Diffusion MRI simulation with the Virtual Imaging Platform

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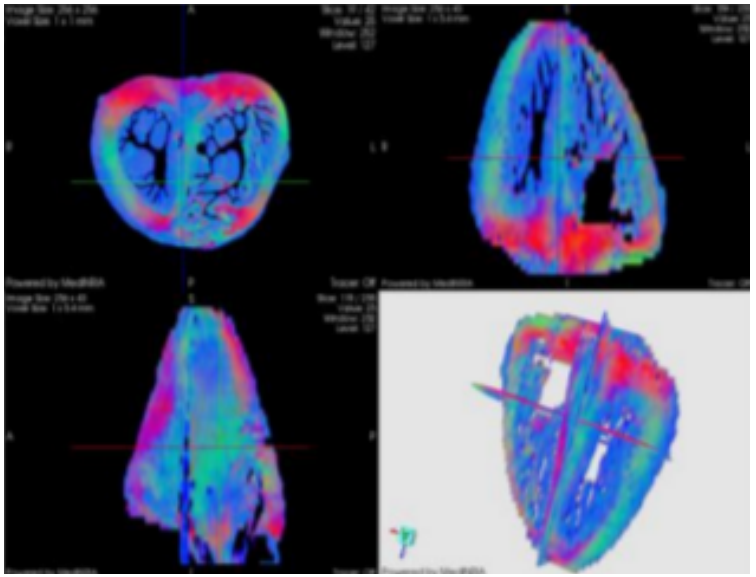
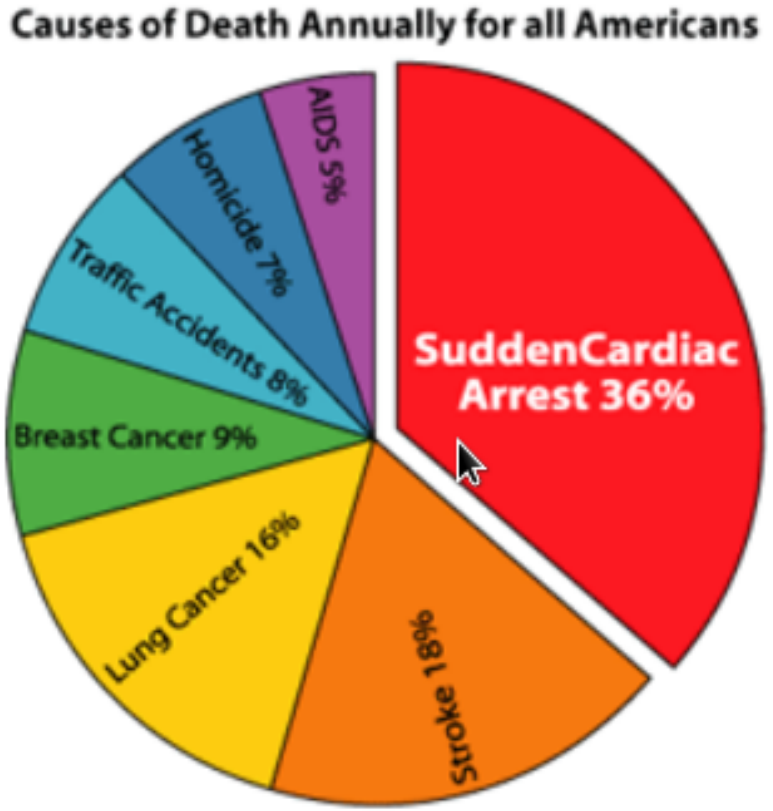
Creatis



Simulation de l'imagerie cardiaque du tenseur de diffusion
(8 ans de calcul)

Ressource de calcul de la VO biomed de EGI
(nombreuses mais non dédiées, hétérogènes, soumises aux pannes)

Background: Why we research the cardiac fiber?



- According to the survey of 2010, the heart disease is mainly responsible for the death of people.
- The cardiac fiber structure plays an important role in ensuring normal mechanical and electrical properties of the heart.
- In order to discover these diseases as early as possible, it is necessary to research the cardiac muscle structure both in normal and pathological states.

Fig1. The pie chart for the causes of death in 2011
http://www.tiptoptens.com/2011/01/12/top-10-leading-causes-of-death-in-the-world-2010-2011/

Background: How to study the cardiac fiber structures ?

- Histological method

  Studying the cardiac fiber structures by sectioning and staining.

  × Distortion and misalignment
  × Not for the whole heart
  × Ex-vivo

- Polarized Light Imaging (PLI)

  Using the birefringent characteristic of cardiac fiber and polarized light properties to investigate the cardiac fiber orientation.

  ✓ High spatial resolution
  ✓ Whole heart imaging
  × Ex-vivo

- Diffusion Magnetic Resonance Imaging (dMRI)

  Mapping the cardiac fiber structure from the displacement of water molecules therein.

  ✓ Ex-vivo and In-vivo
  ✓ The most potential method for clinical analysis of heart disease by researching the cardiac fiber achitecture.

Background: What are the problems and why simulation?

- The spatial resolution of clinical MRI is not enough fine for investigating the cardiac muscle structure in detail.

- The accuracy of cardiac fiber mapping depends greatly on the diffusion image qualities which could be influenced by many factors, such as the scanner noise, the patient motion and the artifacts caused by imperfect gradient etc.

