

Inria



Towards Software Product Lines for (f)MRI analysis

RIPOST WORKSHOP
SIMULA, Oslo,
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MRI analysis challenges

- Various data (organs, people, dimension, resolution,...)
- Noise at acquisition (Movement, residual magnetic fields, ...)
- Computational complexity (interpolation, filtering, ...)
- Analysis noise (floating points error, software configuration, human mistakes / habits, ...)

MRI analysis challenges

- Researchers question the reliability of research based on medical imaging.

- R. Botvinik-Neze *et al.* Variability in the analysis of a single neuroimaging dataset by many teams,” Nature, vol. 582, no. 7810, pp. 84–88, Jun. 2020.
- A. Boucard, A. Marchand, and X. Noguères, “Reliability and validity of structural equation modeling applied to neuroimaging data: a simulation study,” Journal of neuroscience methods, vol. 166, 2007
- A. M. Brandmaier, E. Wenger, N. C. Bodammer, S. Kühn, N. Raz, and U. Lindenberger, “Assessing reliability in neuroimaging research through intra-class effect decomposition (iced),” Elife, vol. 7, 2018.
- R. L. Billingsley-Marshall, P. G. Simos, and A. C. Papanicolaou, “Reliability and validity of functional neuroimaging techniques for identifying language-critical areas in children and adults,” Developmental neuropsychology, vol. 26, 2004
- J. C. Fournier, H. W. Chase, J. Almeida, and M. L. Phillips, “Model specification and the reliability of fmri results: implications for longitudinal neuroimaging studies in psychiatry,” PLoS One, vol. 9, 2014.

NARPS

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- **GOAL** : Evaluate consensuality of 70 research teams over a set of 9 **Research Questions**

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- **RESULTS** : Consensus was never reached.

NARPS : R. Botvinik-Neze *et al.* Variability in the analysis of a single neuroimaging dataset by many teams,” Nature, vol. 582, no. 7810, pp. 84–88, Jun. 2020.

Why NARPS is a good playground ?

- **Exogenous variability is partly controlled :**
 - Dataset quality has been assessed before the study
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- **Variability by design :**
 - \neq Technos (Python, Matlab, ...)
 - \neq Data processing software (SPM, FSL, FreeSurfer, fMRIPrep,...)
 - \neq Pipelines (software suites x configuration x teams habits)

