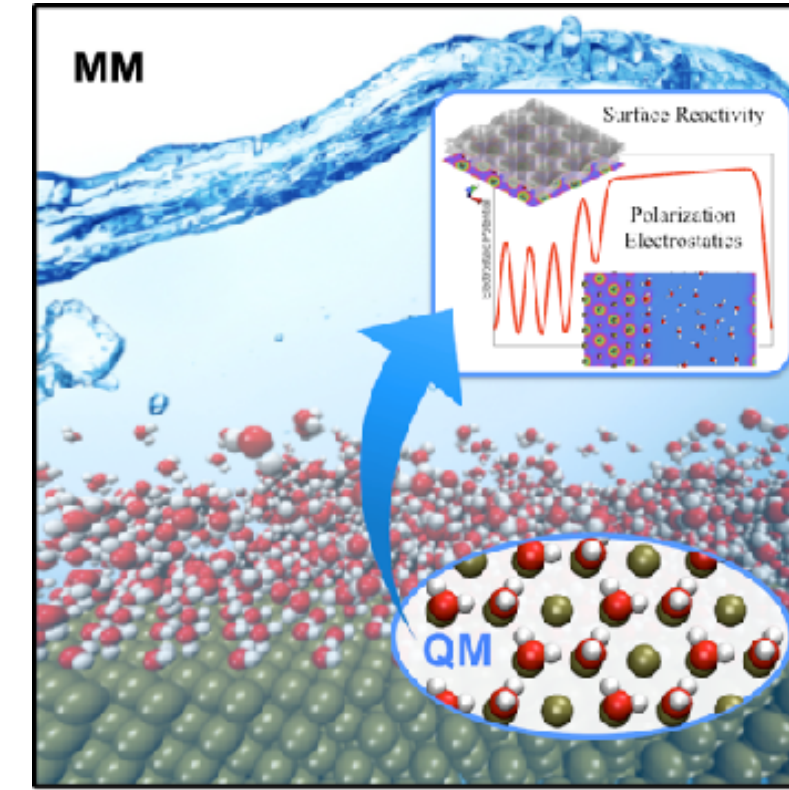




## Industrial automation

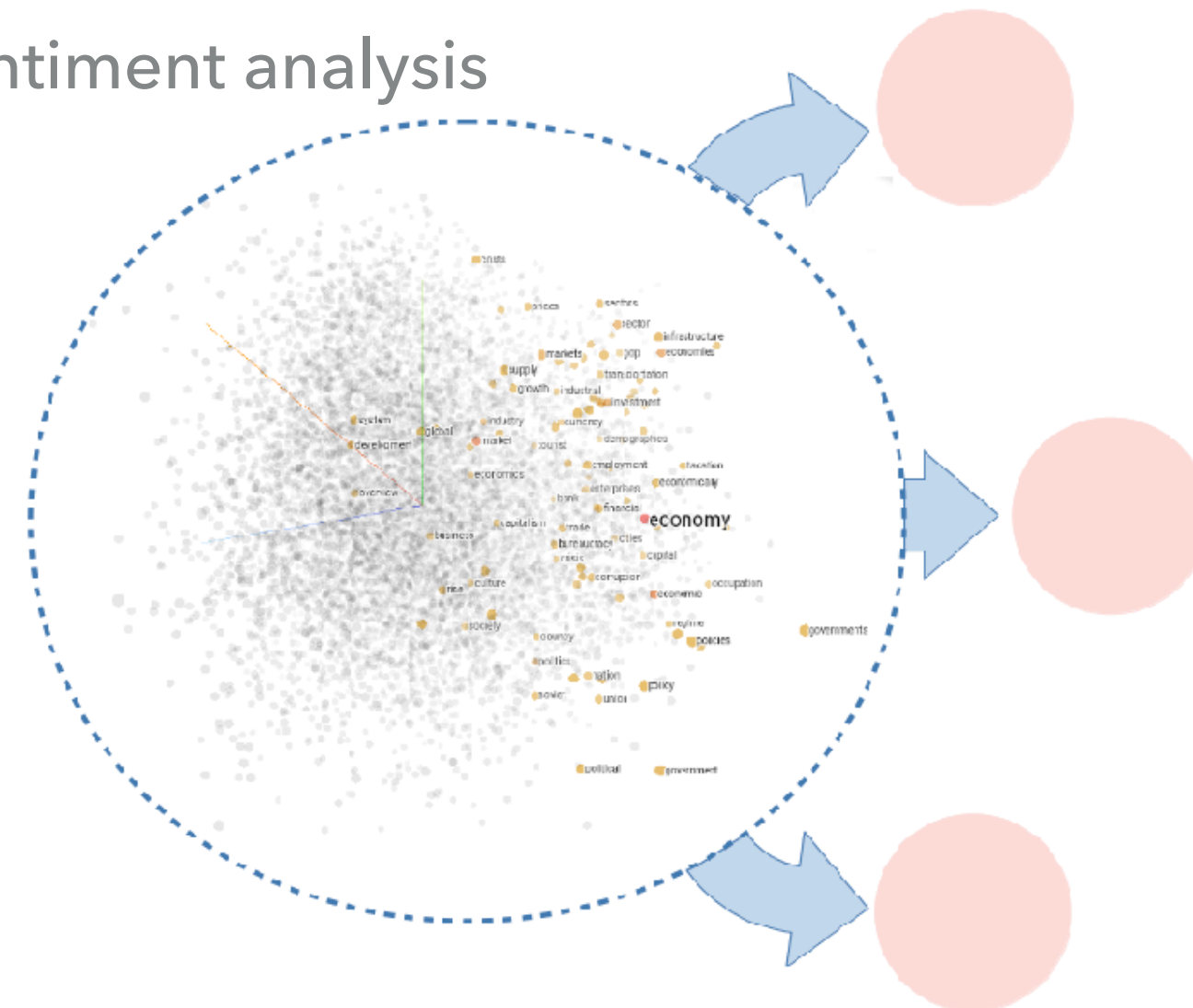


## Electrochemical interfaces

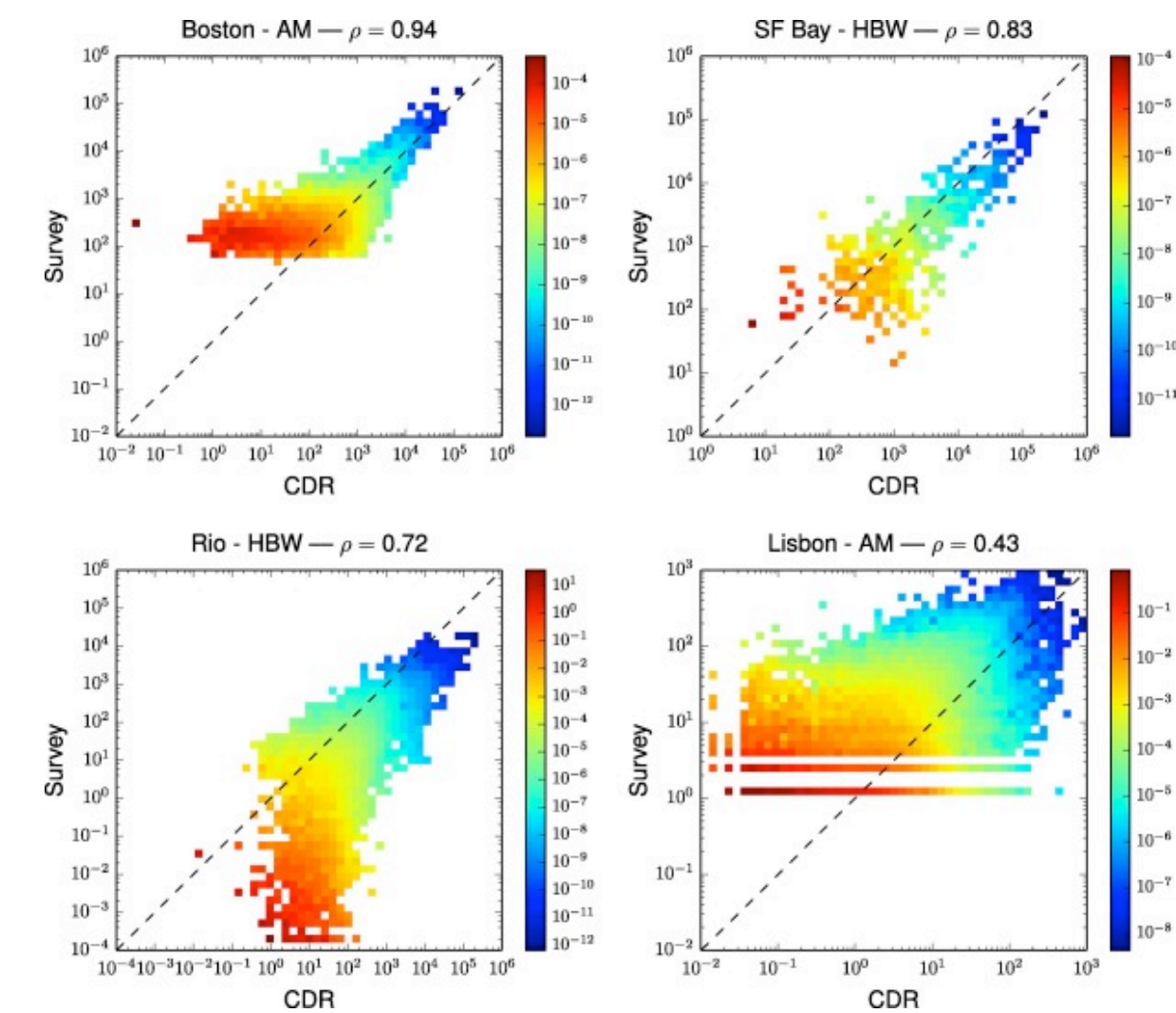


**MACHINE-LEARNING**

## Sentiment analysis



## Transport systems



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The power of RNA:  
Broad application of RNA-based sequencing for transcriptome and genome analysis

Recorded live on September 4, 2018  
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**Chiromagnetic nanoparticles and gels**

Jihyeon Yeom<sup>1,2</sup>, Uallisson S. Santos<sup>3</sup>, Mahshid Chekini<sup>2,4</sup>, Minjeong Cha<sup>2,5</sup>, André F. de Moura<sup>1</sup>  
[+ See all authors and affiliations](#)

Science 19 Jan 2018:  
Vol. 359, Issue 6373, pp. 309-314  
DOI: 10.1126/science.aao7172

BRASIL Acesso à informação Participe Serviços

Instituto Nacional da Propriedade Industrial  
Ministério da Economia

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**Depósito de pedido nacional de Patente**

- (21) Nº do Pedido: **BR 10 2016 021164 6 A2**
- (22) Data do Depósito: 14/09/2016
- (43) Data da Publicação: 03/04/2018
- (47) Data da Concessão: -
- (51) Classificação IPC: **A61K 31/473 ; A61P 31/10**
- (54) Título: **COMPOSIÇÃO FARMACÊUTICA BASEADA NO COMPOSTO 1-CLORO-6-NITRO-2-((2-NITROFENIL)-2,3,3A,4,5,9B-HEXAHIDRO-1H-CICLOPENTA[C]QUINOLINA-4-ÁCIDO CARBOXÍLICO E SEU USO EM MEDICAMENTOS PARA O TRATAMENTO DE INFECÇÕES CAUSADAS POR MICRO-ORGANISMOS DO GÊNERO PARACOCCIDIOIDES SPP**

A presente invenção se enquadra no contexto da química farmacêutica e se refere a composição farmacêutica e o seu uso no combate à infecções causadas por fungos. Mais especificamente, a presente invenção trata-se de uma composição farmacêutica que é útil no tratamento de infecções humanas causadas por microrganismos do gênero Paracoccidioides spp.



ARTICLE  
DOI: 10.1038/s41467-018-04859-5 **OPEN**

**Rational Zika vaccine design via the modulation of antigen membrane anchors in chimpanzee adenoviral vectors**

César López-Camacho<sup>1</sup>, Peter Abbink<sup>2</sup>, Rafael A. Larocca<sup>2</sup>, Wanwisa Dejnirattisai<sup>3</sup>, Michael Boyd<sup>2</sup>, Alex Badamchi-Zadeh<sup>2</sup>, Zoë R. Wallace<sup>4</sup>, Jennifer Doig<sup>5</sup>, Ricardo Sanchez Velazquez<sup>5</sup>, Roberto Dias Lima Neto<sup>6</sup>, Danilo E. Coelho<sup>6</sup>, Young Chan Kim<sup>1</sup>, Claire L. Donald<sup>5</sup>, Anis Qureshi<sup>5</sup>, Giuditta Di Biase<sup>1</sup>, Arvind H. Aravind<sup>1</sup>

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Zika virus (ZIKV) anti-ZIKV immunization



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**Article**

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**Interaction of Water with the Gypsum (010) Surface: Structure and Dynamics from Nonlinear Vibrational Spectroscopy and Ab Initio Molecular Dynamics**

Jaciara C. C. Santos<sup>†§</sup>, Fabio R. Negreiros<sup>†§1</sup>, Luana S. Pedroza<sup>‡</sup>, Gustavo M. Dalpian<sup>‡</sup> , and Paulo B. Miranda<sup>\*†</sup>

<sup>†</sup> Instituto de Física de São Carlos, Universidade de São Paulo, CP 369, São Carlos, São Paulo 13560-970, Brazil  
<sup>‡</sup> Centro de Ciências Naturais e Humanas, Universidade Federal do ABC, Santo André, São Paulo 09210-580, Brazil

*J. Am. Chem. Soc.*, 2018, 140 (49), pp 17141–17152  
DOI: 10.1021/jacs.8b09907  
Publication Date (Web): December 3, 2018  
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[\\*miranda@ifsc.usp.br](mailto:miranda@ifsc.usp.br)

**Cite this:** *J. Am. Chem. Soc.* 2018, 140, 49, 17141-17152

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[References](#)

# ACTIONS RELATED WITH COVID-19

The screenshot shows the SDumont website interface. At the top, there is a navigation bar with the gov.br logo and links for 'ACESSO À INFORMAÇÃO', 'PARTICIPE', 'LEGISLAÇÃO', and 'ÓRGÃOS DO GOVERNO'. Below this, the MCTI | LNCC logo and the SDumont title are displayed, along with the SINAPAD logo and a 40th anniversary emblem. A secondary navigation bar includes 'Chamada ABERTA!', 'A Máquina', 'Programas de Alocação', 'Cursos & Suporte', 'Projetos', and 'Comitês'. The main content area features a large blue banner with a background of binary code and virus particles. The banner text reads: 'Atenção: Chamada 2020 aberta, incluindo alocações Fast-track for COVID-19 SCALAC!' and 'Para lista de projetos de pesquisa relacionados ao coronavírus em andamento no SDumont, clique aqui!'. Below the banner, there is a section for 'Projeto Sistema de Computação Petaflopica do SINAPAD/2014. Processo número 01.14.192.00' with a 'Topo' link. The footer contains logos for Finep, Laboratório Nacional de Computação Científica, Ministério da Ciência, Tecnologia e Inovações, and Pátria Amada Brasil.

The poster is for the Folding@Home campaign. It has an orange background. In the top left corner, it says 'FOLDING @HOME' and in the top right corner, 'TAKE ME HOME'. The central text, in large white letters, reads 'TOGETHER, WE ARE POWERFUL'. Below this, a paragraph states: 'Together, we have created the most powerful supercomputer on the planet, and are using it to help understand SARS-CoV-2/COVID-19 and develop new therapies. We need your help pushing toward a potent, patent-free drug. Use your PC to help fight COVID-19.' A button labeled 'DOWNLOAD FOLDINGATHOME' is positioned below the text, with a note underneath: '[Available for Windows, Mac, Linux]'. At the bottom of the poster, it says 'Progress on the current COVID Moonshot sprint to assess potential drugs'.

# ACTIONS RELATED WITH COVID-19

gov.br

ACESSO À INFORMAÇÃO | PARTICIPE | LEGISLAÇÃO | ATRIBUIÇÕES DO GOVERNO

MCTI | LNCC

## SDumont

Sistema de Computação Petaflopica do SINAPAD

SINAPAD 40 ANOS 2020

Chamada ABERTA! | A Máquina | Programas de Alocação | Cursos & Suporte | Projetos | Comitês

**Atenção: Chamada 2020 aberta, incluindo alocações Fast-track for COVID-19 SCALAC!**

Para lista de projetos de pesquisa relacionados ao coronavírus em andamento no SDumont, clique aqui!

Projeto Sistema de Computação Petaflopica do SINAPAD/2014. Processo número 01.14.192.00 [Topo](#)

**Finep** INOVAÇÃO E PESQUISA

Laboratório Nacional de Computação Científica UNIDADE DE PESQUISA DO MCTI

MINISTÉRIO DA CIÊNCIA, TECNOLOGIA E INOVAÇÕES

PÁTRIA AMADA BRASIL GOVERNO FEDERAL

## dockthor

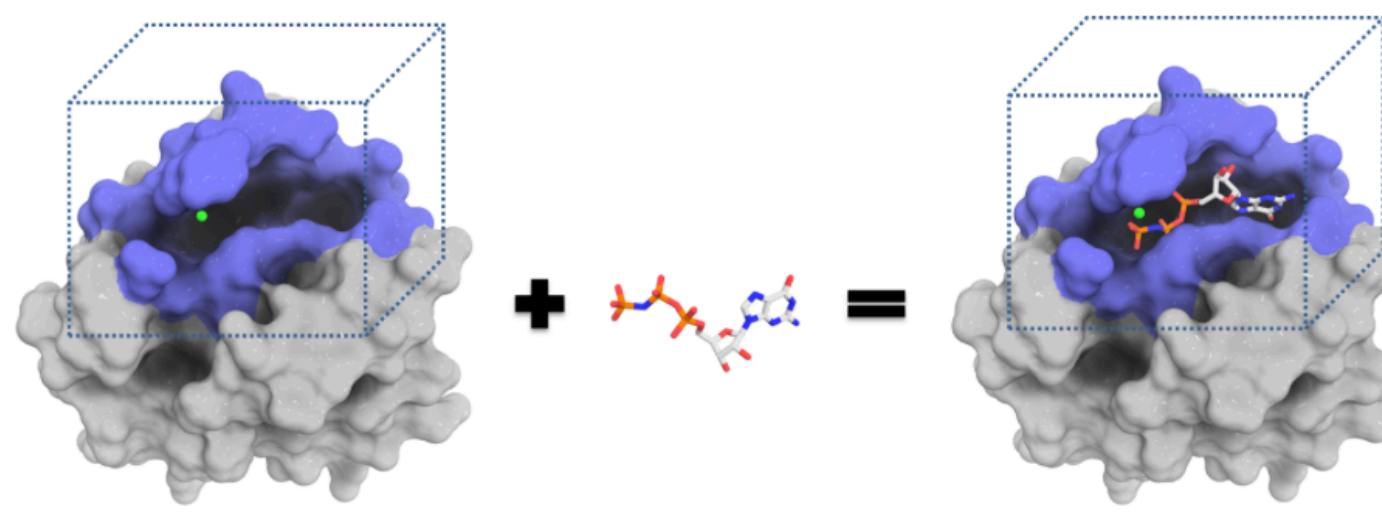
A RECEPTOR-LIGAND DOCKING PROGRAM

Home | Docking | References | About | Support | Login

**COVID-19:** We provide to the DockThor users structures of COVID-19 potential targets already prepared for docking at the Protein tab. New targets and structures will be available soon.