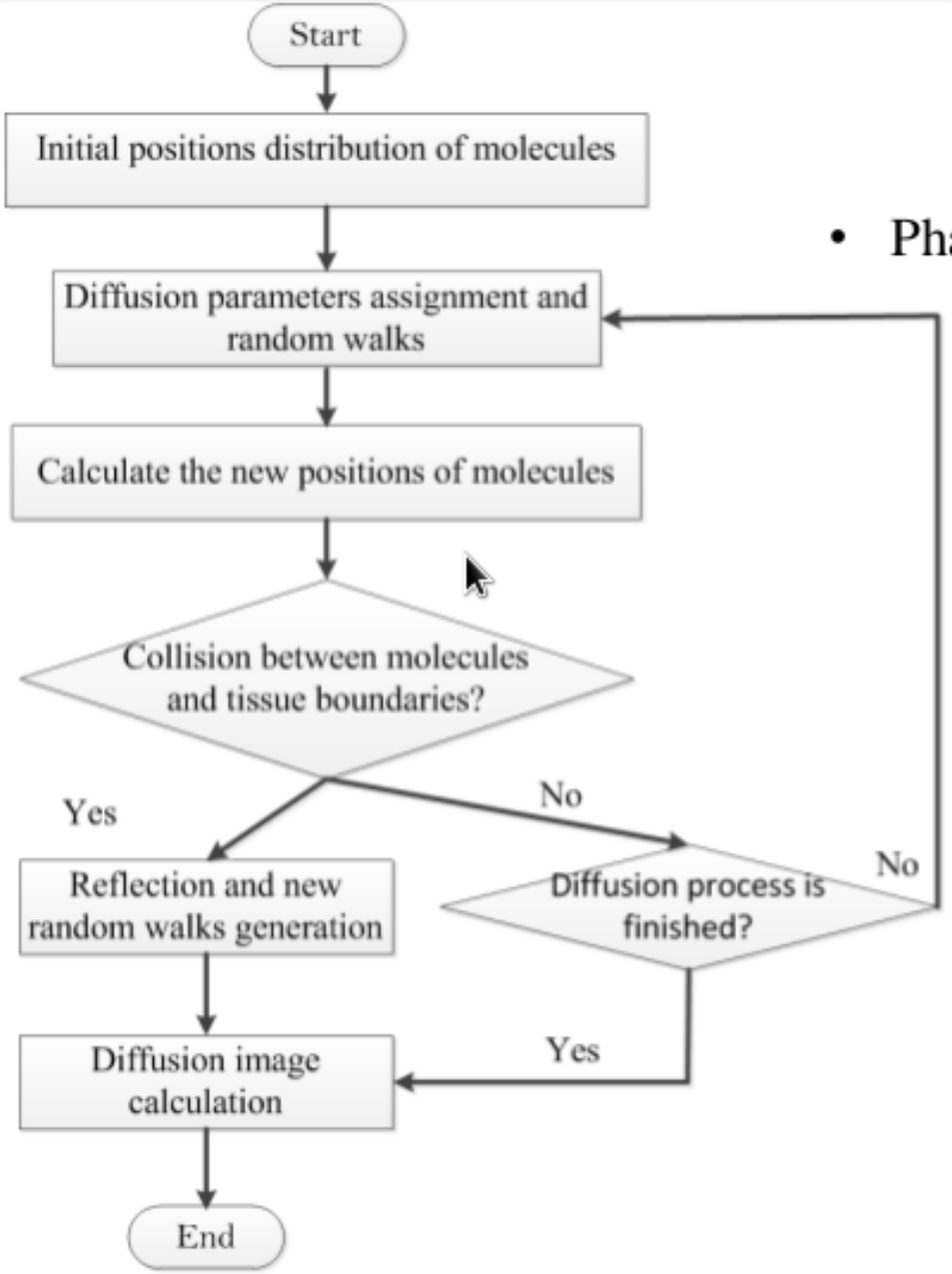
- Using the different imaging parameters will result in different images and therefore various cardiac fiber architectures. Thus in the absence of the ground-truth, it is difficult to evaluate how well the diffusion characteristics calculated from experimental dMRI reflect the actual cardiac fiber microstructure properties.

Methods: construct virtual cardiac fiber

In order to provide a ground-truth for evaluating the dMRI results, the cardiac fiber is modeled based on the PLI data, the process is illustrated as follows:

- ✓ Sample preparation: A fetus heart of 40 weeks was cut into 43 slices
- ✓ PLI: Thorough polarized light imaging, the fiber orientation map was obtained.
- ✓ Modeling: According to the orientation map and the histological knowledge, in each voxel, the cardiac fiber is modeled by a orientated cylinder with diameter ranges from 10 to 20 μm and length of 50 to 100 μm.

Methods: Simulate the diffusion MRI for virtual fiber



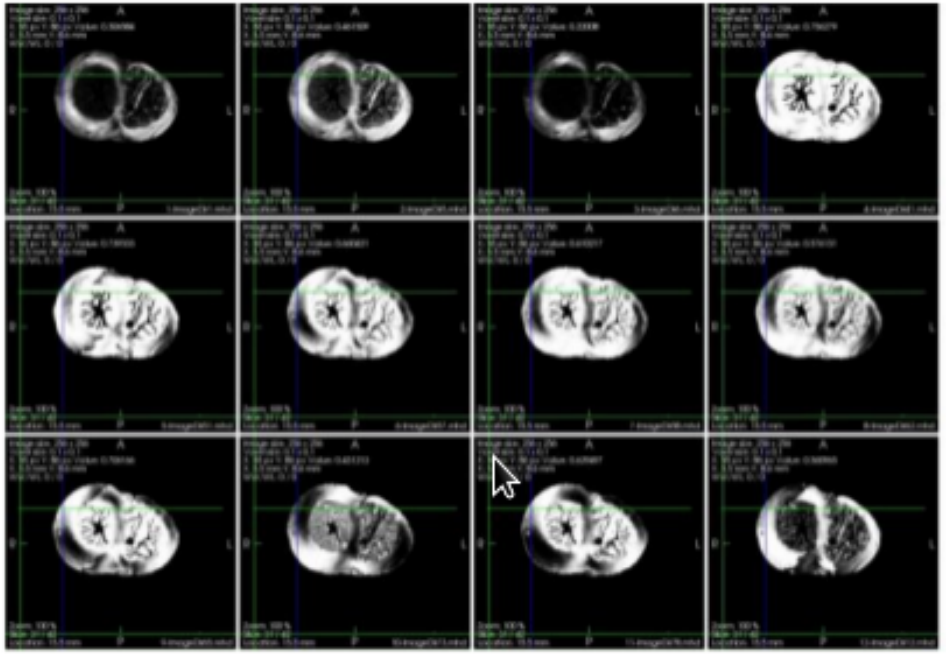
- Phase shift caused by each molecule :

$$\phi_i = \sum_{j=1}^{k} \phi_i^j = 2\pi \sum_{j=1}^{k} q \cdot r_i^j$$

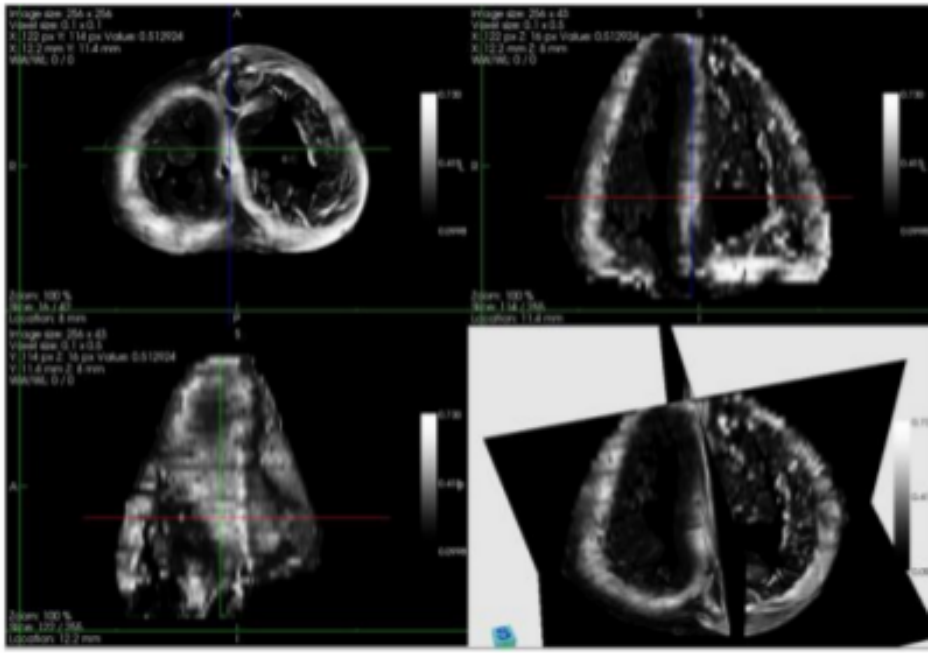
- Signal attenuation caused by the phase shift Of all the molecules:

$$E = \frac{1}{n} \sqrt{(\sum_{i=1}^{n} \cos(\phi_i))^2 + (\sum_{i=1}^{n} \sin(\phi_i))^2}$$

Results : Diffusion weighted (DW) images



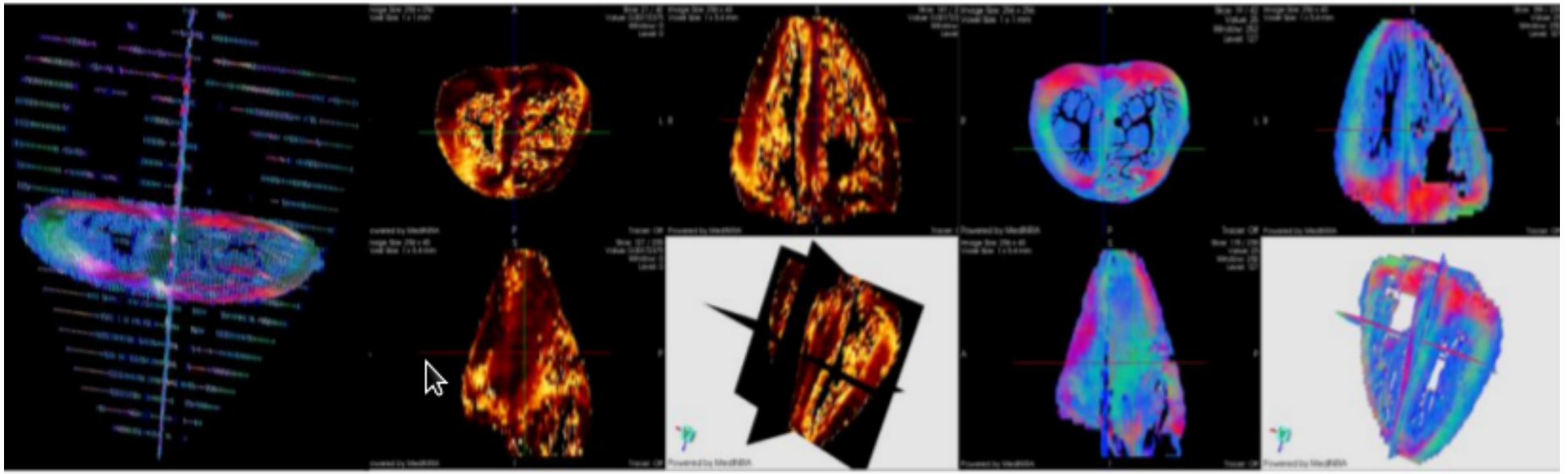
(a) Simulated DW images for one slice in different diffusion gradient directions



(b) Simulated DW images for whole heart in one diffusion gradient direction

Fig2. The simulated diffusion weighted images for ex-vivo fetus heart. Simulation parameters: diffusion time=200 ms, b value= 2288 s/mm2, diffusion gradient directions=162, number of water molecules involved in the simulation= 16 billion.

Results: Diffusion tensor, MD and FA images



(a) Diffusion Tensor Image (b) MD (c) FA

Fig. 3 Diffusion Tensor, MD and FA images. Diffusion coefficient used in the simulation is 10^{-3} mm^2/s, the simulated MD ranges from 4×10^{-4} mm^2/s to 7×10^{-4} mm^2/s, FA changes from 0.31 to 0.96.

The combination of PLI and DWI provides us not only the fiber orientation distribution but also FA and MD information. It takes advantage of the merit of high spatial resolution of PLI which compensates the insufficiency of experimental dMRI.

Perspectives

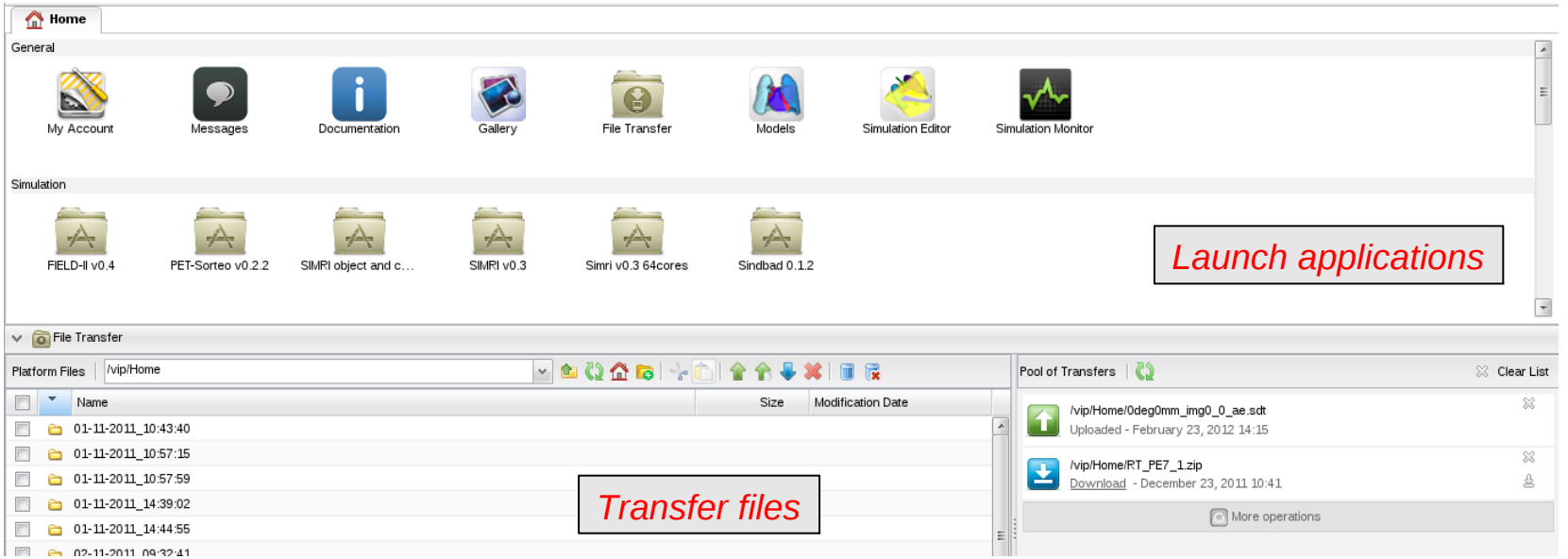
- The simulator allows to simulating the DW images with different imaging sequences and parameters, thus by comparing the simulation results with the ground-truth, the imaging parameters could be optimized.