# Welcome to DockThor

A Free Web Server for Protein-ligand Docking



**Protein**  
Add missing hydrogen atoms, complete side chains, change protonation states. Simple and easy!

**Small molecules**  
Add hydrogen atoms (pH 7), freeze rotatable bonds, get MMFF94S atom types and partial charges. Fast and automatic!

**Cofactors**  
Consider cofactors and structural waters on virtual screening experiments with automatic MMFF94S parametrization.

# ACTIONS RELATED WITH COVID-19



## Desenho racional de anticorpos scFv para desenvolvimento de kits diagnósticos contra COVID-19 (lima\_covid)

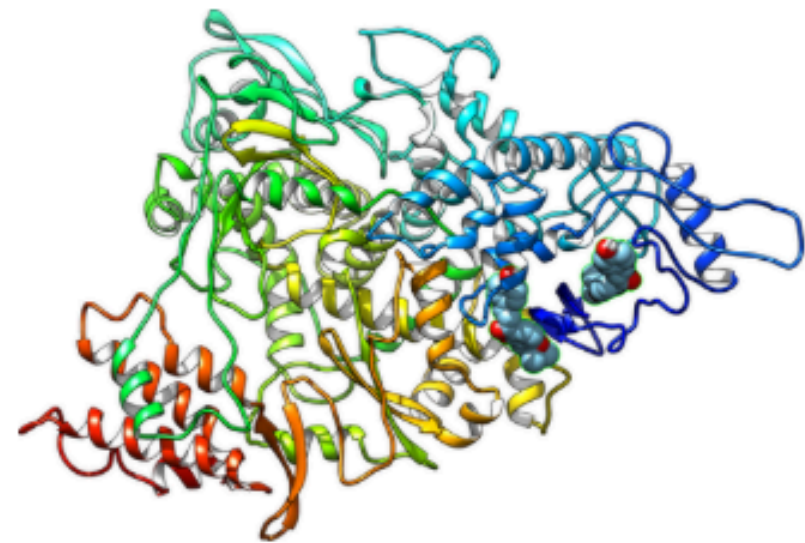
Universidade Federal de Viçosa

Departamento de Bioquímica e Biologia Molecular

**Coordenador:** Gustavo Costa Bressan

**Áreas do conhecimento:** Bioquímica; Ciências biológicas; Ciências da saúde; Farmácia; Química

**Início da vigência:** 26-08-2020



## Determinação de inibidores para as proteínas não estruturais de SARS-CoV-2 com o uso de técnicas computacionais e modelagem molecular (covdock)

Universidade Federal do ABC

Centro de Matemática, Computação e Cognição

**Coordenador:** David Corrêa Martins

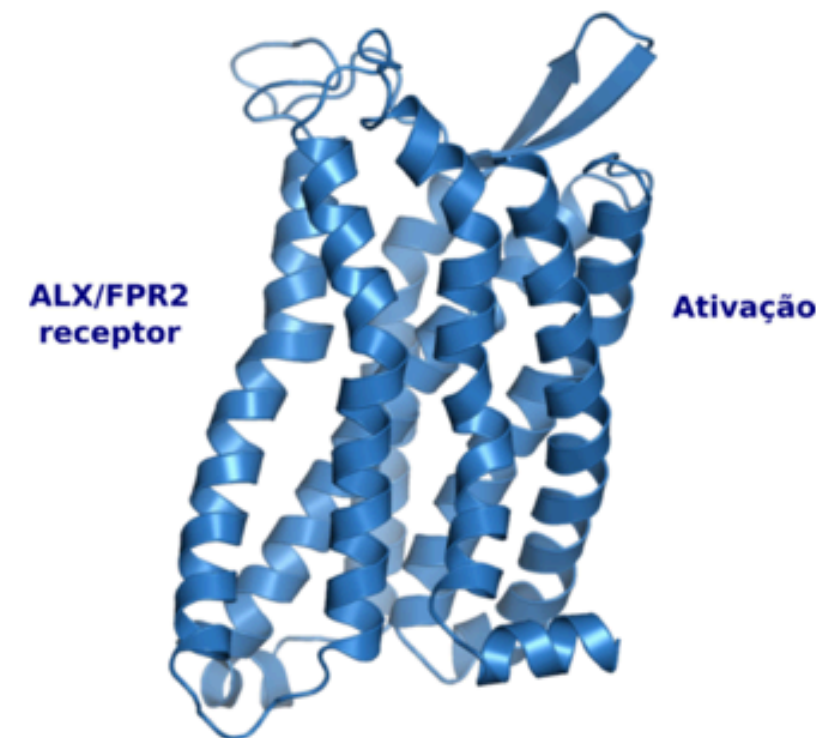
**Áreas do conhecimento:** Ciência da computação; Ciências biológicas; Ciências da saúde; Física; Matemática; Química

**Início da vigência:** 05-06-2020

No dia 11 de março de 2020 foi caracterizada pela Organização Mundial da Saúde (OMS) a COVID-19 como uma pandemia. De acordo com a OMS, até o dia 19 de maio, temos mais de 4,7 milhões de casos confirmados no mundo com mais de 300 mil mortes confirmadas, com casos confirmados em 216 países, no Brasil, temos mais de 270 mil casos e um número próximo a 20 mil mortes. Os casos de COVID-19 são causados pelo virion SARS-CoV-2, e os primeiros casos foram relatados em dezembro de 2019. O virion SARS-CoV ... [Mostre mais](#)

### AGONISTAS

Pro-inflamatórios    Anti-inflamatórios



## Estudo computacional do receptor FPR2 e sua relação com a COVID-19 (fcovid19)

Universidade Federal de Juiz de Fora

Modelagem Computacional

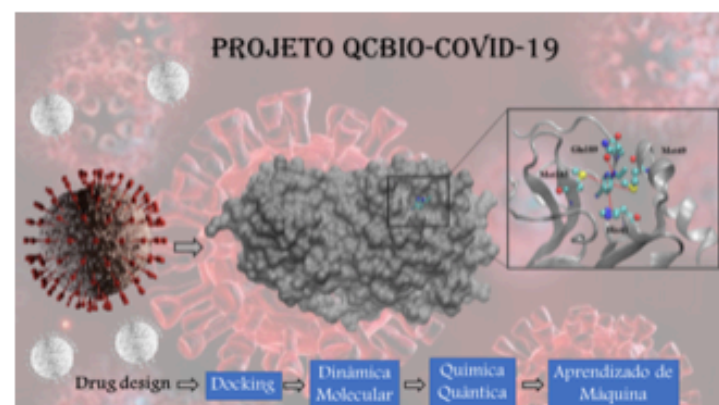
**Coordenador:** Vinicius Schmitz Pereira Nunes

**Áreas do conhecimento:** Ciências biológicas

**Início da vigência:** 24-09-2020

Os receptores de peptídeos formilados (FPR) são um grupo de receptores acoplados à proteína G (GPCR) que desempenham papéis na defesa e inflamação do hospedeiro. Em humanos há três isoformas para FPRs: FPR1, FPR2 e FPR3. Os FPRs, juntamente com os receptores do peptídeo complemento C5a (C5aR), das moléculas lipídicas eicosanoides leucotrienos B4 e prostaglandina D2 (B4LTR e CRTH2), e as moléculas de quimiocinas (receptores de quimiocinas) constituem um grupo de receptores de quimioattractantes aco ... [Mostre mais](#)

# ACTIONS RELATED WITH COVID-19



## Prospecção e testes in vitro de inibidores de proteínas associadas ao vírus SARS-Cov 2 por meio do uso conjunto de ferramentas de bioinformática, simulação molecular, química quântica e aprendizado de máquina (qcbiocovid19)

Universidade Federal da Paraíba

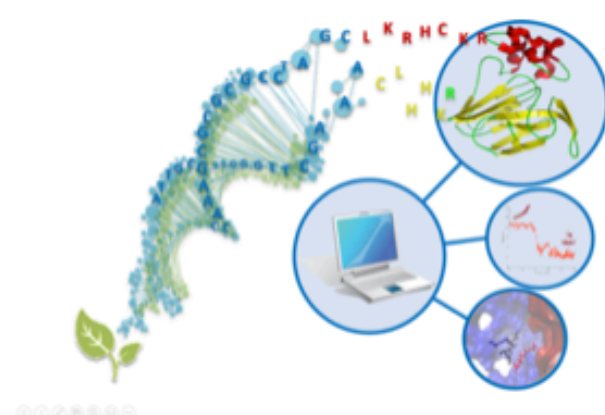
Departamento de Química

**Coordenador:** Gerd Bruno da Rocha

**Áreas do conhecimento:** Ciência da computação; Ciências biológicas; Química

**Início da vigência:** 05-05-2020

O surto de um vírus novo, o SARS-Cov 2, têm afetado, em um curtíssimo tempo, o mundo inteiro numa pandemia sem igual precedente na história moderna. Esse evento impulsionou os cientistas do mundo todo a darem uma resposta imediata, atuando em diversas frentes de batalha, para conter essa pandemia de proporções catastróficas. Uma dessas frentes têm sido o estudo em nível molecular do funcionamento do vírus e sua infecção em células humanas. Nesse sentido, muitas proteínas (ex. SARS-Cov 2 Spike e ... [Mostre mais](#))



## Rationally Designed Antimicrobial Peptides against SARS-CoV-2 (rdap)

Universidade Federal de Pernambuco

Departamento de Genética

**Coordenador:** Ana Maria Benko Iseppon

**Áreas do conhecimento:**

**Início da vigência:** 08-06-2020

Atualmente, como coordenadora deste projeto, possui o financiamento de agências de fomento como CAPES e CNPq que permitem a concessão de bolsas aos estudantes implicados neste projeto, bem como a manutenção de atividades biotecnológicas no laboratório (etapa posterior as análises de bioinformática). Tenho 124 artigos científicos publicados em revistas de relevância nacional e internacional, e 28 capítulos de livro de grande prestígio acadêmico. Deste modo, este projeto visa complementar as pesqu ... [Mostre mais](#)



## Regulação da tempestade de citocinas como estratégia para COVID-19: busca por novos sítios de ligação para planejamento de inibidores seletivos de IRAKs (irak)

Universidade Federal do Rio de Janeiro

Instituto de Química

**Coordenador:** Bruno Araujo Cautiero Horta

**Áreas do conhecimento:** Química

**Início da vigência:** 28-07-2020

## Segmentação e Classificação de exames de imagens: Detectando COVID-19 utilizando Inteligência Artificial (coviseq)

Centro Brasileiro de Pesquisas Físicas

Coordenação de Atividades Técnicas

**Coordenador:** Clecio Roque De Bom

**Áreas do conhecimento:** Ciência da computação

**Início da vigência:** 19-08-2020

Em função da pandemia do COVID-19, soluções inovadoras com potencial para contribuir no enfrentamento da pandemia de COVID-19 são consideradas prioridade. Um dessas formas é o apoio científico automatizado e inteligente às análises de Tomografia Computadorizada (TC) na região do pneumotórax. A técnica já é bastante aplicada na atual pandemia, porém alguns desses exames feitos em pacientes com COVID19 apresentaram achados importantes, tais como: (i) opacidades em vidro fosco; (ii) consolidação pu ... [Mostre mais](#)



MACHINE-LEARNING

# ACTIONS RELATED WITH COVID-19



## **Estudo da interação e especificidade da proteína N de coronavirus com RNA: papel na regulação da tradução (covidntd)**

Universidade Federal do Rio de Janeiro

Instituto de Bioquímica Médica Leopoldo de Meis

**Coordenador:** Fabio Ceneviva Lacerda Almeida

**Áreas do conhecimento:** Ciências biológicas; Ciências da saúde

**Início da vigência:** 16-04-2020



## **Estudo SPIRA: Sistema de Detecção Precoce de Insuficiência Respiratória por Análise de Áudio (spira)**

Universidade de São Paulo

Instituto de Matemática e Estatística

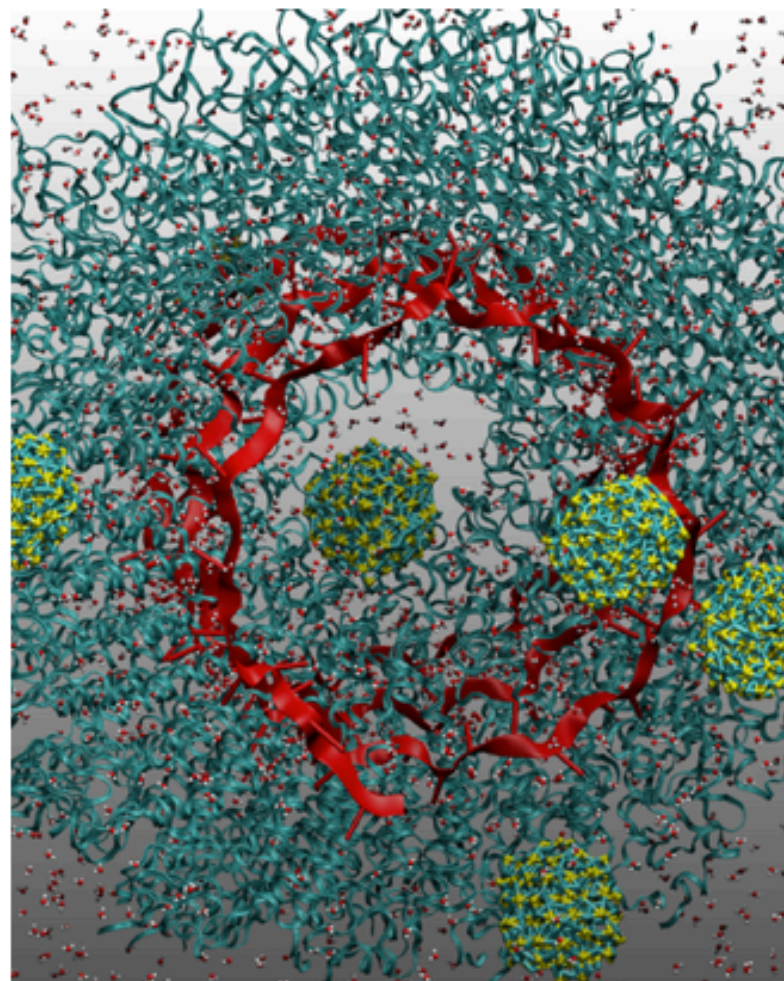
**Coordenador:** Marcelo Finger

**Áreas do conhecimento:** Ciência da computação; Ciências da saúde

**Início da vigência:** 16-07-2020

O objetivo deste estudo é desenvolver uma ferramenta que possa detectar precocemente as pessoas com insuficiência respiratória devido a COVID-19 usando dados de fala. Para tanto iremos coletar registros em áudio de pessoas infectadas bem como de pessoas normais, a fim de explorar diferenças associadas à saturação de O<sub>2</sub> e à frequência respiratória que permitam distinguir os dois grupos.