- In vivo cardiac fiber models can be constructed based on PLI data and motion information derived from MRI cine sequences and as a result in vivo DW images can be simulated.

- The simulated noise-free and non-artifact images can be used for evaluating diffusion image processing algorithms, such as de-noising, k-space reconstruction, and motion correction.

Déploiement sur la grille

- **Disponible dans la "Virtual Imaging Platform" (VIP)**
  - http://vip.creatis.insa-lyon.fr



- **Ressources de calcul et de stockage**
  - Grille EGI, organisation virtuelle biomed
  - Environ 150 sites de calcul et de stockage
- **Pour cette expérience**
  - Temps CPU total : 8 ans, calculé en 1 mois

Parallélisation statique

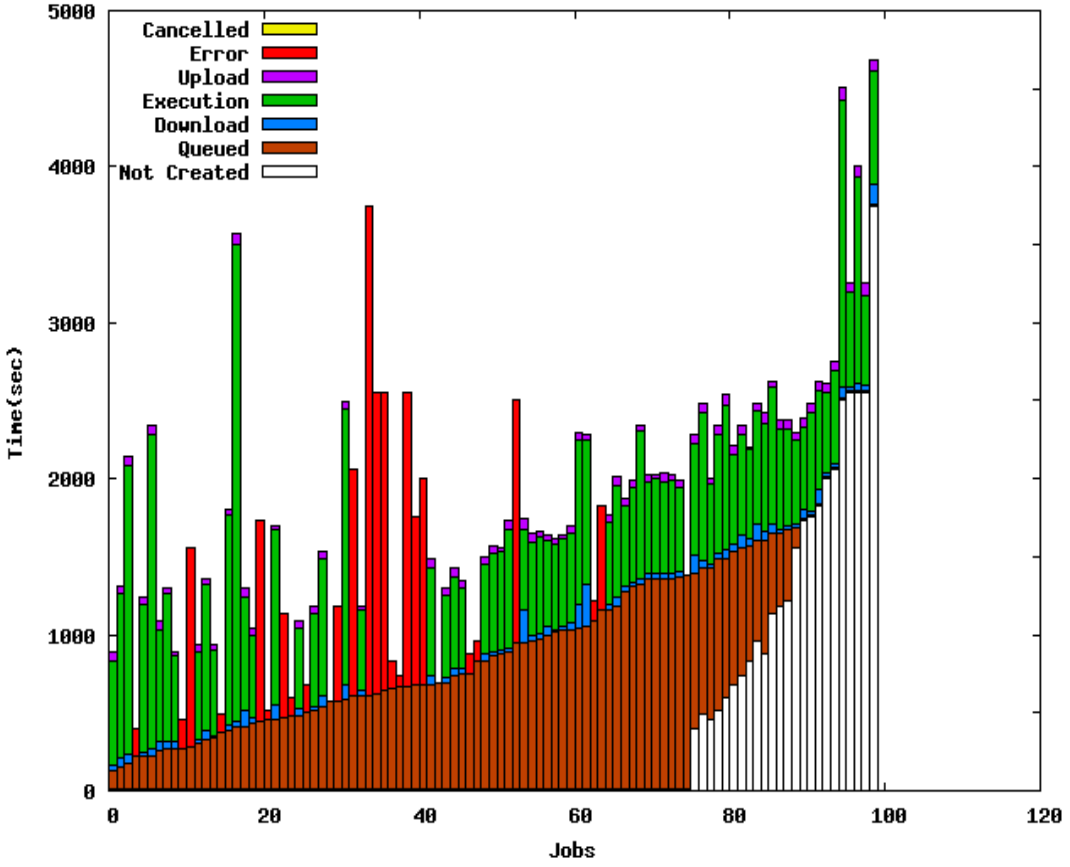
- **Chaque tâche simule m molécules dans f fibres parmi F**

Worker:

1. **Input:** n_1, ..., n_f: the f indices of the cardiac fibers to simulate
2. Download input data and simulation code
3. **for** i **from** 1 **to** f
4. **for** j **from** 1 **to** m
5. randomly choose one initial molecule position in fiber n_i
6. simulate diffusion of molecule and contribution to DWI signal
7. **end**
8. **end**
9. write and upload molecule positions and signal contributions

Parallélisation statique (2)

- **Les tâches**
  - ont des durées très variables
  - sont toutes nécessaires à la simulation
  - doivent être re-soumises si elles échouent
  - ne contribuent pas à la simulation si elles échouent



Solution proposée

- **Chaque tâche simule “tant qu'elle peut”**

Master:

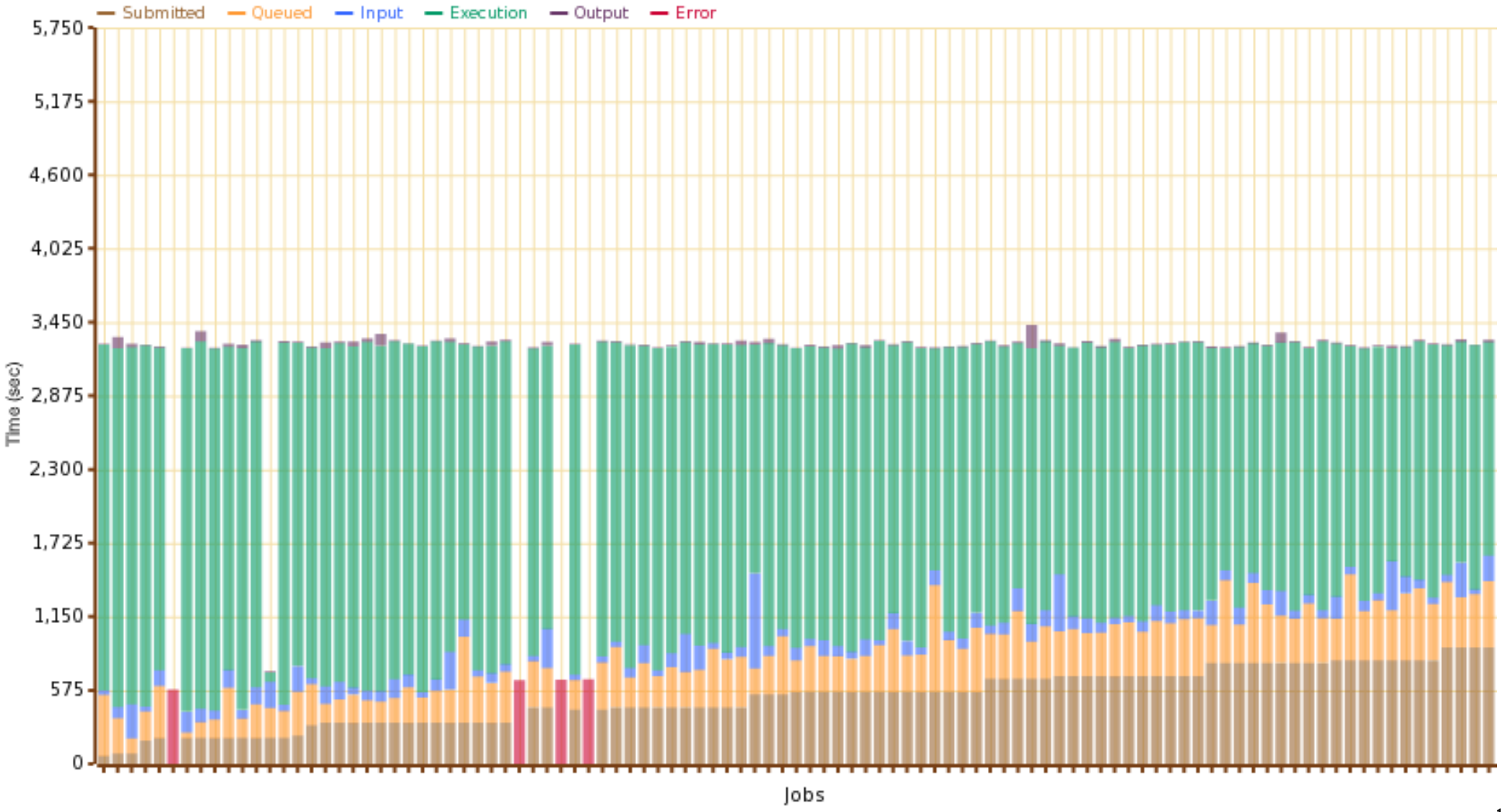
```
1. N = F x m
2. n = 0
3. while ( n < N ) do
4.   n = number of water molecules simulated by running and completed tasks
5. end
6. send stop signal to all tasks
7. cancel queued tasks
```

Worker:

```
1. Download input data and simulation code
2. N = F x m
3. while stop signal not received and n < N do
4.     randomly select one cardiac fiber from uniform distribution
5.     randomly select one initial molecule position in the previously selected cardiac
   fiber
6.     simulate diffusion of the molecule and contribution to DWI signal
7.     report total number n of simulated molecules to master
8. end
```

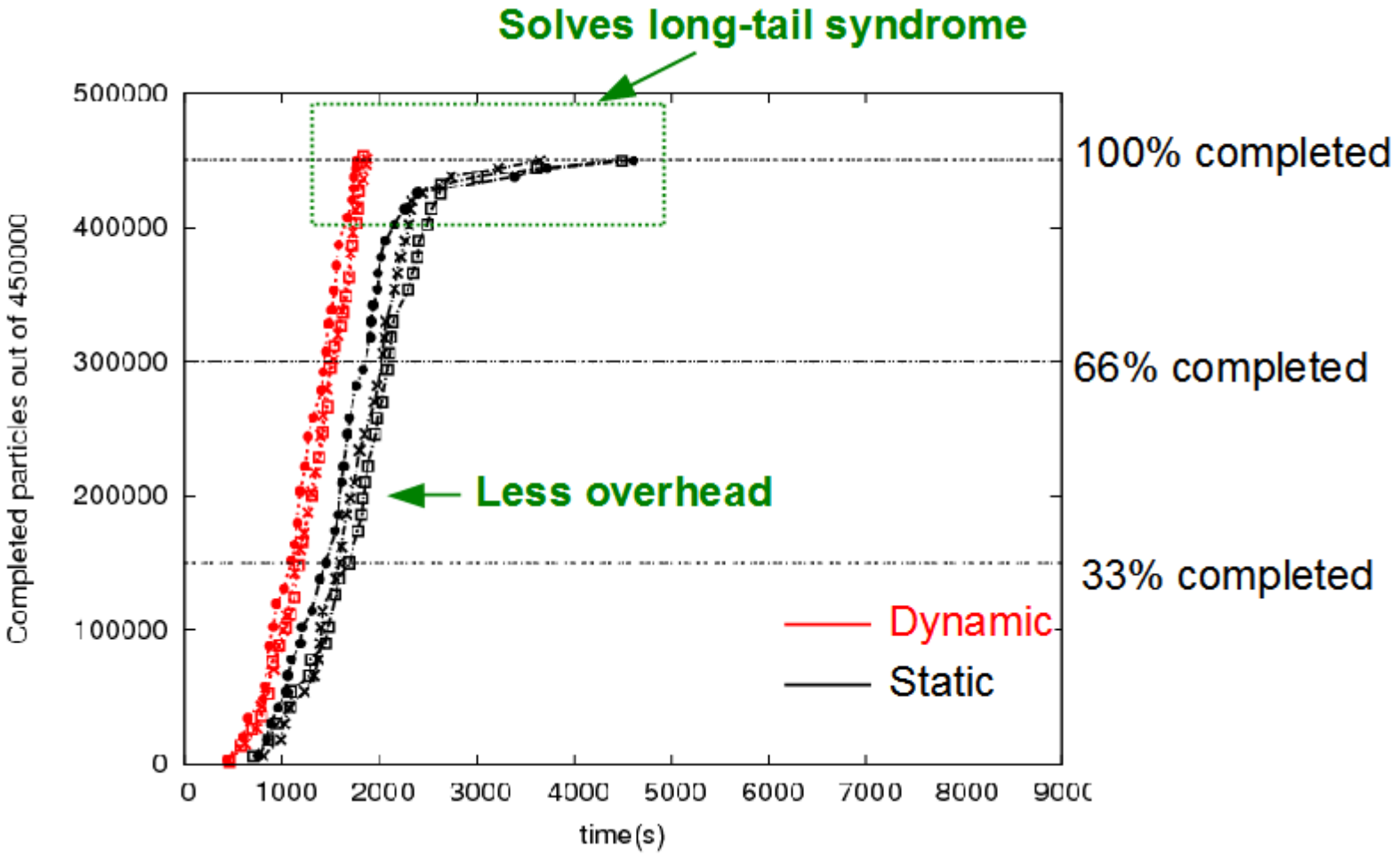
Résultat

- **Répartition de charge quasi-optimale**



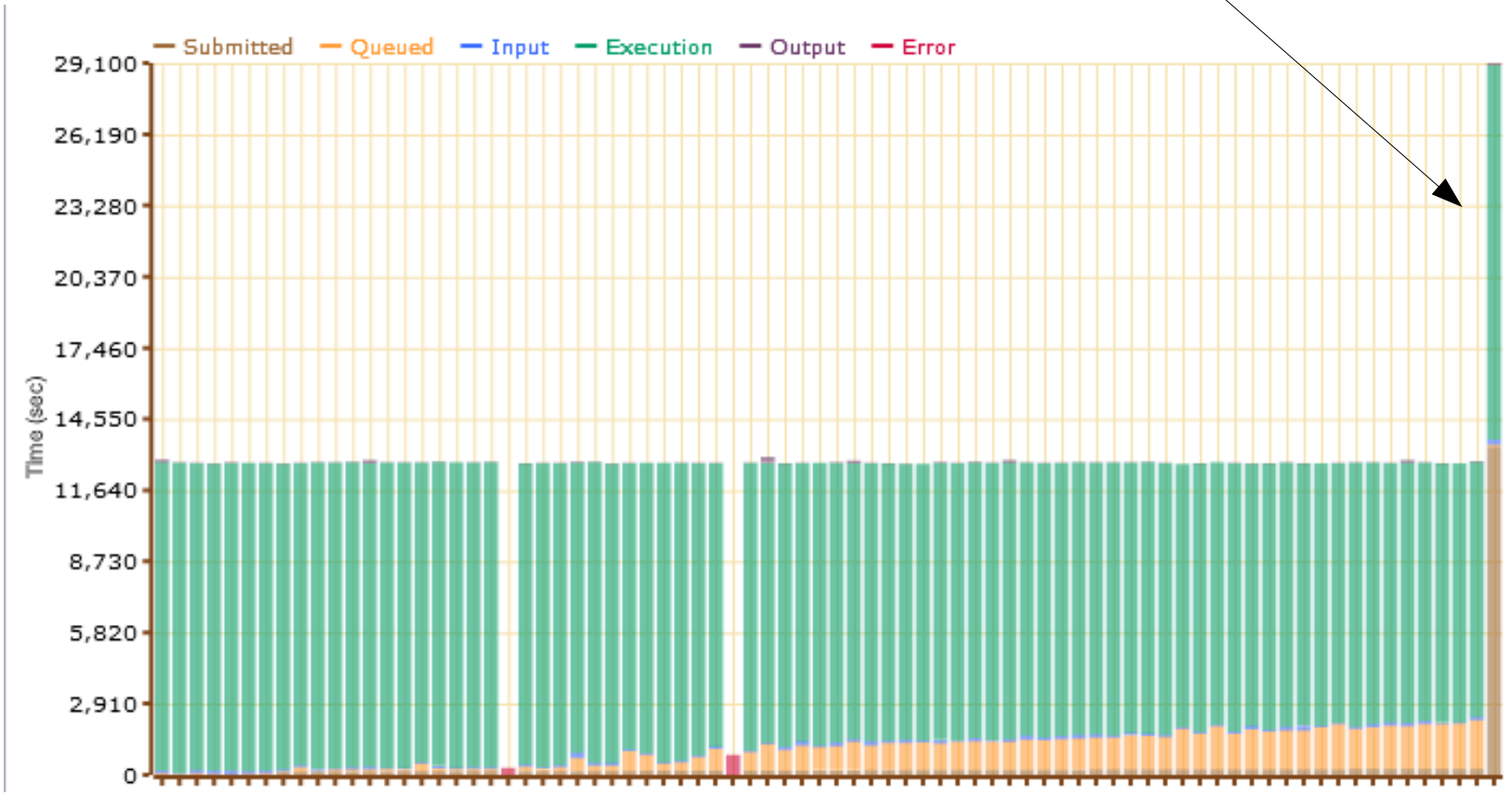
Résultat (2)