A ferramenta de classificação automática proposta será baseada em técnicas de inteligência artificial, pr ... [Mostre mais](#)



## **Estudo Teórico-Experimental de Moléculas e Nanomateriais Inativantes do SARS-CoV-2 (covidufscar)**

Universidade Federal de São Carlos

Departamento de Química

**Coordenador:** Andre Farias de Moura

**Áreas do conhecimento:** Ciência dos materiais; Ciências biológicas; Ciências da saúde; Engenharias; Física; Química

**Início da vigência:** 30-07-2020

A emergência da pandemia de COVID-19 nos coloca o desafio de reposicionamento de projetos de pesquisa para atender às demandas por novas tecnologias em diagnóstico, prevenção e tratamento desta grave doença. Evidentemente, este reposicionamento de linhas pesquisa não é praticável em todas as áreas do conhecimento com a mesma facilidade, mas especificamente na química teórica computacional existe uma grande versatilidade que deve ser abraçada neste cenário de crise. É nesse contexto que estamos a ... [Mostre mais](#)

**MACHINE-LEARNING**



# ACTIONS RELATED WITH COVID-19



## Arquitetura de Aprendizado de Máquina Multimodal para Auxílio do Diagnóstico da Covid-19 (covnet-ufcspa)

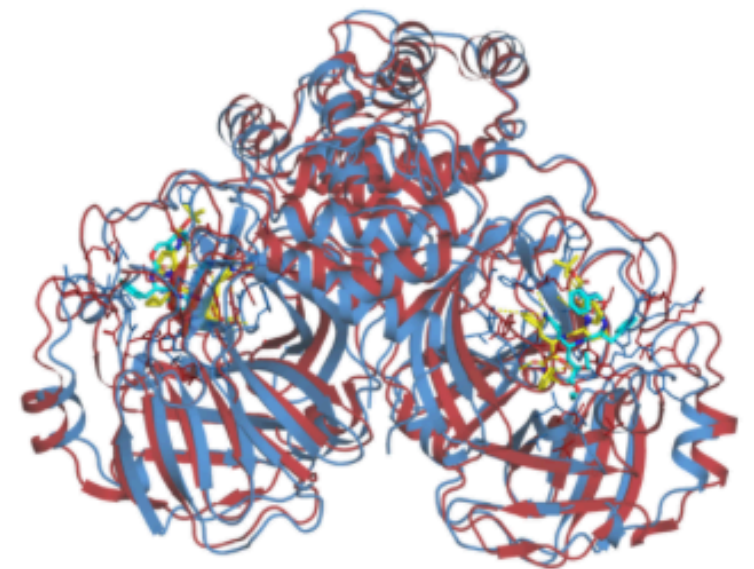
Universidade Federal de Ciências da Saúde de Porto Alegre  
Departamento de Ciências Exatas e Sociais Aplicadas

**Coordenador:** Carla Diniz Lopes Becker

**Áreas do conhecimento:** Ciência da computação; Engenharias; Matemática

**Início da vigência:** 26-08-2020

Com a chegada do SARS-CoV-2, devido às suas características regionais e populacionais, um alto índice de contágio é verificado, sobrecarregando o Sistema de Saúde Pública (SUS) e causando um número significativo de óbitos (até o dia 30/07/20, 90 mil mortes), segundo o consórcio de veículos da imprensa. As estratégias para a identificação do SARS-CoV-2 variam entre a aplicação de testes sorológicos, a realização de testes por reação em cadeia da polimerase por transcrição reversa (RT-PCR), vigil ... [Mostre mais](#)



## Avaliação da estabilidade e formas de ligação de análogos de cloroquina, anti-hipertensivos e anti-inflamatórios sobre proteínas envolvidas na infecção pelo vírus SARS-CoV-2 (covid19jf)

Universidade Federal de Juiz de Fora  
Departamento de Ciência da Computação

**Coordenador:** Priscila Vanessa Zabala Capriles Goliatt

**Áreas do conhecimento:** Ciência da computação; Ciências biológicas; Ciências da saúde; Química

**Início da vigência:** 23-04-2020



## Click Covid

Ferramenta de Informação

## Click-Covid: Uma ferramenta de informação (clickcovid)

Laboratório Nacional de Computação Científica  
Coordenação de Matemática Aplicada e Computacional

**Coordenador:** Sandra Mara Cardoso Malta

**Áreas do conhecimento:** Ciência da computação; Ciências biológicas; Matemática

**Início da vigência:** 30-07-2020

A ideia desse projeto surgiu a partir da solução Click Covid - Ferramenta de Informação Interativa submetido ao Hackcaton Hackcovid19 (<https://devpost.com/software/click-covid-ferramenta-de-informacao-interativa>). O Click Covid implementou um modelo epidemiológico de equações diferenciais não lineares, o SEIRDS, que considera indivíduos em período de incubação, implementação de quarentena, uso de máscaras ... [Mostre mais](#)

**MACHINE-LEARNING**

**SOBRE QUEM USA  
(, QUEM PROGRAMA) E  
QUEM OPERA**

## WHERE TO BEGIN

# MODULES, MODULES, MODULES...

```
abyss/2.1
align_m/2.3
anaconda2/2018.12
anaconda2/2019.10
anaconda3/2018.12
antismash/4.2.0
antlr/2.7.7_gnu
aspera-desktopclient/3.9.6
autodock-vina/1.1.2
automake/1.14
aws/current
bagel/1.1_intel
bagel/1.1_openmpi_gnu
bamtools/2.5.1
bcftools/1.9
bcl2fastq2/2.20
beagle/current
beast/1.10
beast/1.8.4
beast/2.5
beast/2.6
bedtools/2.29.0
berkeleygw/2.1_intel
bie/current_openmpi+intel
binutils/2.32
blast/2.2.31
blast/2.2.9
blast/2.6.0
blast/2.9.0
boost/1.59_gnu
boost/1.59_openmpi-2.0_intel
boost/1.69_gnu
boost/1.69_intel
boost/1.72_gnu
boost/1.73_gnu
bowtie2/2.3
bucky/1.4.4
bullxmpi/bullxmpi-1.2.8.4
bullxmpi_gnu/bullxmpi_gnu-1.2.8.4
```

```
gnu-parallel/20190422
gnuplot/5.2
go/1.12
g-phocs/1.3
grace/5.1.25
great/current
gromacs/2016_intel
gromacs/2018.4_intel17
gromacs/2018.4_openmpi_gnu+cuda
gromacs/2018.7_openmpi_gnu
gromacs/2018.8_openmpi_gnu+plumed
gromacs/2019.1_openmpi_gnu
gromacs/2019.3_openmpi_gnu
gromacs/2020.3_openmpi_gnu+cuda
gromacs/4.6.7_intel
gromacs/4.6.7_openmpi-3.1_gnu
gromacs/5.1.5_openmpi_gnu
gsl/2.4_gnu
gsl/2.5_gnu
 hdf4/4.2.13
 hdf4/4.2.14_openmpi-2.0.4.2_gnu
 hdf5/1.8
 hdf5/1.8_intel
 hdf5/1.8_openmpi-2.0_gnu
 hdf5/1.8_openmpi-2.0_intel
 hdfEOS/2.20
 healpix/3.40_gnu
 healpix/3.50_gnu
 hmmer/2.3.2
 hmmer/3.1b2
 hmmer/3.2_openmpi-2.0_gnu
 hpctoolkit/5.3.2_4712
 htlib/1.9_gnu
 humann2/current
 hypre/2.15_intel
 hypre/2.15_openmpi-2.0_gnu
 hypre/2.15_openmpi-2.0_intel
 intel-omp/2017
 intel-omp/2018
```

/scratch/app/modules

```
openmpi/gnu/2.0.4.2+cuda
openmpi/gnu/3.1.4
openmpi/gnu/3.1.5_gcc-7.4
openmpi/gnu/4.0.1
openmpi/gnu/4.0.1+cuda
openmpi/gnu/4.0.1_gcc-7.4
openmpi/gnu/4.0.4_gcc-7.4-cuda
openmpi/gnu/4.0.4_ucx_1.6
openmpi/gnu/ilp64/2.0.4.2
openmpi/gnu/mt/2.0.4.2
openmpi/gnu/mt/ilp64/2.0.4.2
openmpi/icc/2.0.4.2
openmpi/icc/4.0.4
openmpi/icc/debug/2.0.2.10
openmpi/icc/ilp64/2.0.4.2
openmpi/icc/mt/2.0.4.2
openmpi/icc/mt/debug/2.0.2.10
openmpi/icc/mt/ilp64/2.0.4.2
openmx/3.8_intel
openssl/1.0.0
orca/4.0.1
orca/4.1.1
orca/4.1.2
orca/4.2.0
orca/4.2.1
paml/4.9
paraview/5.5
paraview/5.6
paraview/5.6_osmesa
paraview/5.8
parmetis/4.0.3_intel
parmetis/4.0.3_openmpi-2.0_gnu
parmetis/4.0.3_openmpi-2.0_gnu-6.5
parmetis/4.0.3_openmpi-2.0_gnu-7.4
partitionfinder/2.1.1
perl/5.20
petsc/3.10_openmpi-2.0_gnu
petsc/3.6.0_openmpi-1.8.6_gnu
pgdspider/2.1.1
```

## WHERE TO BEGIN

# MODULES, MODULES, MODULES...

```
bwa/0.7
casino/2.14_intel
ccfits/2.5_gnu
cfitsio/3.450_gnu
cfitsio/3.450_intel
cgal/5.0.2
charmm/40b2
checkm/current
clhep/2.4_gnu
clumpy/3.0.1_gnu
clustal/w-2.1
cmake/3.12
cmake/3.17.3
cp2k/6.1_intel
cp2k/6.1_intel_no-mkl
cp2k/6.1_openmpi_gnu
cp2k/7.1_intel
cp2k/7.1_openmpi_gnu
crpropa2/2014
crpropa3/3.1.6
crpropa3/3.1.6_openmpi-2.0_gnu
crpropa3/current
ctools/1.6.3_gnu
cube/4.4
cuda/10.0
cuda/10.1
cuda/10.2
cuda/11.0
cuda/11.1
cuda/8.0
cuda/9.0
cudnn/7.3_cuda-10.0
cudnn/7.4_cuda-10.0
cudnn/7.5_cuda-10.0
cudnn/7.6_cuda-10.0
cudnn/7.6_cuda-10.1
cudnn/8.0_cuda-10.1
darshan/3.1.6_openmpi-2.0_gnu
darshan/3.1.7_openmpi-2.0_gnu
darshan/3.1.7_util
deepl/conda3-deeplearn
deepl/deeplearn-py2.7
deepl/deeplearn-py3.7
deepl/deeplearn-py3.7.4
deepl/deeplearn-py3.7.old
deepl/deeplearn-pyAtos
intel_psxe/2016
intel_psxe/2017
intel_psxe/2018
intel_psxe/2019
intel_psxe/2020
interproscan/5.36
iqtree/2.1.1
jasper/2.0.14_gnu
java/jdk-11
java/jdk-12
java/jdk-8u201
jellyfish/2.2.10
jpeg/9b
julia/1.4.2
kaiju/1.7.0
kaiju/1.7.2
kalign2/current
kraken2/2.0.7
lammps/12Dec18_intel
lammps/18Sep20_openmpi_cuda_gnu_double
lammps/18Sep20_openmpi_cuda_gnu_mixed
lammps/18Sep20_openmpi_cuda_gnu_openmp_double
lammps/18Sep20_openmpi_cuda_gnu_openmp_mixed
lammps/18Sep20_openmpi_cuda_gnu_openmp_single
lammps/18Sep20_openmpi_cuda_gnu_single
lammps/18Sep20_openmpi_openmp_gnu
lammps/3Mar20_openmpi_gnu
lammps/5Nov16_intel
lammps/5Nov16_openmpi_gnu
leptonica/1.79.0
libdap/3.18.1_gnu
libgd/2.3.0
libmagic/5.18
libqglviewer/2.7.2
libqglviewer/3.2.1
llvm/5.0
llvm/6.0
llvm/9.0
loki/0.1.7
lsdalton/2018_intel
lua/5.2
mafft/7.4
mathlibs/atlas/3.10
mathlibs/fftw/3.3.8_intel
mathlibs/fftw/3.3.8_openmpi-2.0_gnu
mathlibs/fftw/3.3.8_openmpi-2.0_intel
pgi/compilers-18.10
pgi/compilers-19.10
pgi/compilers-19.4
pgi/cuda-10.0-18.10
pgi/cuda-10.0-19.10
pgi/cuda-10.0-19.4
pgi/cuda-10.1-19.10
pgi/cuda-10.1-19.4
pgi/cuda-9.1-18.10
pgi/cuda-9.2-18.10
pgi/cuda-9.2-19.10
pgi/cuda-9.2-19.4
pgi/openmpi-2.1.2_18.10
pgi/openmpi-3.1.3_19.10
pgi/openmpi-3.1.3_19.4
php/7.4.2
phylip/3.6
picard/2.18
plplot/5.14
plumed/2.5_intel
pnetcdf/1.10_intel
pnetcdf/1.10_openmpi-2.0_gnu
pnetcdf/1.10_openmpi-2.0_intel
poco/1.9
prinseq/0.20.4
probcons/1.12
prodigal/2.6.3
proj/5.2
proj/6.0
python/2.7
python/2.7.18
python/3.6.9
python/3.7.2
python/3.8.2
q6/6.0.8
quantum-espresso/5.4_intel
quantum-espresso/6.0_intel
quantum-espresso/6.3_intel
quantum-espresso/6.4_envIRON_intel
quantum-espresso/6.4_intel
quantum-espresso/6.5_intel
quantum-espresso/6.6_intel
R/3.5.2_openmpi-2.0_gnu
rapsearch/2.24
raxml/8.2_openmpi-2.0_gnu
ray/2.3_openmpi-2.0_gnu
```

## WHERE TO BEGIN

# MODULES, MODULES, MODULES...

eggnog-mapper/1.0.3  
eigen/3.3.7\_gnu  
eigen/3.3.8\_gnu  
elpa/2016.11\_intel  
elpa/2016.11\_openmpi-2.0\_gnu  
elpa/2018.11\_intel  
energyplus/9.0.1  
energyplus/9.1  
energyplus/9.3.0  
esmf/7.1.0r\_openmpi-2.0\_gnu  
examl/2.0\_openmpi-2.0\_gnu  
fastsimcoal/2.6.0.3  
fasttree/2.1.7  
fasttree/2.1.9  
ffmpeg/4.2  
fluka/2011-2x  
fluka/2011-2x.old  
fluka/2011-3x-gfort7  
FragGeneScan/1.31  
freelut/3.2.1  
g2clib/1.6.0  
galprop/56.0.2870\_gnu  
galtoolslib/1.0.855\_gnu  
gamess/2016\_intel  
gamess/2018\_intel  
gamess/2019\_intel  
gatk/4.1  
gblocks/0.9  
gcc/6.5  
gcc/7.4  
gcc/8.3  
gdal/2.4  
gdb/9.2  
gdl/0.9  
geant4/10.6  
genemarks/4.30  
git/2.23  
glimmer/3.02  
glimmerHMM/3.0.4  
globalarrays/5.6\_intel  
globalarrays/5.6\_openmpi-gcc  
globalarrays/5.7\_intel  
gnu-common/1.8

meps/1.0  
meme/4.11.2  
mesa/18.3  
metabat/2\_gnu  
metis/5.1.0-64bits\_gnu  
metis/5.1.0\_gnu  
metis/5.1.0\_intel  
modelgenerator/85  
mrbayes/3.2.7a-OpenMPI-4.0.4  
multiwfn/3.6\_intel  
mummer/4.0  
mumps/5.1.2\_intel19  
mumps/5.1.2\_openmpi-2.0\_gnu  
muscle/3.8  
namd/2.11-ibverbs  
namd/2.11-ibverbs-smp-CUDA  
namd/2.11-verbs  
namd/2.12-ibverbs  
namd/2.12-ibverbs-CUDA  
namd/2.12-verbs  
namd/2.12-verbs-CUDA  
namd/2.13-ibverbs  
namd/2.13-ibverbs-CUDA  
namd/2.13-sd-verbs  
namd/2.13-sd-verbs-CUDA  
namd/2.13-verbs  
namd/2.13-verbs-CUDA  
ncbi-ngs/2.10.1  
nccl/2.4\_cuda-10.0  
nco/4.9.3\_gnu  
netcdf/4.6\_intel  
netcdf/4.6\_openmpi-2.0\_gnu  
netcdf/4.6\_openmpi-2.0\_intel  
nvptx-tools/1.0  
nwchem/6.8\_intel  
nxtrim/0.4  
oligoarrayaux/3.8  
opencoarrays/2.7.0  
openmolcas/intel  
openmolcas/openmpi-gcc  
openmpi/gnu/1.8.6  
openmpi/gnu/2.0.4.14  
openmpi/gnu/2.0.4.2

rosetta/3.10-2019.07\_openmpi  
rsem/1.3  
samtools/1.9  
sequana/current  
siesta/4.1\_intel  
spades/3.13  
spades-hpc/3.14  
spades-hpc/3.15  
spark/2.3+hadoop2.7  
spark/2.4+hadoop2.7  
sqlite/3.27  
sqlite/3.32.3  
sratoolkit/2.10.5  
stacks/2.52  
star/2.7.3a  
sundials/2.7\_gnu  
sundials/5.3.0  
svm-light5/current  
swift/0.96.2  
swiftT/1.4\_openmpi-2.0\_gnu  
swig/3.0.4  
swig/4.0.1  
szip/2.1.1  
t-coffee/12.0  
tensorrt/5.1  
tesseract/5.0.0  
trimal/1.4  
ucx/1.4  
ucx/1.5+cuda  
ucx/1.6  
ucx/1.6+cuda  
udunits/2.2.26  
vcftools/0.1.17  
vtk/8.1\_intel  
vtk/8.2\_intel  
vtk/9.0.1\_gnu  
wannier90/3.0\_intel  
wcslib/6.2\_gnu  
xcrysdn/1.6.2  
xerces/3.2\_gnu  
xtb/6.2.3\_intel  
zlib/1.2.11

# MODULES, MODULES, MODULES...

```
----- /usr/share/Modules/modulefiles -----  
debuggers/padb-bind/3.3      modules      openmpi/gnu/mt/2.0.4.2      openmpi/icc/mt/2.0.4.14      profilers/mpiprof-openmpi/1.0.1  
deepl/conda3-deeplearn      null        openmpi/gnu/mt/ilp64/2.0.4.14  openmpi/icc/mt/2.0.4.2      scalasca/2.4_openmpi_gnu  
deepl/deeplearn-py2.7      openmpi/gnu/2.0.4.14      openmpi/gnu/mt/ilp64/2.0.4.2  openmpi/icc/mt/ilp64/2.0.4.14  use.own  
deepl/deeplearn-py3.7      openmpi/gnu/2.0.4.2      openmpi/icc/2.0.4.14        openmpi/icc/mt/ilp64/2.0.4.2  
dot                          openmpi/gnu/ilp64/2.0.4.14  openmpi/icc/2.0.4.2        papi/5.5.1.0  
module-git                  openmpi/gnu/ilp64/2.0.4.2  openmpi/icc/ilp64/2.0.4.14  papi-devel/5.5.1.0  
module-info                 openmpi/gnu/mt/2.0.4.14    openmpi/icc/ilp64/2.0.4.2    profilers/mpiprof-intelmpi/1.0.1  
  
----- /etc/modulefiles -----  
mpi/compat-openmpi16-x86_64  mpi/mpich-3.0-x86_64      mpi/mpich-x86_64            mpi/mvapich23-x86_64        mpi/openmpi3-x86_64        mpi/openmpi-x86_64
```