- **Le problème de la fin de simulation est résolu**



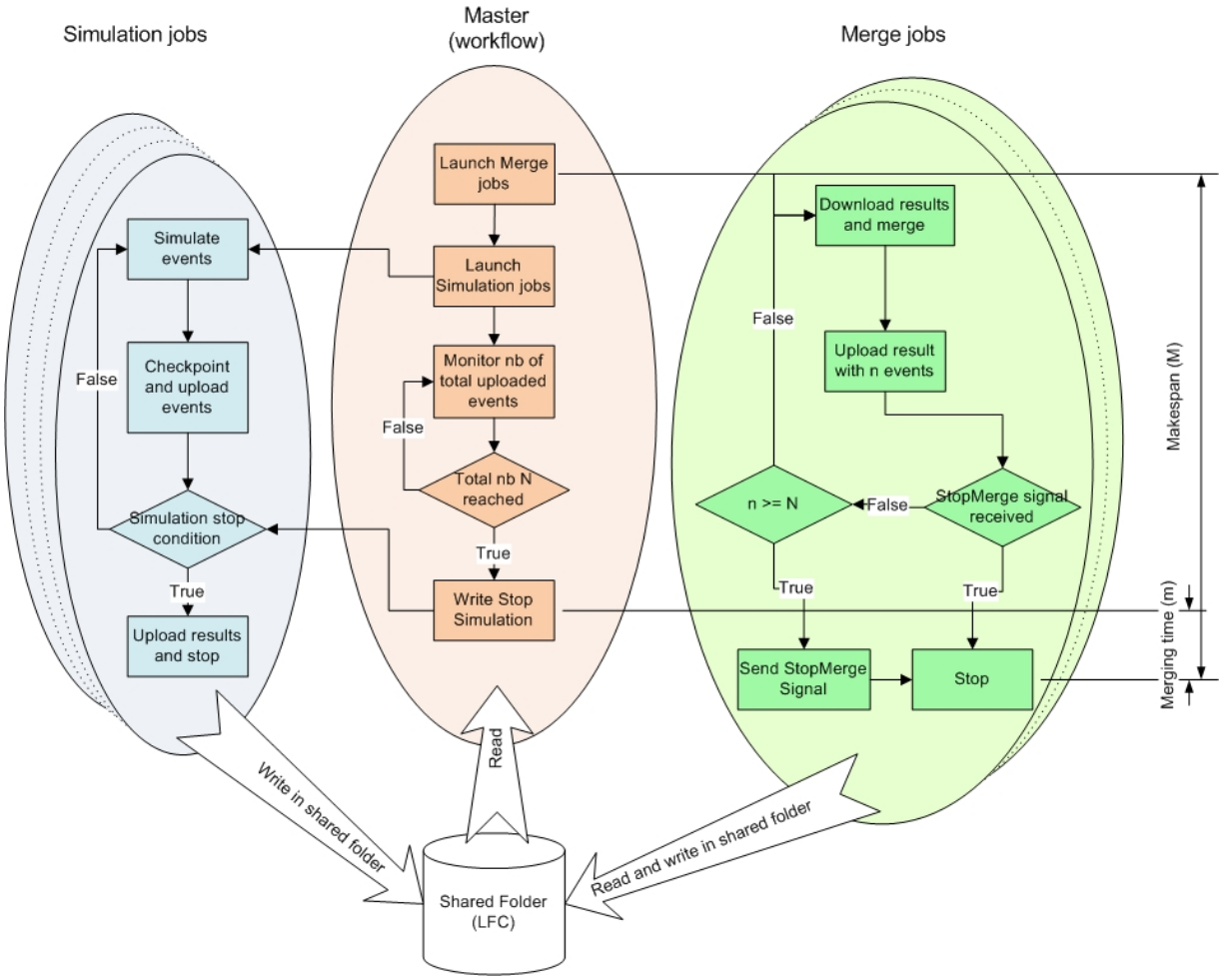
Fusion des résultats partiels

- **Peut durer aussi longtemps que la simulation**

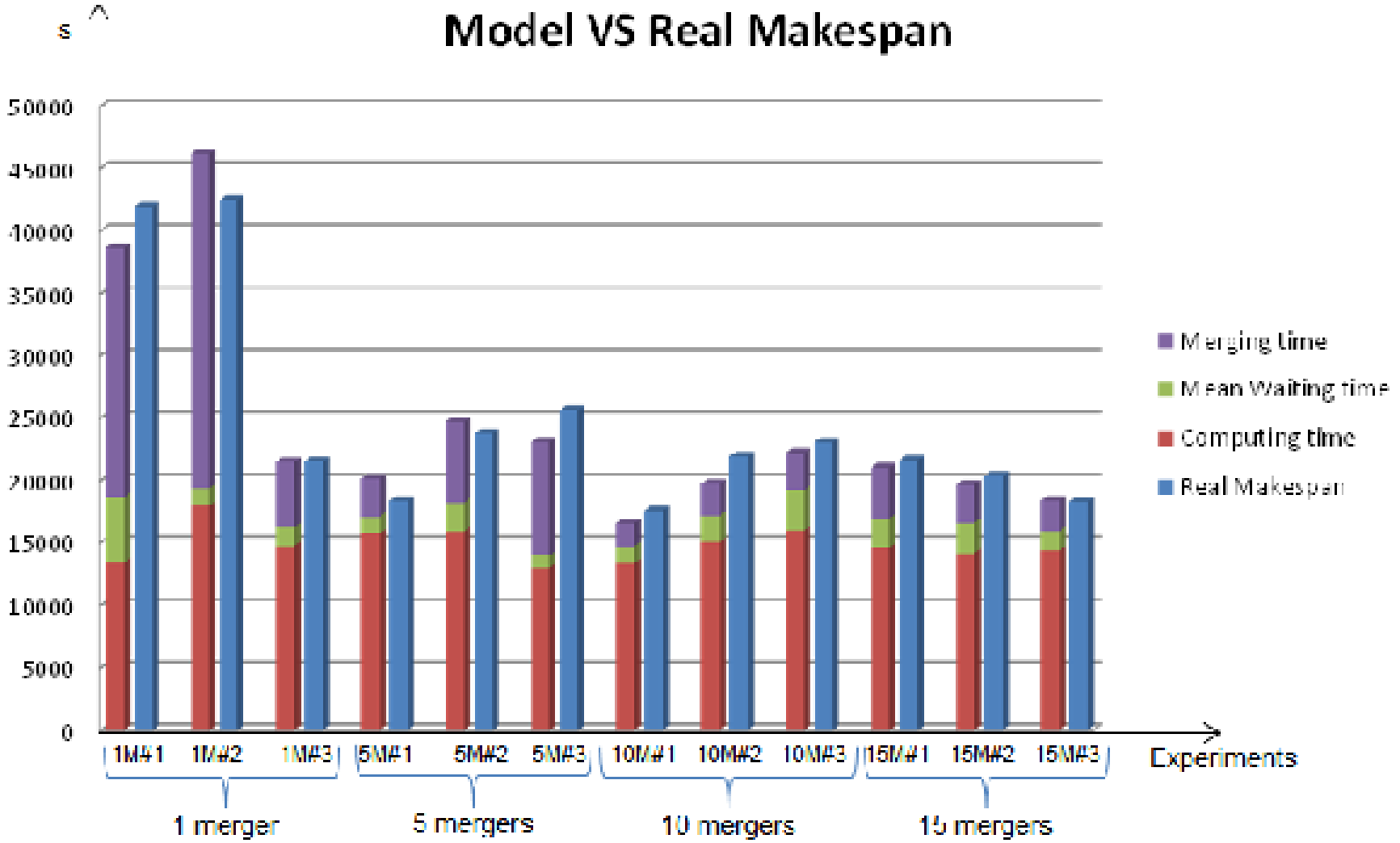


Solutions proposées

- **Fusion parallèle**
  - Plusieurs tâches de fusion
  - Fusion commutative et associative
- **Fusion incrémentale**
  - Tâches de fusion lancées en début de simulation
  - Nécessite un *checkpointing*
- **Checkpointing**
  - Fréquence adaptée au débit des tâches de fusion
  - $C_{[mol]} = N_{[tâches]} * T_{[s]} * \theta_{[mol/s]}$