# QUEUES, QUEUES, QUEUES...

Fila	Wall-clock máximo (em horas)	Número mínimo de nós (núcleos+ dispositivos)	Número máximo de nós (núcleos+ dispositivos)	Número máximo de tarefas em execução por usuário	Número máximo de tarefas em fila por usuário	Custo em Unidade de Alocação (UA)
cpu (Nós B710)	96	21 (504)	50 (1200)	4	24	1,0
nvidia (Nós B715)	48	21 (504+42)	50 (1200+100)	4	24	1,5
gdl <sup>6</sup> (Nós Sequana IA)	48	1 (40+8)	1 (40+8)	1	6	2,0
mesca2 <sup>5</sup>	48	1 (240)	1 (240)	1	6	2,0
cpu_small	72	1 (24)	20 (480)	16	96	1,0
nvidia_small	1	1 (24+2)	20 (480+40)	4	24	1,5
cpu_dev <sup>1</sup>	0:20	1 (24)	4 (96)	1	1	1,0
nvidia_dev <sup>1</sup>	0:20	1 (24+2)	4 (96+8)	1	1	1,5
cpu_scal <sup>2</sup>	18	51 (1224)	128 (3072)	1	8	1,0
nvidia_scal <sup>2</sup>	18	51 (1224+102)	128 (3072+256)	1	8	1,5
cpu_long <sup>3</sup>	744 (31 dias)	1 (24)	10 (240)	3	18	1,0
nvidia_long <sup>3</sup>	744 (31 dias)	1 (24+2)	10 (240+20)	2	4	1,5
cpu_shared <sup>7</sup>	72	1 (24)	20 (480)	16	96	1
Requisições especiais <sup>4</sup>	24	-	-	-	-	1,0
Todos os thin nodes <sup>4</sup>	24	-	756 (18144)	1	1	2,0
<b>Filas da expansão</b>						
sequana_cpu	96	1 (48)	50 (2400)	4	24	1,0
sequana_cpu_dev <sup>1</sup>	0:20	1 (48)	4 (192)	1	1	1,0
sequana_cpu_long <sup>3</sup>	744 (31 dias)	1 (48)	10 (480)	3	18	1,0
sequana_gpu	96	1 (48+4)	21 (1008+84)	4	24	1,5
sequana_gpu_dev <sup>1</sup>	0:20	1 (48+4)	4 (192+16)	1	1	1,5
sequana_gpu_long <sup>3</sup>	744 (31 dias)	1 (48+4)	10 (480+40)	3	18	1,5

## WHERE TO BEGIN

# SALLOC, SRUN, SBATCH, SQUEUE, SACCT...

```
#!/bin/bash
#SBATCH --nodes=N                #Numero de Nós
#SBATCH --ntasks-per-node=TPN   #Numero de tarefas por Nó
#SBATCH --ntasks=T              #Numero total de tarefas MPI
#SBATCH -p FILA                 #Fila (partition) a ser utilizada
#SBATCH -J JOB                  #Nome job
#SBATCH --exclusive             #Utilização exclusiva dos nós durante a execução do job

#Exibe os nós alocados para o Job
echo $SLURM_JOB_NODELIST
nodeset -e $SLURM_JOB_NODELIST

cd $SLURM_SUBMIT_DIR

#Configura os compiladores
#-----#

## 1) Utilizando o OpenMPI com Intel PSXE (2016, 2017, 2018 ou 2019)
source /scratch/app/modulos/intel-psxe-2016.sh
##### ou #####
source /scratch/app/modulos/intel-psxe-2017.sh
##### ou #####
source /scratch/app/modulos/intel-psxe-2018.sh
##### ou #####
source /scratch/app/modulos/intel-psxe-2019.sh
module load openmpi/icc/2.0.4.2

##### ou #####
## 2) Utilizando o OpenMPI com GNU
module load openmpi/gnu/2.0.4.2

#Configura o executavel
EXEC=/scratch/CAMINHO/PARA/O/EXECUTAVEL

#exibe informações sobre o executável
/usr/bin/ldd $EXEC

srun -n $SLURM_NTASKS $EXEC
```

## THE ANATOMY OF A JOB IN SDUMONT

```
sacct --jobs=556827.0 --format=JobID,MaxVMSize,AveVMSize,MaxRSS,AveRSS,MaxPages,AvePages,MinCPU,AveCPU,Elapsed,ElapsedRaw,CPUTime,CPUTimeRaw,SystemCPU,TotalCPU,UserCPU
JobID  MaxVMSize  AveVMSize  MaxRSS  AveRSS  MaxPages  AvePages  MinCPU  AveCPU  Elapsed  ElapsedRaw  CPUTime  CPUTimeRaw  SystemCPU  TotalCPU  UserCPU
-----
556827.0  31229860K  3369084K  26044684K  2897089K  53K  48.50K  02:01:14  02:02:20  00:23:56  1436  19:08:48  68928  03:04.338  08:12:34  08:09:30
```

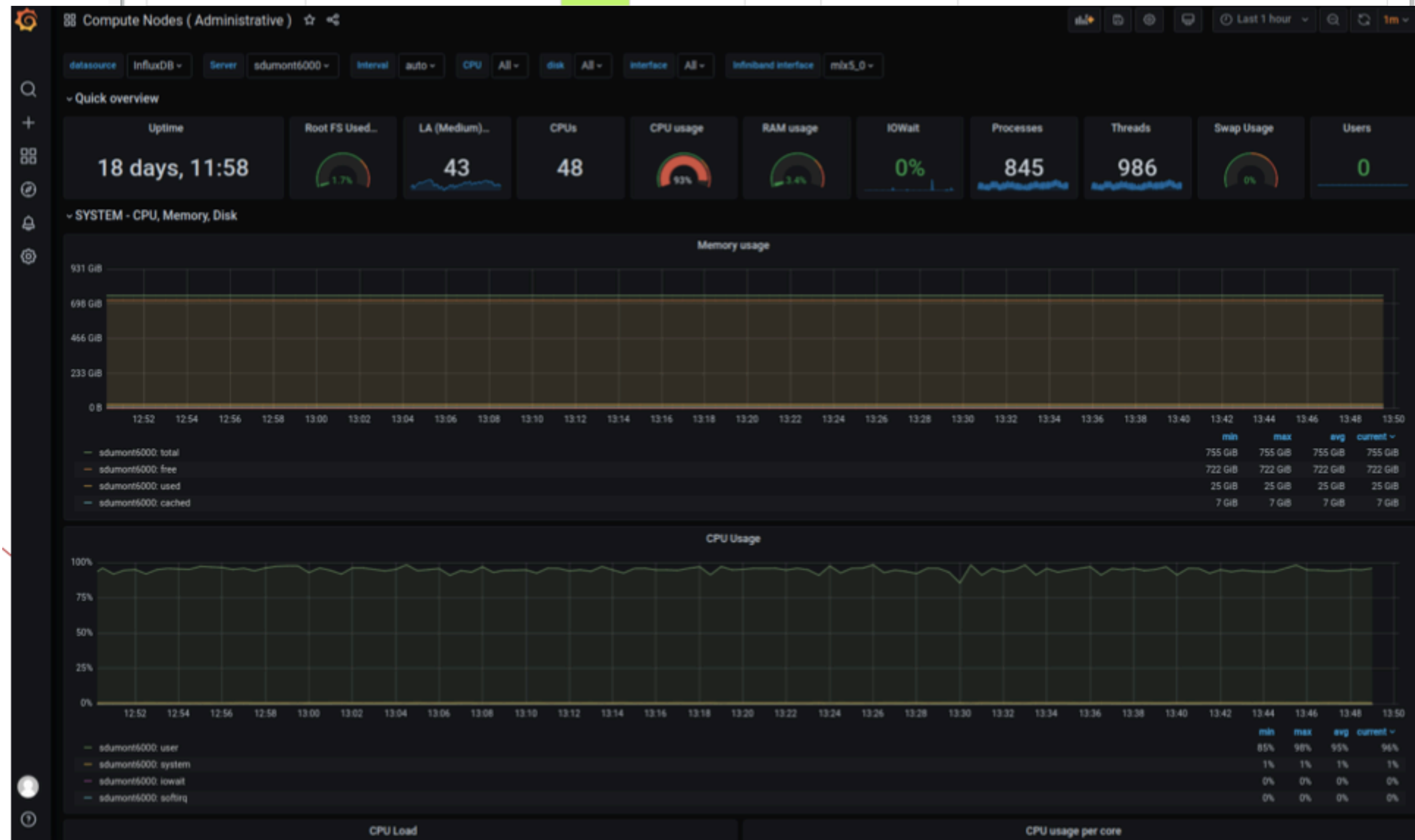


**SOBRE QUEM OPERA**

# MONITORING

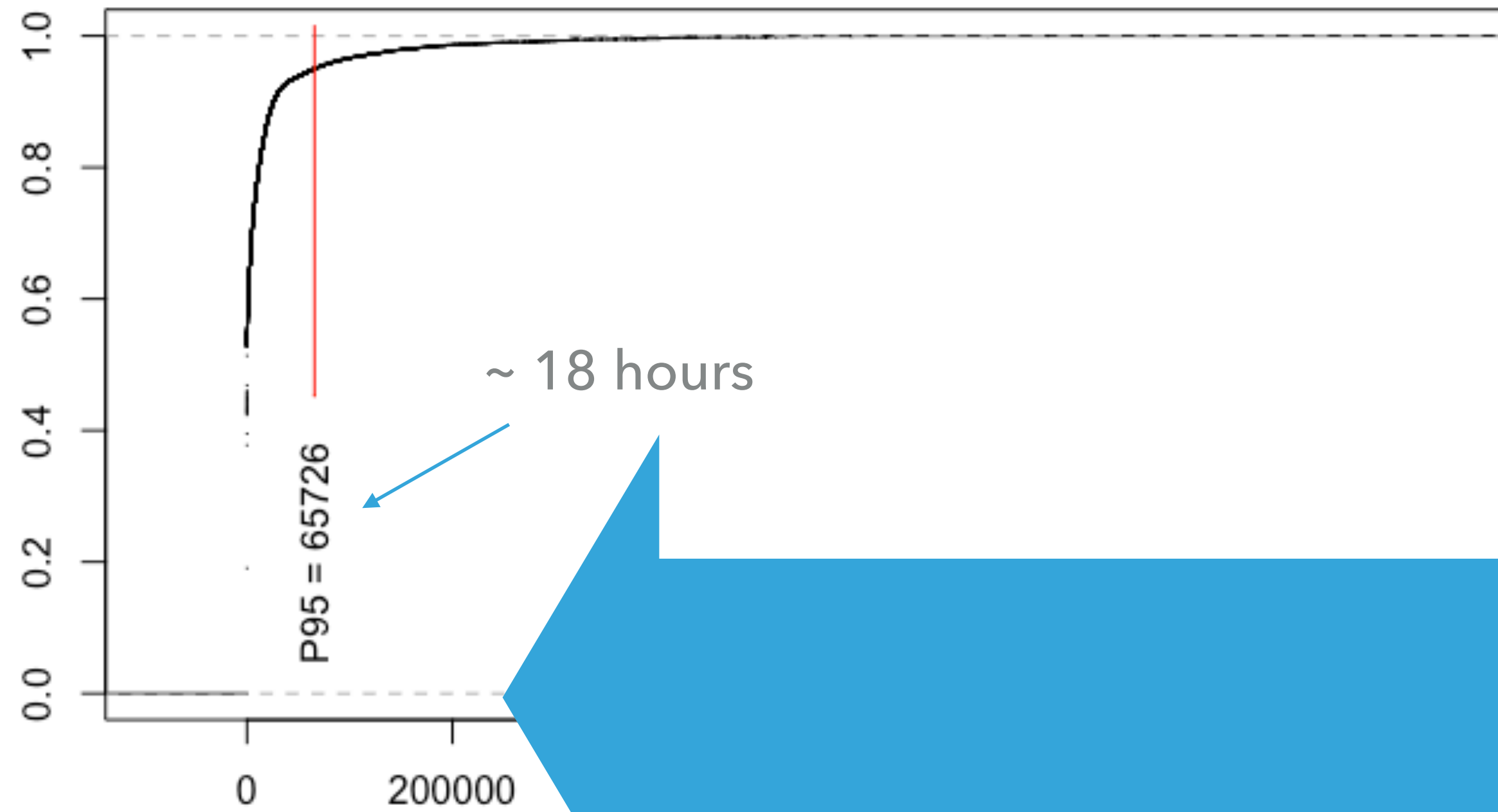
- ▶ Shared operation
  - ▶ LNCC: user services
  - ▶ ATOS/Bull: availability (power outages, cooling problems...)
- ▶ 24x7 / 8x5
- ▶ NAGIOS (automated) + GRAFANA (manual/analysis)
- ▶ Control version
- ▶ Monthly reports

Service	Status	Uptime	Progress	Last Check	Message
INROW 5.9 Temperature	Unknown	1d 2h 45m 36s	3/3	2020-06-08 11:23:51	146.134.143.250: UNKNOWN: Falha ao coletar a temperatura do inrow ip 192.168.5.9, verificar status do mesmo
LOGIN CHECK SSH E /SCRATCH	Ok	3d 5h 50m 26s	1/5	2020-06-08 11:20:03	146.134.143.250: OK : sdumont11 e sdumont14 OK!
Mobull Temperature	Ok	3d 5h 48m 38s	1/3	2020-06-08 11:22:40	146.134.143.250: OK : Media de temperatura de 19,7 graus
Nodes lbstat	Critical	3d 5h 51m 30s	5/5	2020-06-08 11:21:10	146.134.143.250: CRITICAL - Há 16 erros no IBLINKINFO, favor verificar a saída do comando iblinkinfo
Nodes Megaraid	Ok	3d 5h 52m 31s	1/5	2020-06-08 10:57:37	146.134.143.250: OK - Todos os servidores estao com discos online, mas com problema na coleta
NODES TEMPERATURE VIA AIR	Ok	3d 5h 50m 39s	1/5	2020-06-08 10:59:28	146.134.143.250: OK : Media de temperatura de 24 graus
NTP SYNC	Ok	3d 5h 47m 27s	1/5	2020-06-08 05:37:38	146.134.143.252: CRITICAL - O LOG /home/bulladm/monitor/monitor_nodes_ntp.log não está atualizado
PROCESS NODES	Warning	1d 3h 40m 45s	5/5	2020-06-08 10:43:37	146.134.143.250: WARNING - Porcentagem de servidores disponiveis 95 % (726 up, 32 down)
RMC HYB Pressao RMC14	Ok	3d 5h 52m 11s	1/3	2020-06-08 11:24:20	146.134.143.252: OK : A HYB_2 ativa da RMC14 tem a pressao eh de 180 Kpa



# THE SYSTEMS' BEHAVIOR

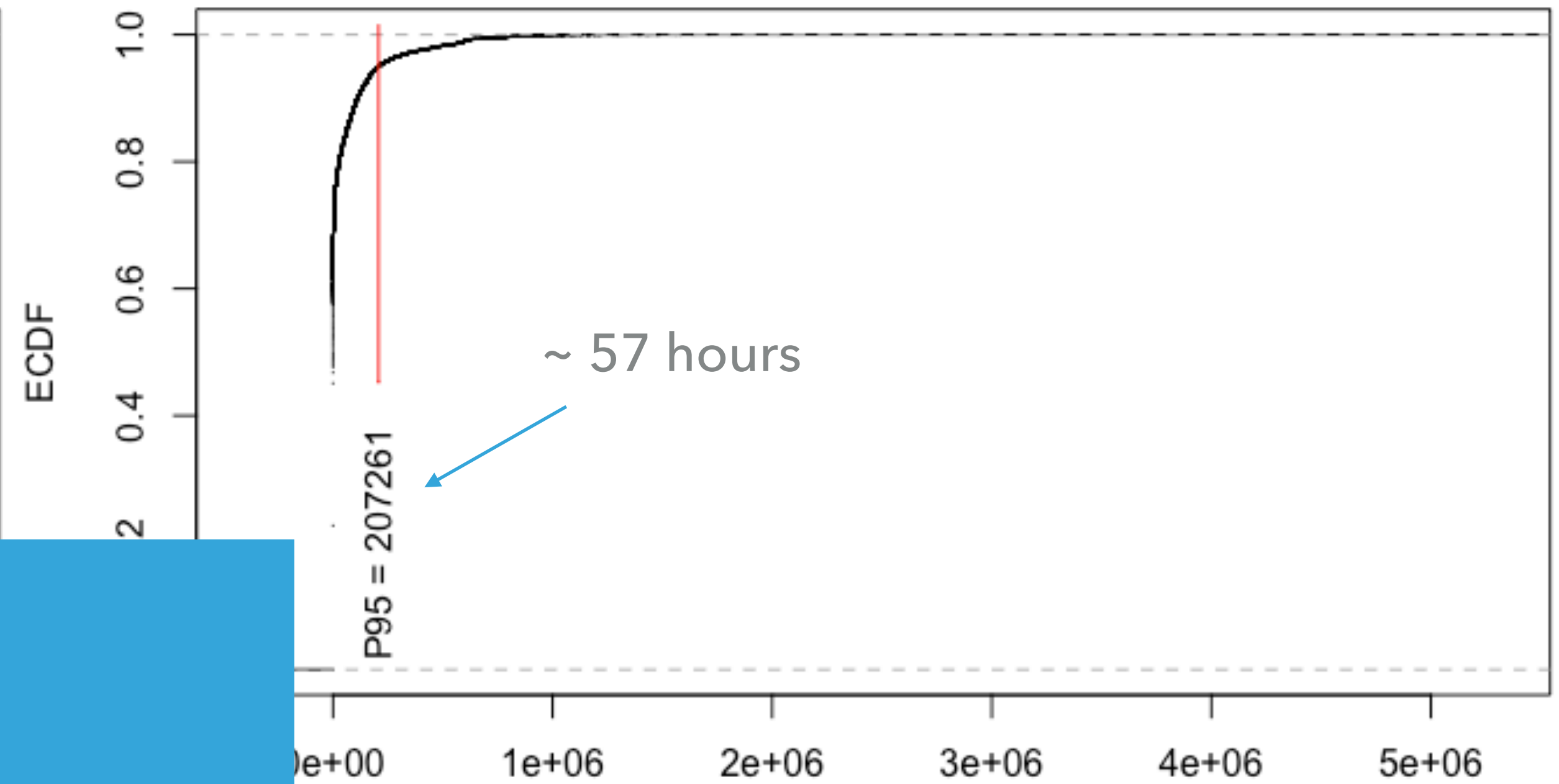
Queue waiting times of completed jobs



90 %	25827
100 %	1088599

Between  
7 hours and 12 days!

Queue waiting times of completed jobs



90 %	112358
100 %	4920842

Between  
1 and 23 days!



**SOBRE QUEM OPERA  
(E QUEM USA)**

## INTRANET

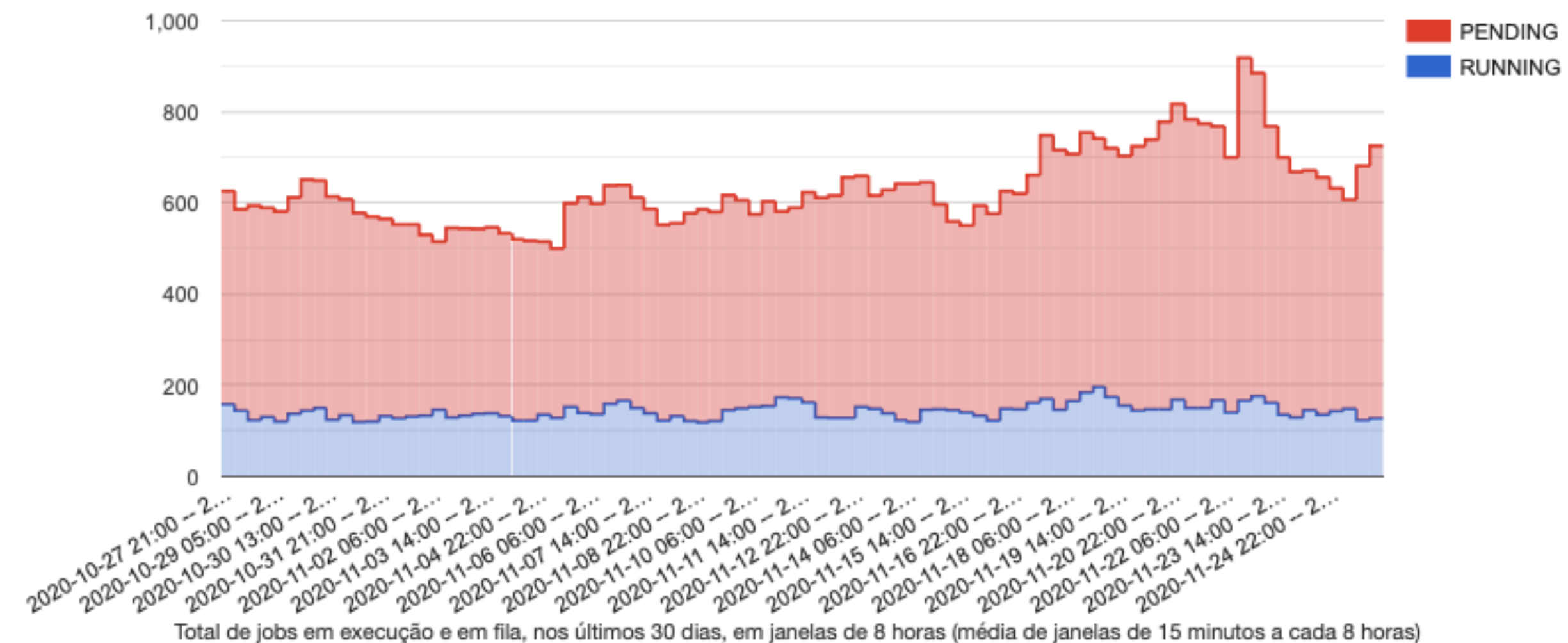
### Consumo de UAs

Total\*

\* Total: Dados coletados automaticamente a cada hora. Última coleta realizada em 2020-11-26 11:00:18

Total

**Total de jobs executados:** 717.995,00  
**Total de UAs solicitadas:** 947.376.858,00  
**Total de UAs consumidas:** 580.395.033,00  
**Percentual total de consumo de UAs:** 61,26%



Projetos com UAs solicitadas

Projetos sem UAs solicitadas

Ordenar por:

Mais UAs Consumidas

Exibir:

Todos

Status

Ativo

GID	Sigla	Tipo	Status	Ciclo	Prioridade em fila <sup>i</sup>	Início / Término	Jobs Executados	UAs Solicitadas	UAs Consumidas	Porcentagem de UAs Consumidas	Notificações <sup>i</sup>
61045	asmsol	Premium	Ativo	1	N/A	2016-09-28 / 2019-09-28	5.122	2.200.000,00	15.562.265,00	707,38%	
61219	achspecfem	Standard	Ativo	1	N/A	2020-03-04 / 2021-03-04	9	4.800.000,00	15.375.283,00	320,32%	
61160	ctws-fwi	Standard	Ativo	1	N/A	2019-06-07 / 2020-06-	339	3.000.000,00	10.752.148,00	358,40%	

# PROJECT MANAGEMENT

## INTRANET

Ano	Produção bibliográfica									Projetos		Produção técnica e de inovação			
	APP	AAP	LC	TAC	DMA	DMD	TDA	TDD	OPB	PP	PDT	PAT	PCSR	MR	OPT
2020	12	5	13	8	4	7	12	6	38	2	0	1	3	0	6
2019	108	9	12	91	29	21	21	24	33	22	0	4	10	0	27
2018	104	6	6	89	28	36	27	24	52	24	5	3	6	1	42
2017	94	16	2	121	24	16	54	15	69	37	1	1	17	0	59
2016	29	0	3	18	4	8	25	4	3	24	0	0	0	0	20
2015	0	0	0	0	1	0	18	0	0	11	0	0	0	0	0
2014	0	0	0	0	0	0	7	0	0	8	0	0	0	0	0
2013	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
2012	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
2011	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
2010	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0

Legenda:

### Produção bibliográfica

**APP** Artigos completos publicados em periódicos  
**AAP** Artigos aceitos para publicação  
**LC** Livros e capítulos  
**TAC** Trabalhos publicados em anais de congressos  
**DMA** Dissertações de mestrado em andamento  
**DMD** Dissertações de mestrado defendidas  
**TDA** Teses de doutorado em andamento  
**TDD** Teses de doutorado defendidas  
**OPB** Outras produções bibliográficas

### Projetos

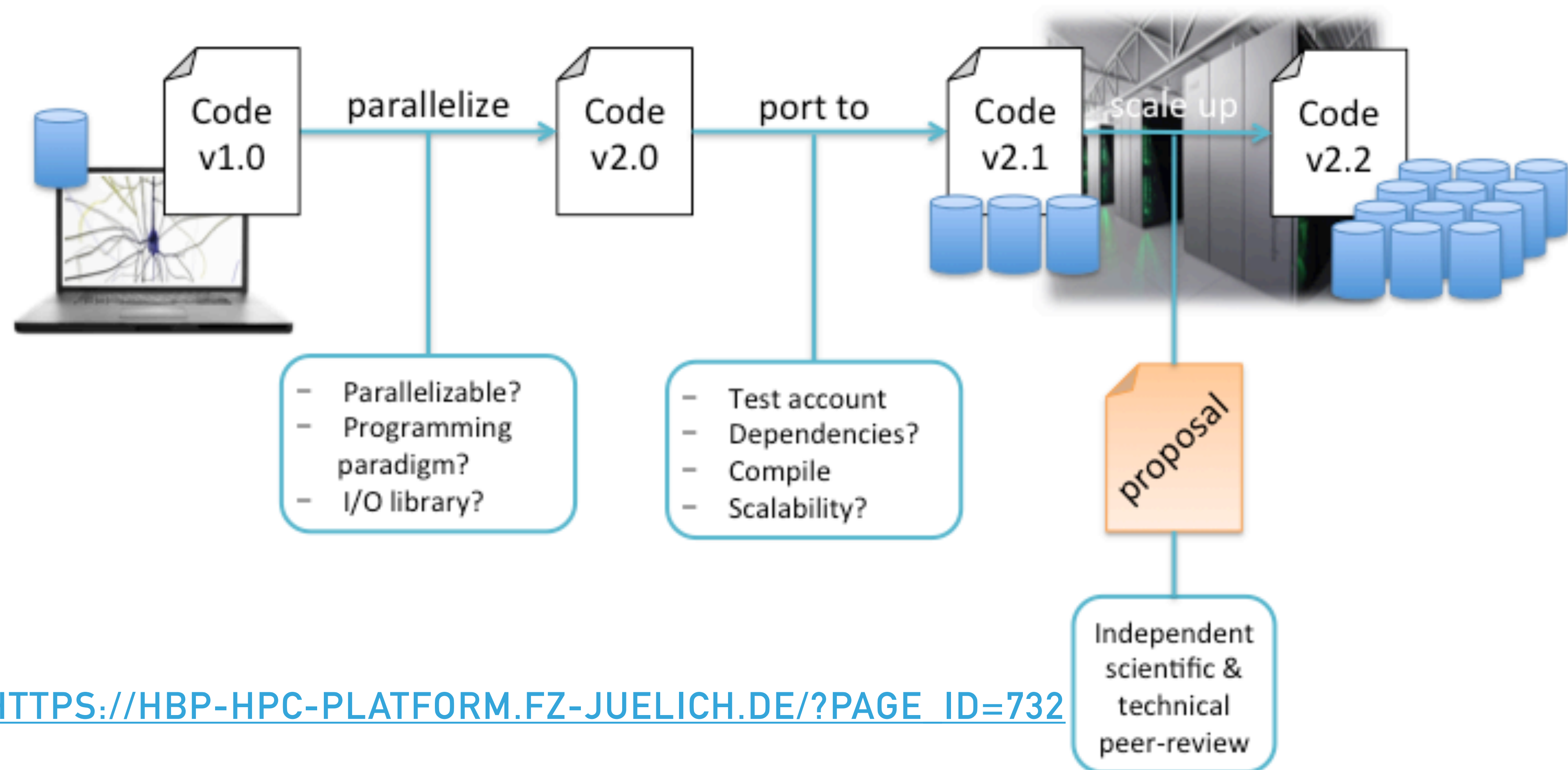
**PP** Projetos de pesquisa  
**PDT** Projeto de desenvolvimento tecnológico

### Produção técnica e de inovação

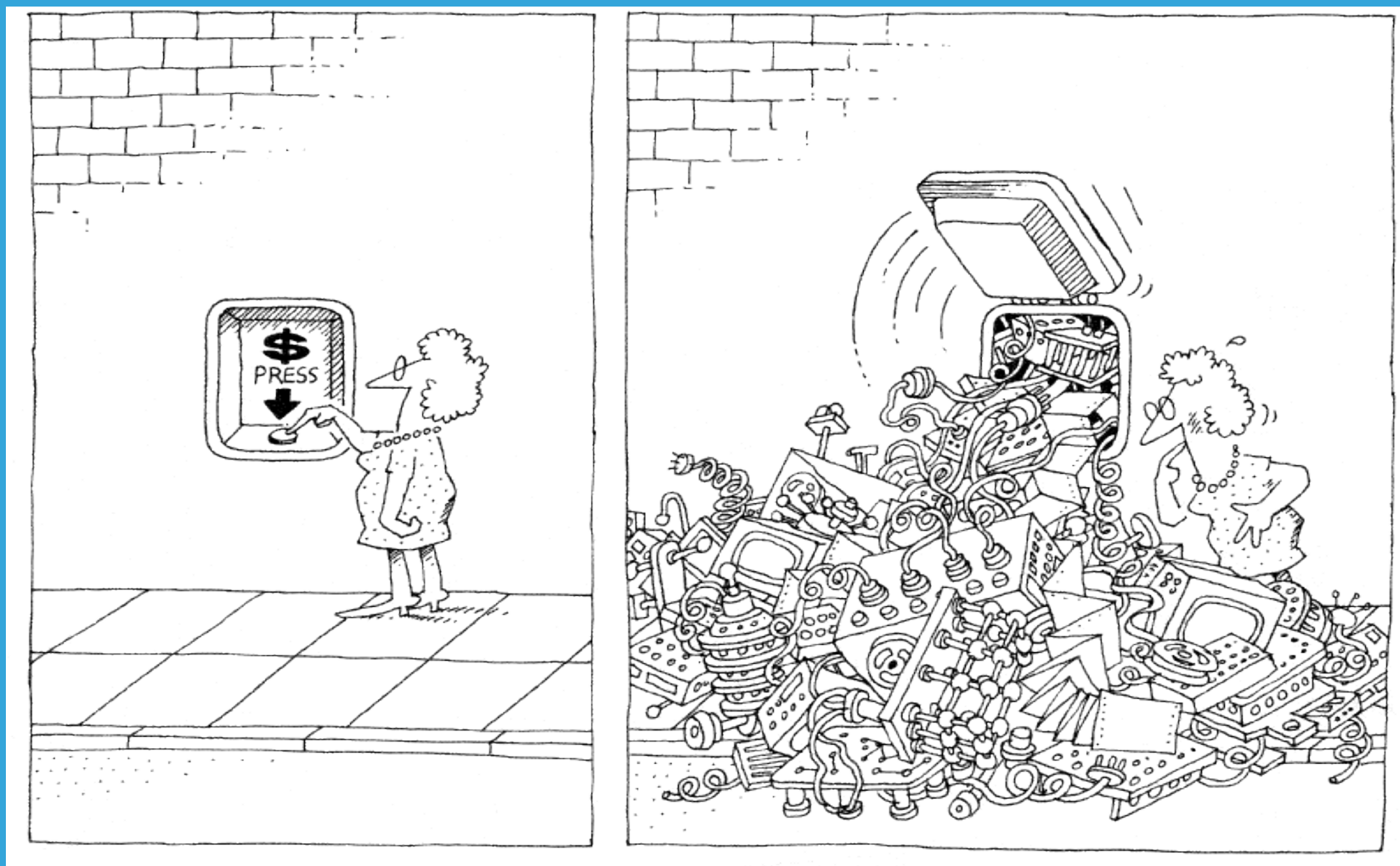
**PAT** Patentes  
**PCSR** Programas de computador sem registro  
**MR** Marca registrada  
**OPT** Outras produções técnicas

**SOBRE QUEM  
DESENVOLVE**

## THE APPLICATION PORTING WORKFLOW:







SOURCE: Booch, G. Object- Oriented Analysis and Design with Applications (2007)

**"THE FUNCTION OF GOOD SOFTWARE IS TO MAKE THE COMPLEX APPEAR TO BE SIMPLE"**

**Grady Booch**

# SCIENTIFIC SOFTWARE

“open, well-documented, and well-tested scientific code is essential not only to **reproducibility** in modern scientific research, but to the very **progression of research** itself”

“academia has been singularly successful at **discouraging** these very practices that would contribute to its success”

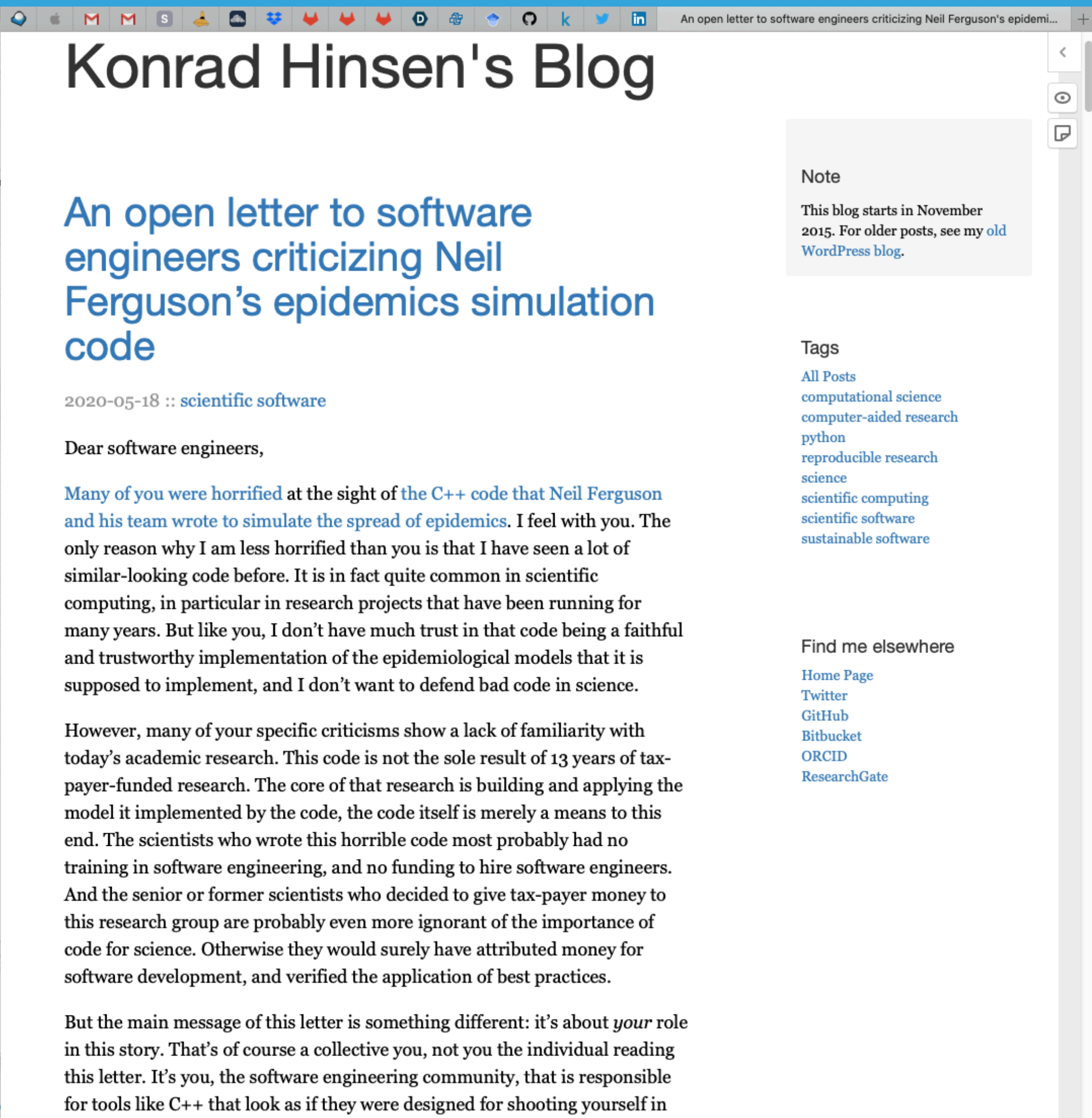
“the new breed of scientist must be a broadly-trained expert in statistics, in computing, in algorithm-building, in **software design**”

“an article about computational science in a scientific publication is not the scholarship itself, it is merely **advertising** of the scholarship. The **actual** scholarship is the complete software development environment and the complete set of instructions which generated the figures.”