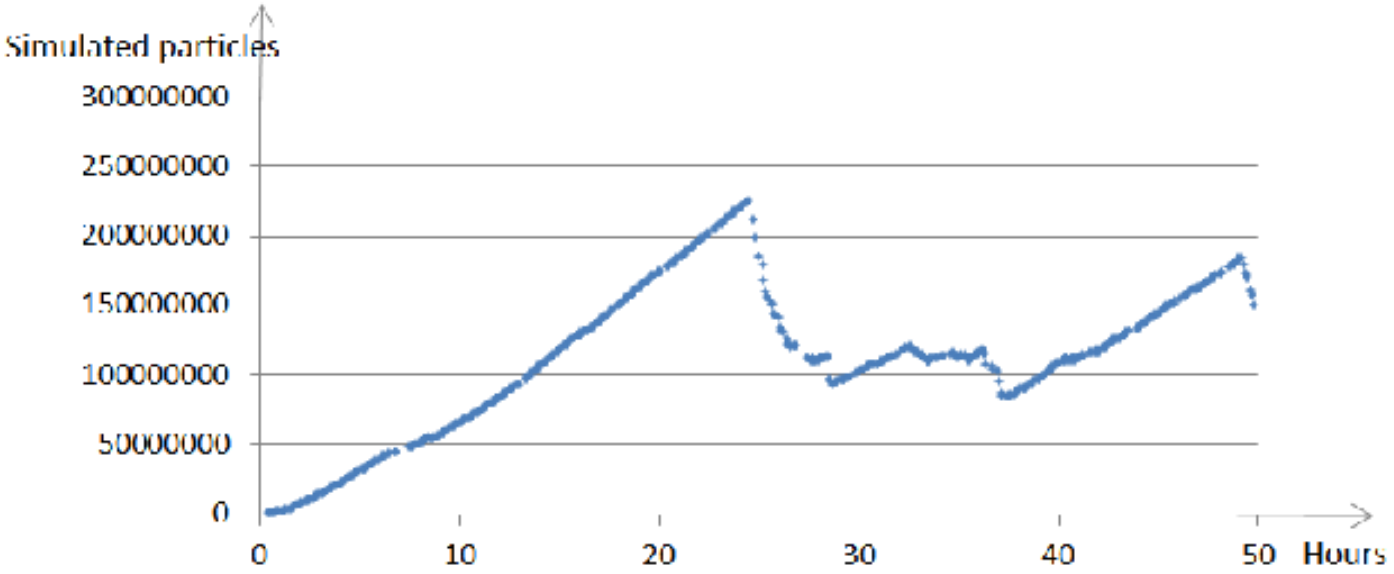


Impact de la fusion parallèle

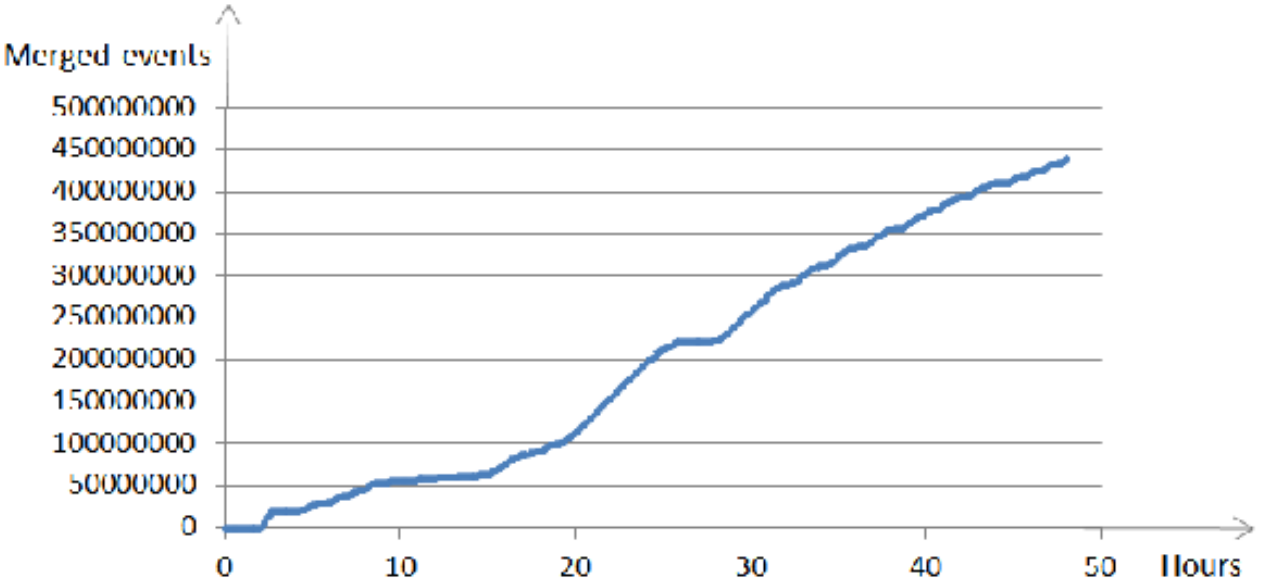


Impact du *checkpointing*

- **Sans**



- **Avec**



Conclusion

- **Exploitation quasi-optimale des ressources de calcul**
  - Tâches pilotes + équilibrage de charge dynamique
  - Utilisable pour la plupart des simulations Monte-Carlo
- **La fusion des résultats reste bloquante**
  - Fusion parallèle, incrémentale avec checkpointing
  - Intervention manuelle souvent nécessaire
  - Perspective : optimiser le placement des résultats partiels

Références

- **Parallélisation dynamique des simulations Monte-Carlo**

S. Camarasu-Pop, T. Glatard, J. T. Moscicki, H. Benoit-Cattin, and D. Sarrut, "*Dynamic partitioning of GATE Monte-Carlo simulations on EGEE*", Journal of Grid Computing, vol. 8, no. 2, pp. 241-259, mar, 2010

- **Fusion incrémentale et parallèle, avec *checkpointing***

S. Camarasu-Pop, T. Glatard, R. Ferreira da Silva, P. Gueth, D. Sarrut, and H. Benoit-Cattin, "*Monte-Carlo Simulation on Heterogeneous Distributed Systems : a Computing Framework with Parallel Merging and Checkpointing Strategies*", Future Generation Computer Systems, 2012, in press.