Jake Vanderplas: <http://jakevdp.github.io/blog/2013/10/26/big-data-brain-drain/>

Buckheit & Donoho: “Wavelab and Reproducible Research” <http://www-stat.stanford.edu/~wavelab/>

Elsevier Executable Paper Challenge: <http://www.executablepapers.com/>



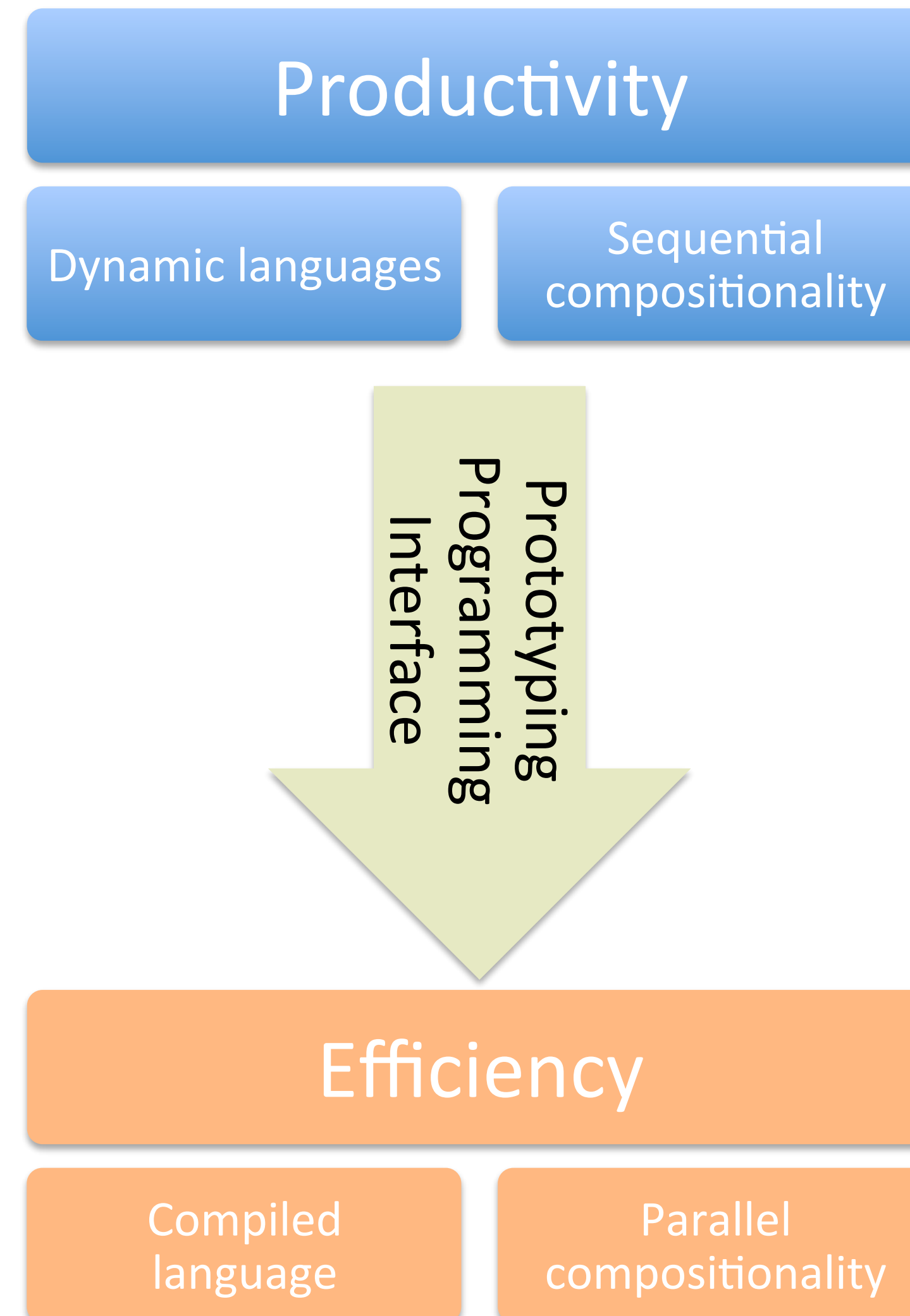
# WHAT'S YOUR ROLE IN THIS STORY?

Gilles Allain

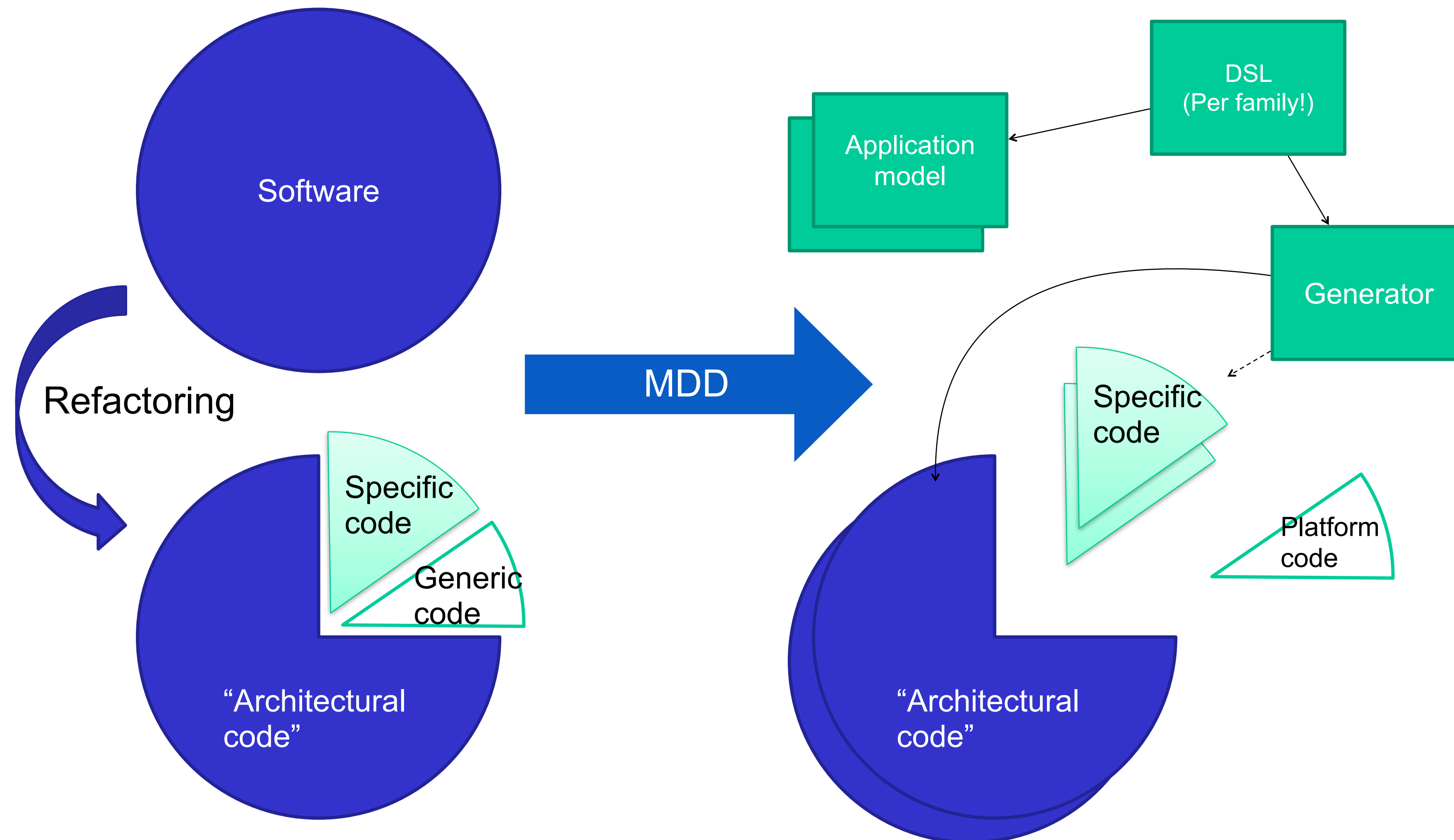
## TECHNIQUES FOR TAMING TECHNICAL COMPLEXITY

- ▶ Rapid prototyping
- ▶ Model-driven development
- ▶ (To mention my beloved ones...)

# RAPID PROTOTYPING



# MODEL-DRIVEN DEVELOPMENT

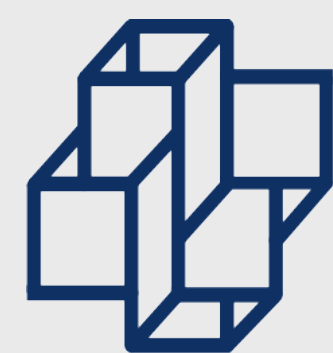


# INNOVATIVE PARALLEL FINITE ELEMENT SOLVERS — IPES

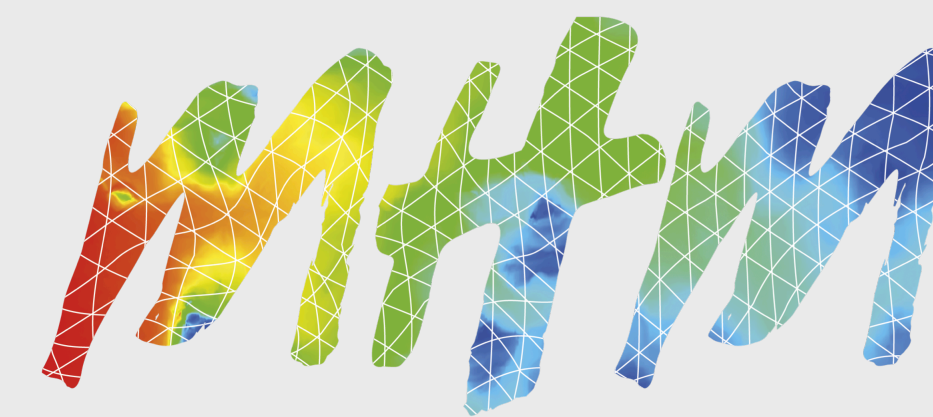
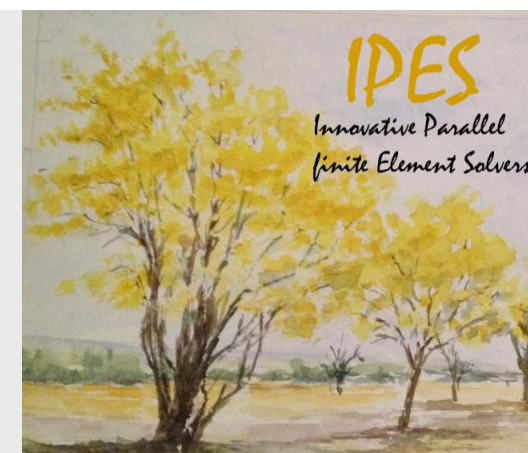
Develop, analyze and validate innovative multiscale numerical models and methods through the use of modern mathematical and computational techniques and strategies for deployment on massively parallel architectures

Contribute to multidisciplinary human-resources training

PETROBRAS, INRIA, UDEC, IUT Lyon, Univ. of  
Straitclyde, Univ. Grenoble Alpes



Laboratório  
Nacional de  
Computação  
Científica

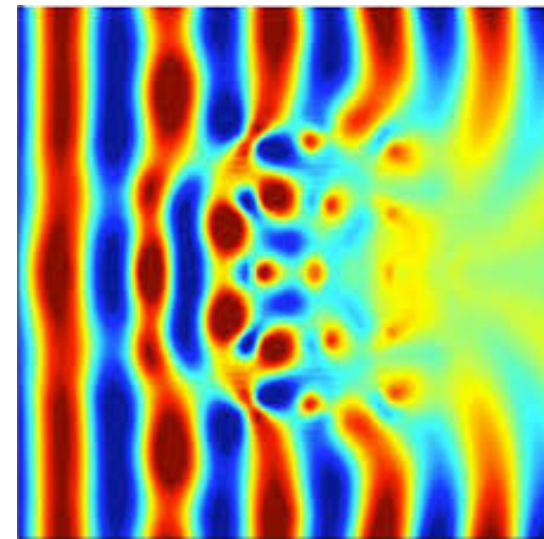


MULTISCALE  
NUMERICAL  
ALGORITHMS  
FOR HPC

## PROJECTS INVOLVING MHM

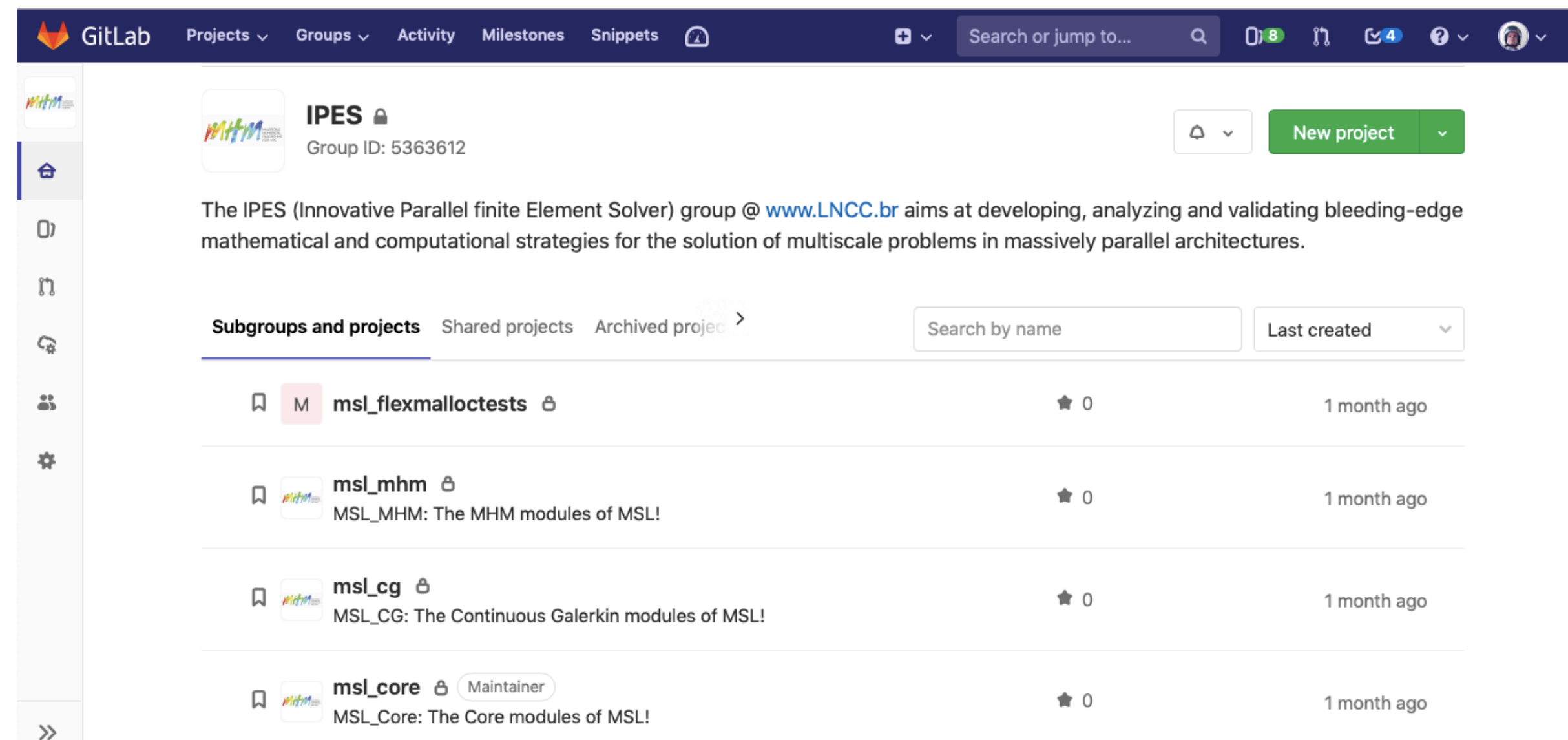
- ▶ My role in these projects: the software of course!

Hoscar



**PHOTOM**  
Math/Amsud Program

**PADEF**



The screenshot shows the GitLab interface for the IPES group. The group name is IPES (Innovative Parallel finite Element Solver) and its ID is 5363612. The description states that the group aims at developing, analyzing and validating bleeding-edge mathematical and computational strategies for the solution of multiscale problems in massively parallel architectures. Below the description, there is a list of subgroups and projects:

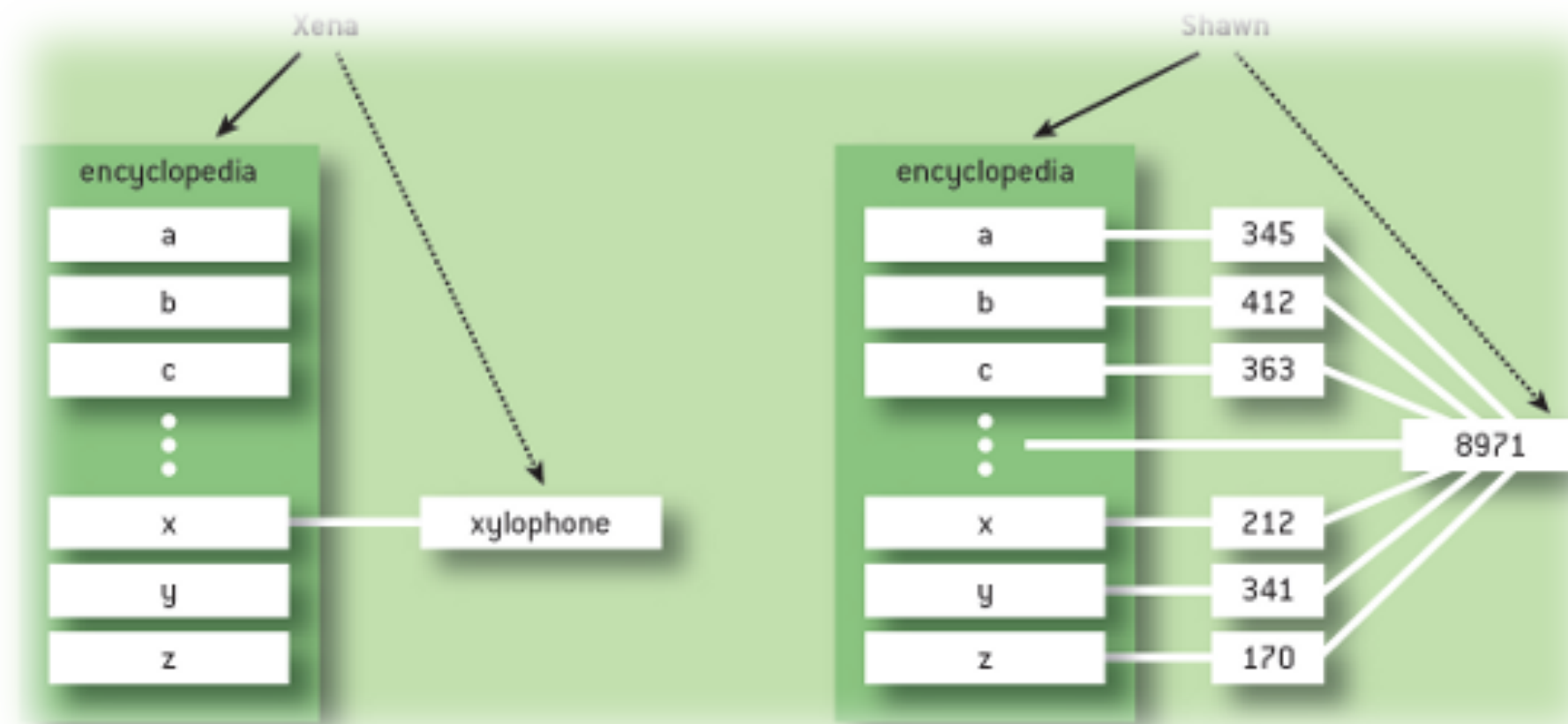
Subgroups and projects	Shared projects	Archived projects	Search by name	Last created
msl_flexmalloctests				1 month ago
msl_mhm				1 month ago
msl_cg				1 month ago
msl_core (Maintainer)				1 month ago



## THE MSL SET OF LIBRARIES

- ▶ Expresses **variational formulations** symbolically evaluated at compile-time and numerically evaluated at runtime
- ▶ Supports **classical and MHM**-based variational formulations
- ▶ **Hybrid** parallelization (OpenMP and MPI):
  - ▶ Assembly of integrals
  - ▶ Solution of linear system(s)
  - ▶ Post-processing of solution

## EFFICIENCY-ORIENTED DEBUGGING



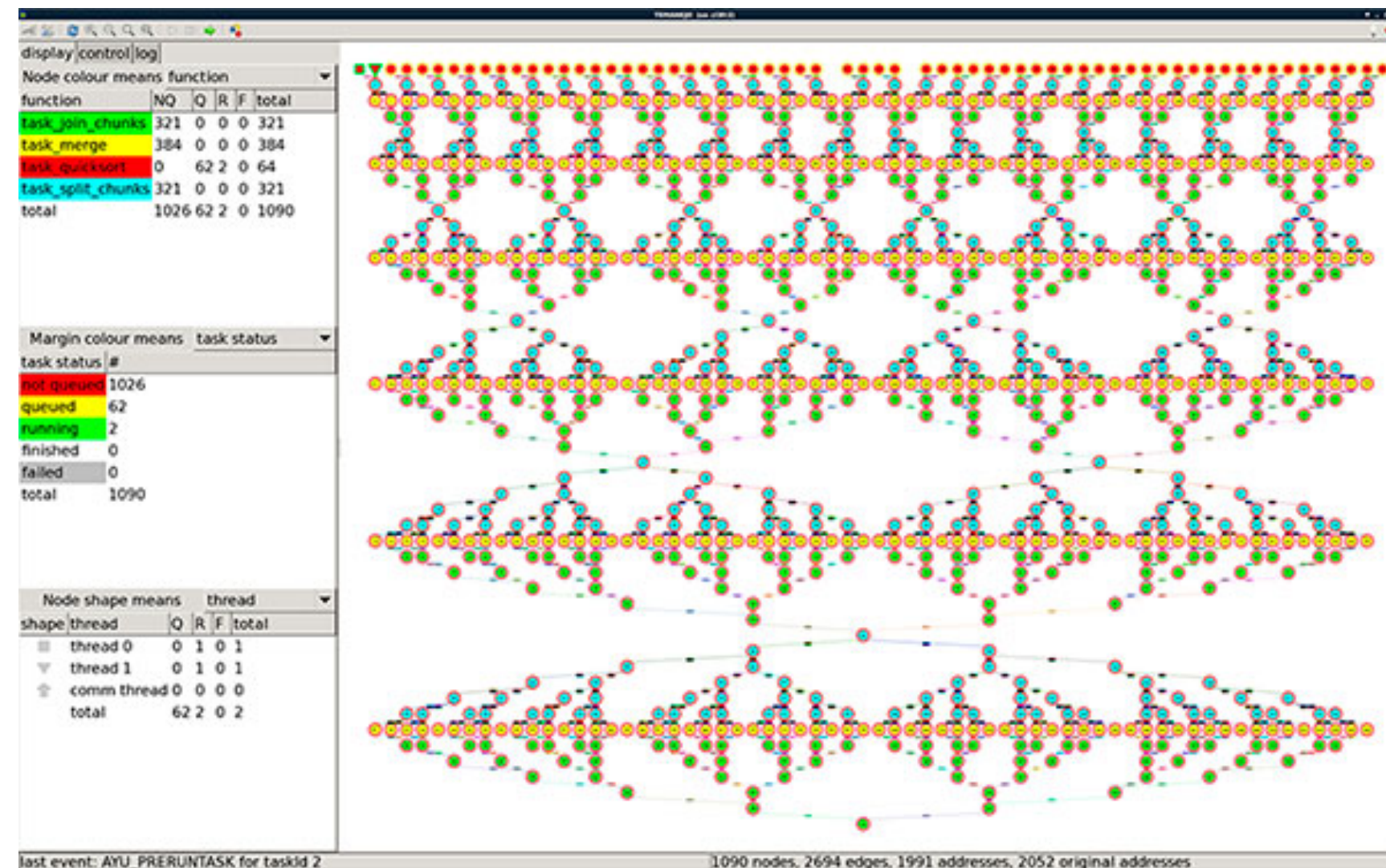
Total free memory available for allocation.



Dynamically allocated three blocks of memory (A, B, C).



Out of these three continuous blocks of allocated memory, consider that the middle block B is released. It is not possible to use the freed block B, if the memory to be allocated is larger than the size of block B.



**List of Stack Frames**

Name	Declared Type	Value	Actual Type
b2	Boolean	false	signed char
count	Integer	13	long int
inStatements	record<Interactive.Statements.IS...	record<Interactive.State...	void *
interactiveStmtList	list<record<Interactive.Statemen...	<1 item>	void *
[1]	record<Interactive.Statement.LEX...	record<Interactive.State...	void *
exp	record<Absyn.Exp.CALL>	record<Absyn.Exp.CALL>	void *
function_	record<Absyn.ComponentRef.C...	record<Absyn.Compon...	void *
name	String	"loadModel"	void *
subscri	list<Any>	<0 item>	void *
functionAr	record<Absyn.FunctionArgs.FUN...	record<Absyn.Function...	void *
semicolon	Integer	1	void *
	record<Interactive.SymbolTable	record<Interactive.Sym...	void *

**Variables View**

```

then
(resstr, st):
case (istmts, st as SYMBOLTABLE(ast = p))
equation
matchApiFunction(istmts, "getIconAnnotation");
(Absyn.CREF(componentRef = cr)) = getApiFunctionArgs(istmts);
modelpath = Absyn.crefToPath(cr);
ErrorExt.setCheckpoint("getIconAnnotation");
RTOpts.setEvaluateParametersInAnnotations(true);
resstr = getIconAnnotation(modelpath, p);
RTOpts.setEvaluateParametersInAnnotations(false);
ErrorExt.rollback("getIconAnnotation");
    
```

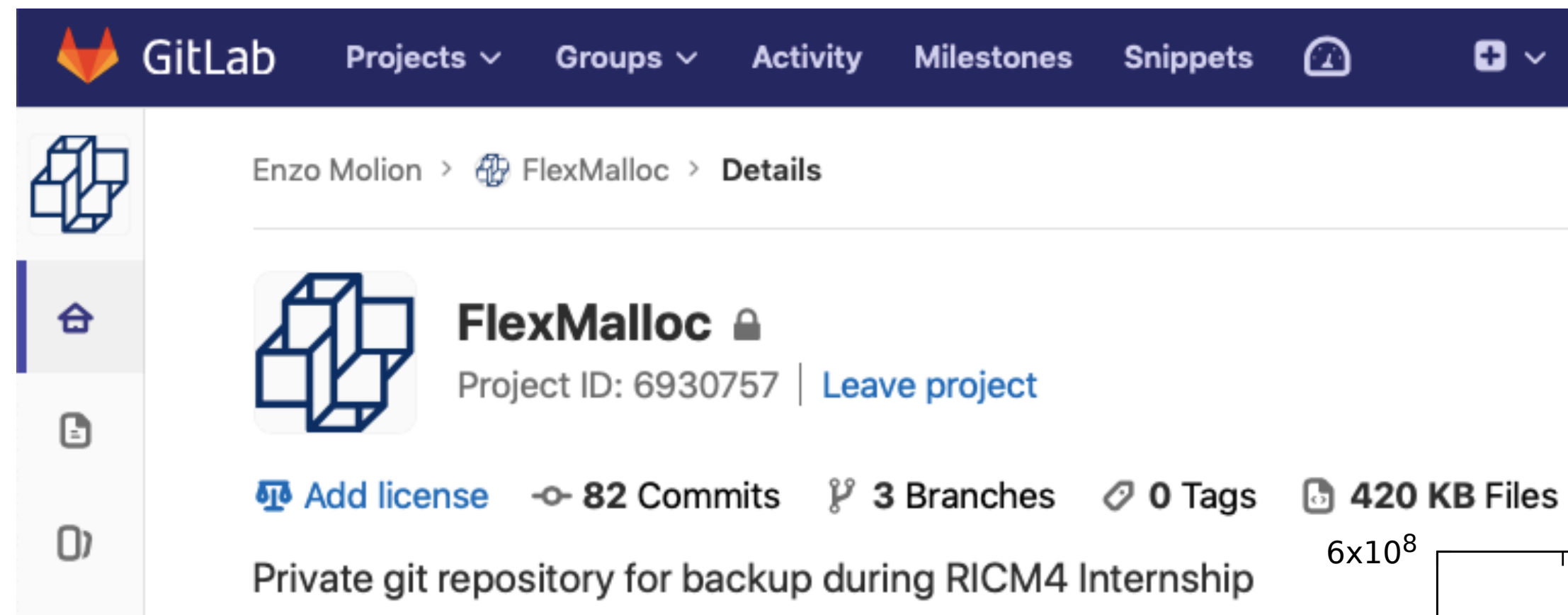
**Output View**

```

dumpCompiledFunctions(SymbolTable in:
dumpComponentsToString(Components i
eltsHasLocalClass(list<Absyn.ElementItem
emptyComponentReplacementRules(Com
emptyComponents(Components inComp
evaluate(Statements inStatements, Symbol
evaluate2(Statements inStatements, Symbc
evaluateAlgStmt(Absyn.AlgorithmItem inA
evaluateAlgStmtList(list<Absyn.Algorithmit
evaluateExpr(Absyn.Exp inExp, SymbolTabl
evaluateExprToStr(Absyn.Exp inExp, Symb
evaluateForStmt(String iter, list<Values.Val
    
```

# CHARACTERIZING AND FIXING MEMORY ALLOCATION ANOMALIES

([HTTPS://GITLAB.COM/ENZOMOLION/PROFILING-LIBRARY](https://gitlab.com/enzomolion/profiling-library))



## Concurrency and Computation Practice and Experience

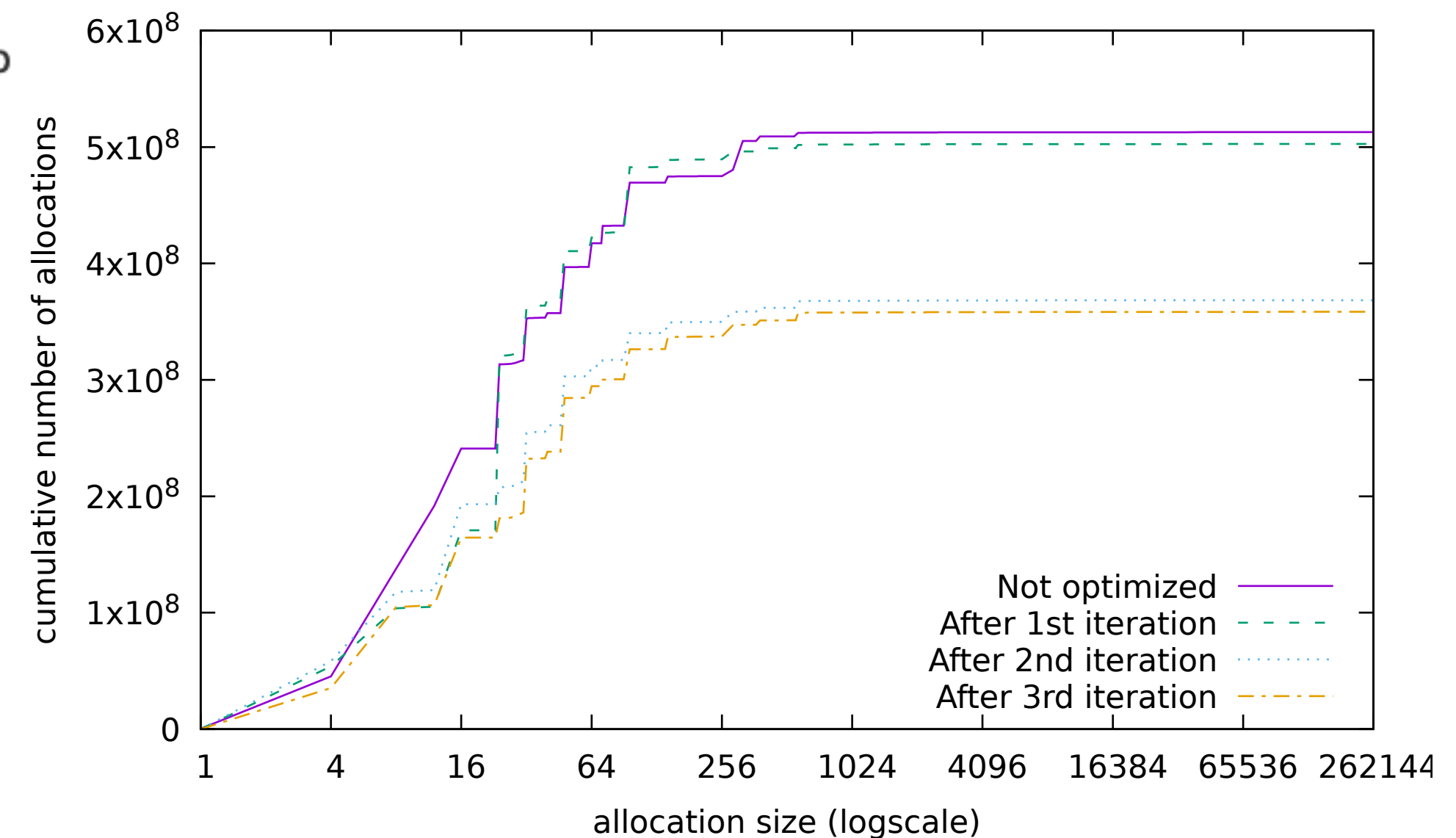
SPECIAL ISSUE PAPER

### Memory allocation anomalies in high-performance computing applications: A study with numerical simulations

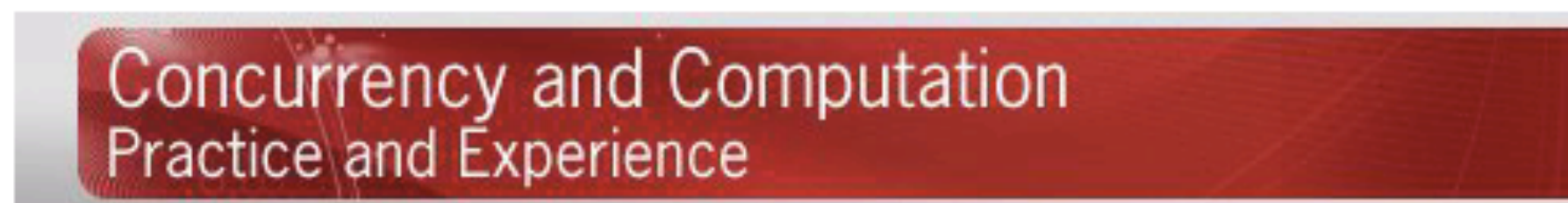
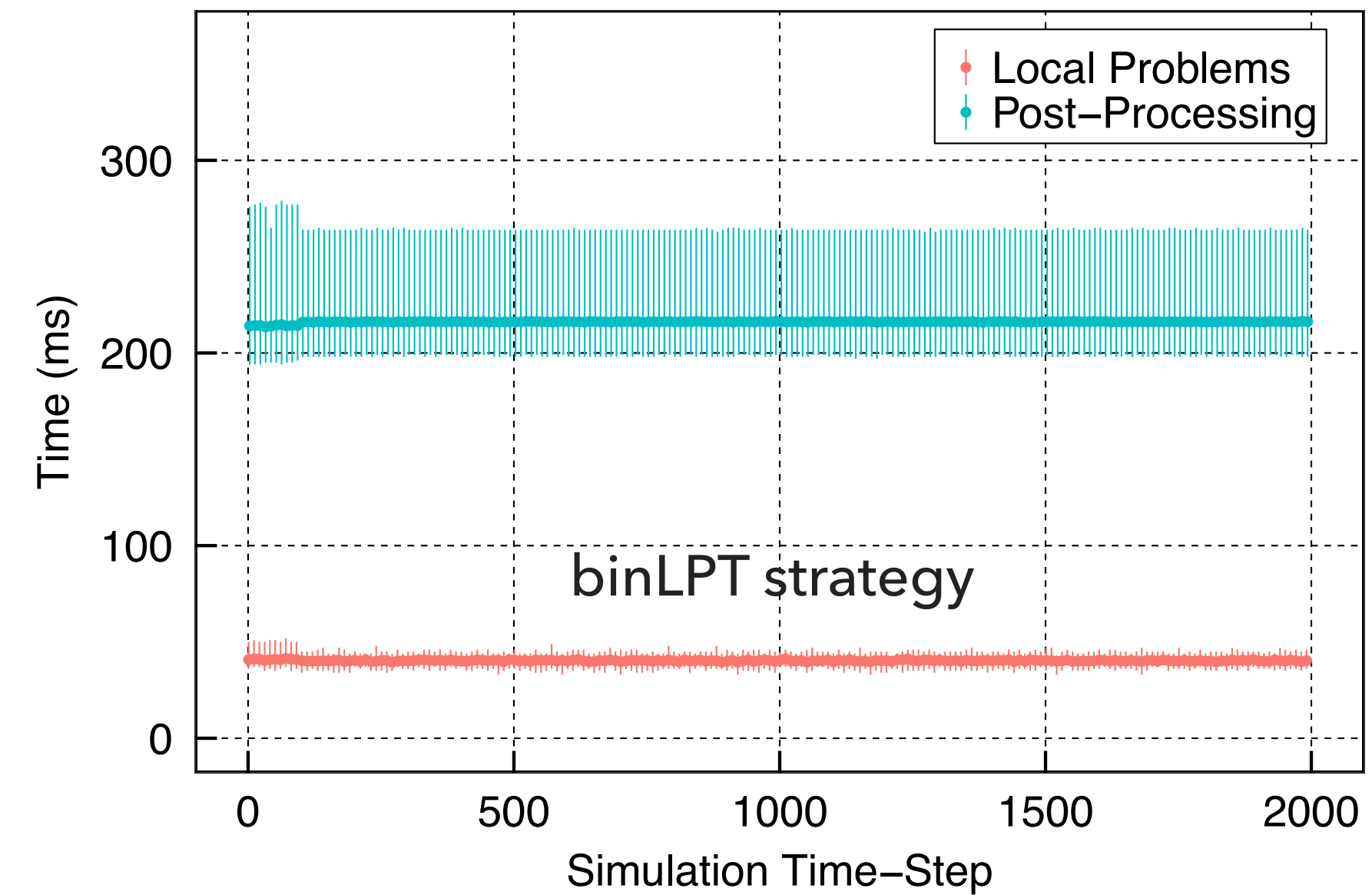
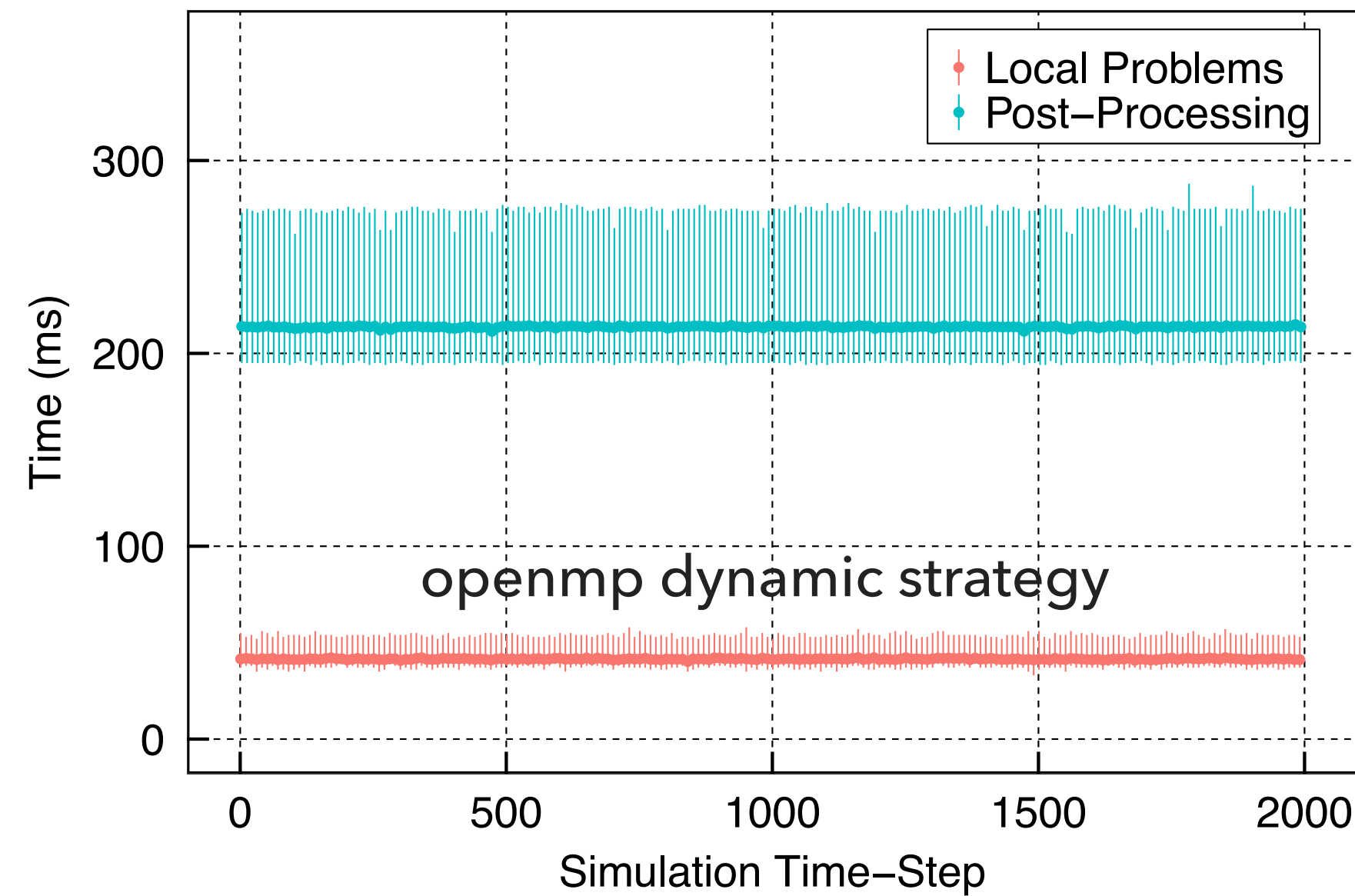
Antônio Tadeu A. Gomes ✉, Enzo Molion, Roberto P. Souto, Jean-François Méhaut

First published: 23 November 2020 | <https://doi.org/10.1002/cpe.6094>

**Funding information:** Conselho Nacional de Desenvolvimento Científico e Tecnológico; 314816/2018-6; Petrobras; 2017/00751-7



# IMBALANCE ASSESSMENT ([WWW.GITHUB.COM/LAPESD/LIBGOMP](http://www.github.com/LAPESD/LIBGOMP))



SPECIAL ISSUE PAPER | [Full Access](#)

## A comprehensive performance evaluation of the BinLPT workload-aware loop scheduler

Pedro Henrique Penna [✉](#), Antônio Tadeu A. Gomes, Márcio Castro ... [See all authors](#) [v](#)

First published: 19 February 2019 | <https://doi.org/10.1002/cpe.5170>

## REAL APPLICATIONS



Accueil Dépôt Consultation Recherche Documentation

hal-02931170, version 2

Pré-publication, Document de travail

### The MHM Method for Elasticity on Polytopal Meshes

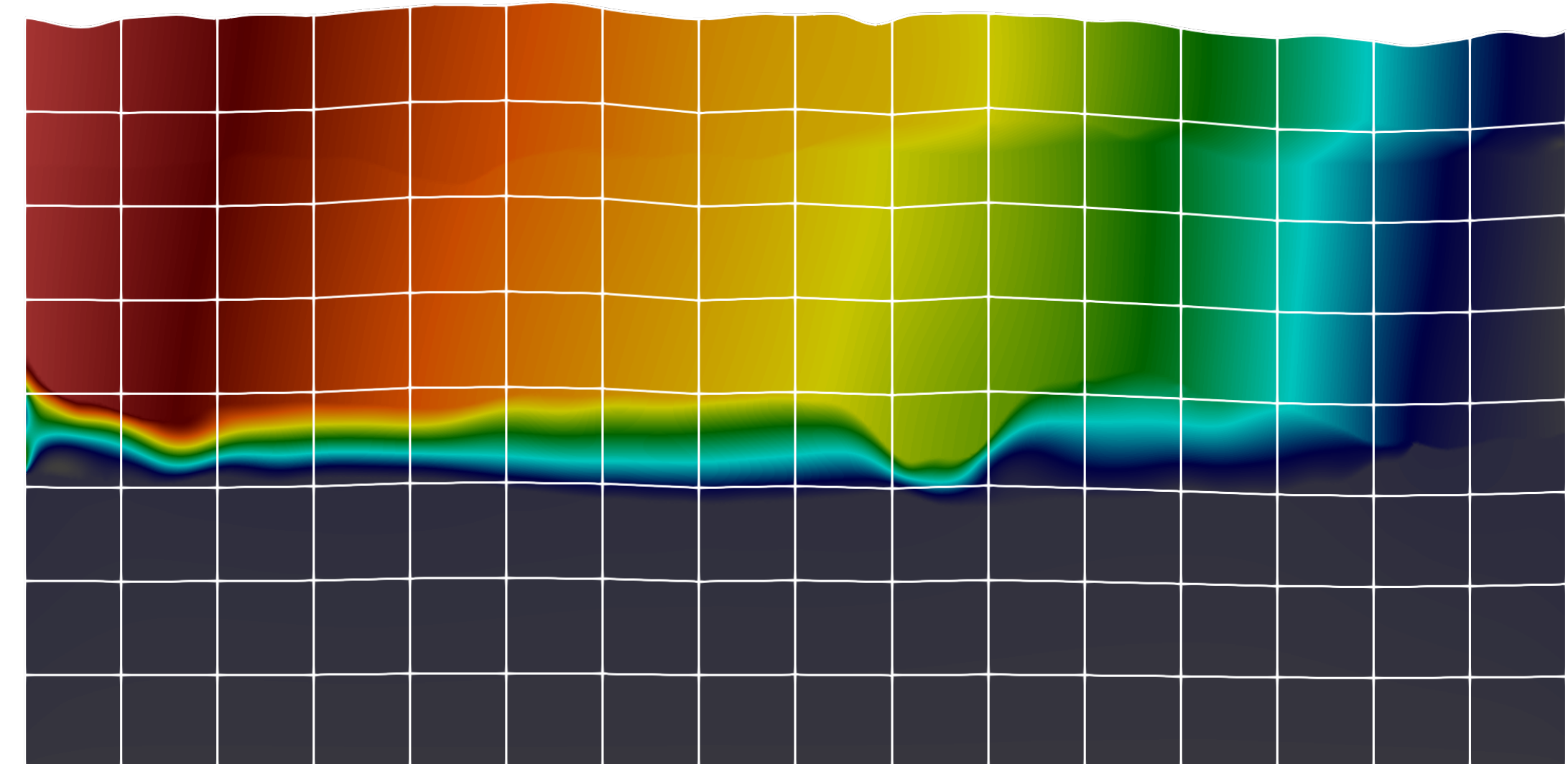
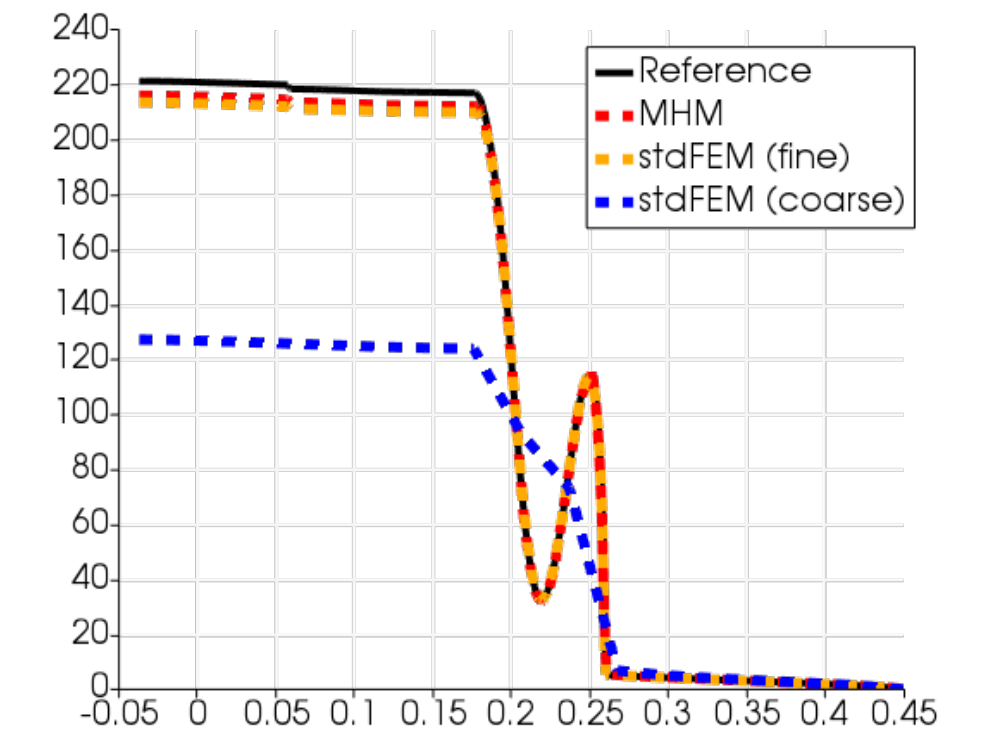
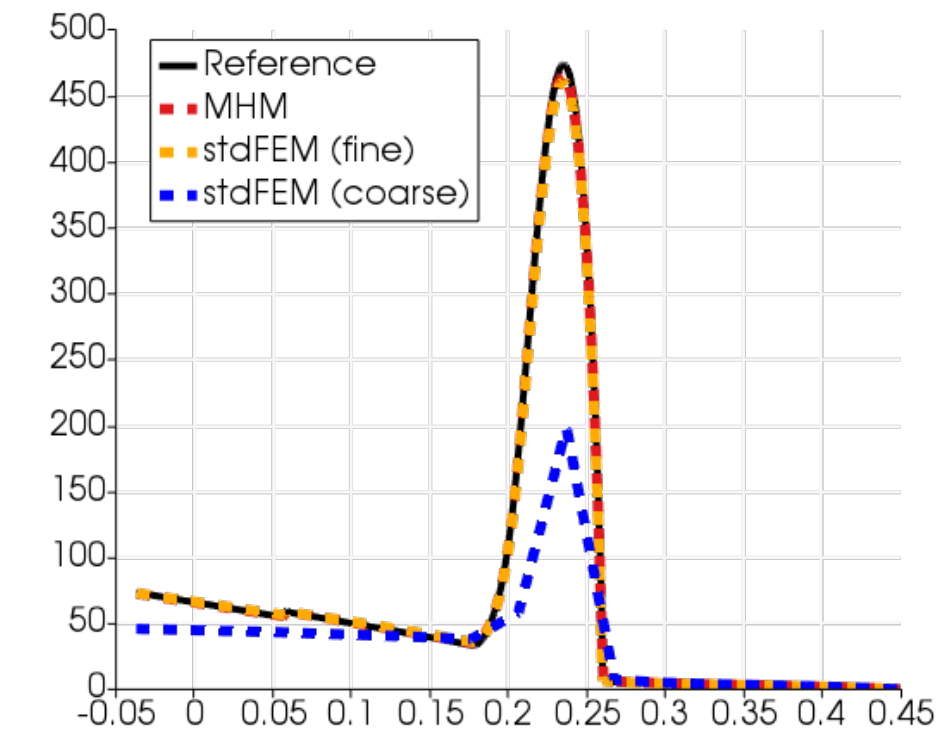
Antônio Tadeu A. Gomes<sup>1</sup>, Wesley S. Pereira<sup>1,2</sup>, Frédéric Valentin<sup>1,3</sup> [Détails](#)

<sup>1</sup> LNCC / MCT - Laboratório Nacional de Computação Científica [Rio de Janeiro]

<sup>2</sup> UFJF - Universidade Federal de Juiz de Fora

<sup>3</sup> CRISAM - Inria Sophia Antipolis - Méditerranée

**Abstract :** The multiscale hybrid-mixed (MHM) method consists of a multi-level strategy to approximate the solution of boundary value problems with heterogeneous coefficients. In this context, we propose a new family of finite elements for the linear elasticity equation defined on coarse polytopal partitions of the domain. The finite elements rely on face degrees of freedom associated with multiscale bases obtained from local Neumann problems with polynomial interpolations on faces. We establish sufficient conditions on the fine-scale interpolations such that the MHM method is well-posed. Also, discrete traction stays in local equilibrium with external forces. We show by means of a multi-level analysis that the MHM method achieves optimal convergence under local regularity conditions without refining the coarse partition. The upshot is that the Poincaré and Korn's inequalities do not degenerate, and then convergence arises on general meshes. We employ two- and three-dimensional numerical tests to assess theoretical results and to verify the robustness of the method through a multi-layer media case. Also, we address computational aspects of the underlying parallel algorithm associated with different configurations of the MHM method; our aim is to find the best compromise between execution time and memory allocation to achieve a given error threshold.

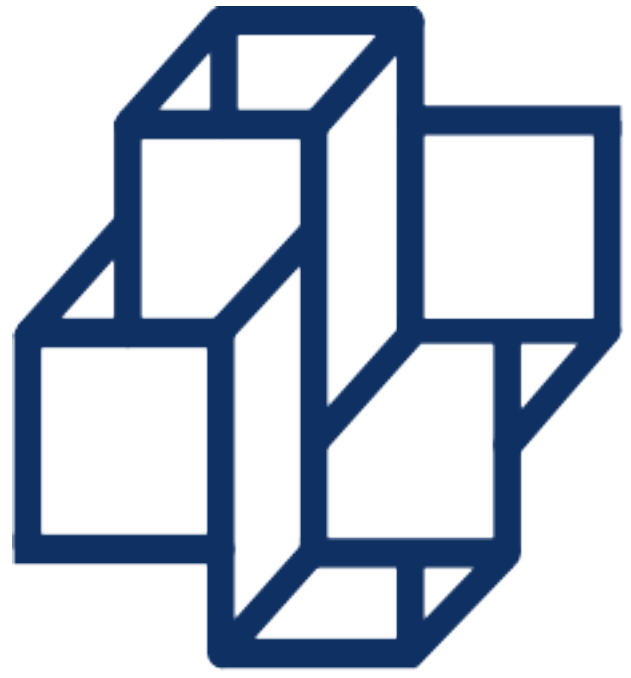


# COMENTÁRIOS FINAIS

# HPC

- ▶ Many dimensions, none simple
- ▶ Need for human resources, more than physical resources!
- ▶ Approximation between domain experts and HPC experts





Laboratório  
Nacional de  
Computação  
Científica

[ATAGOMES@LNCC.BR](mailto:ATAGOMES@LNCC.BR)

[HTTP://WWW.LNCC.BR/~ATAGOMES](http://www.lncc.br/~atagomes)

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**OBRIGADO! THANK YOU!**

**¡GRACIAS! MERCI! DANKE!**