Variability layers

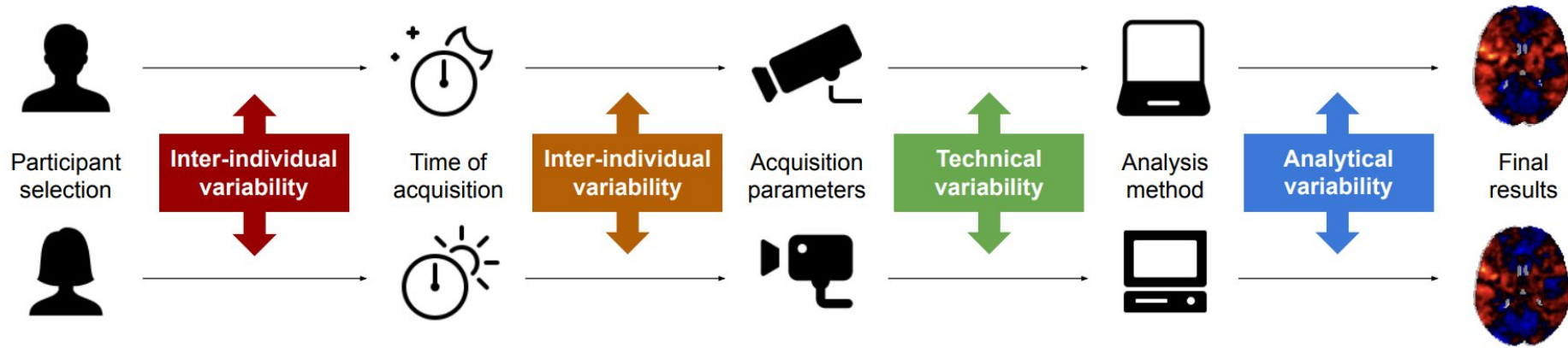


Figure 2.1 – Different sources of variability in neuroimaging studies

Variability layers

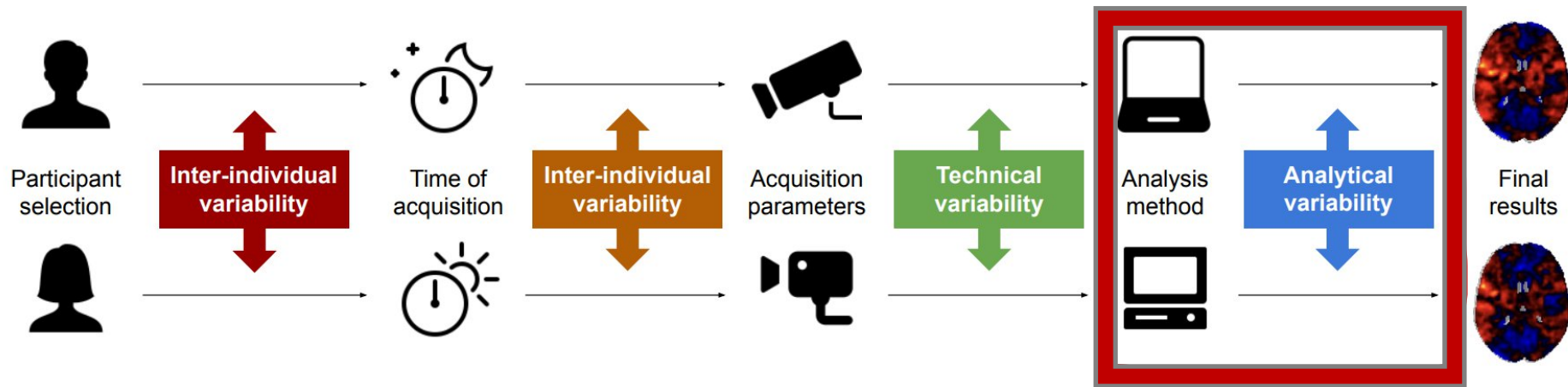
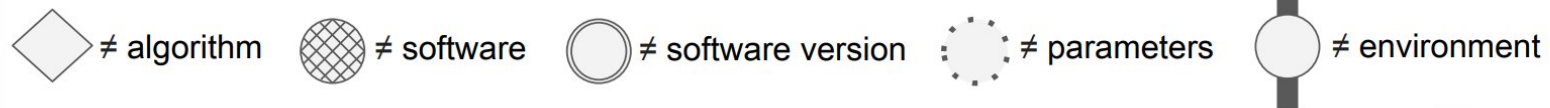
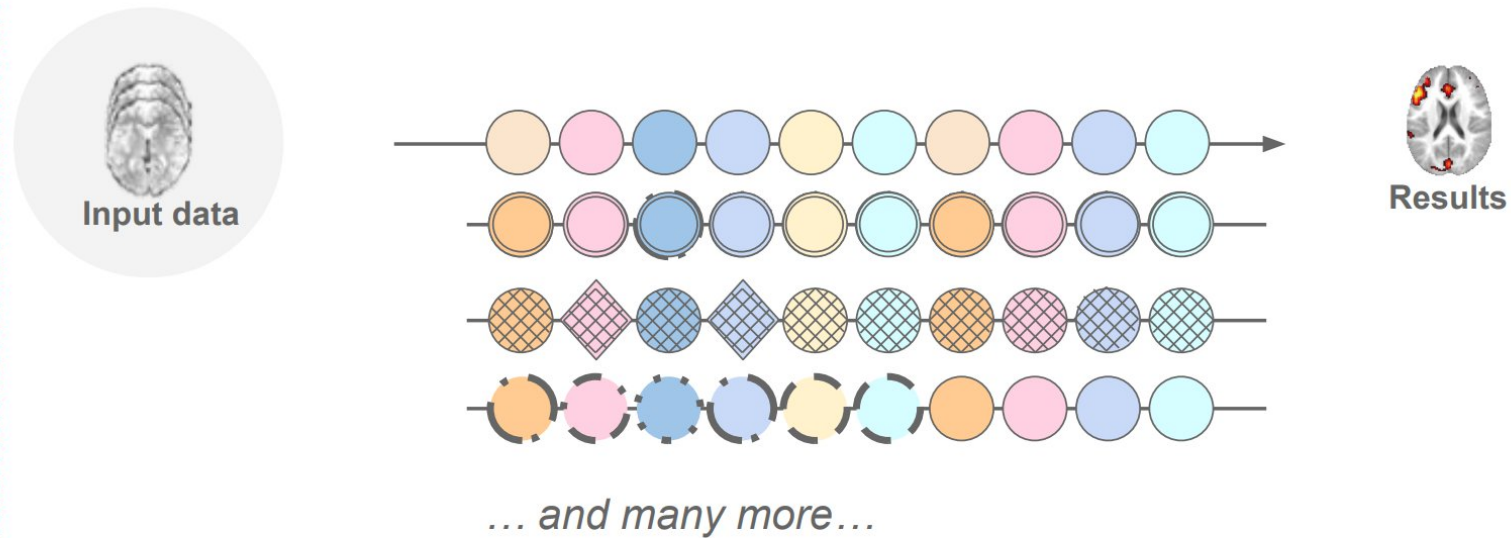


Figure 2.1 – Different sources of variability in neuroimaging studies

A multiplicity of analysis pipelines



A family of acceptable pipelines
over 10^{30} combinations...

**Software
Variants**

Deep Software Variability

Introducing Deep Variability

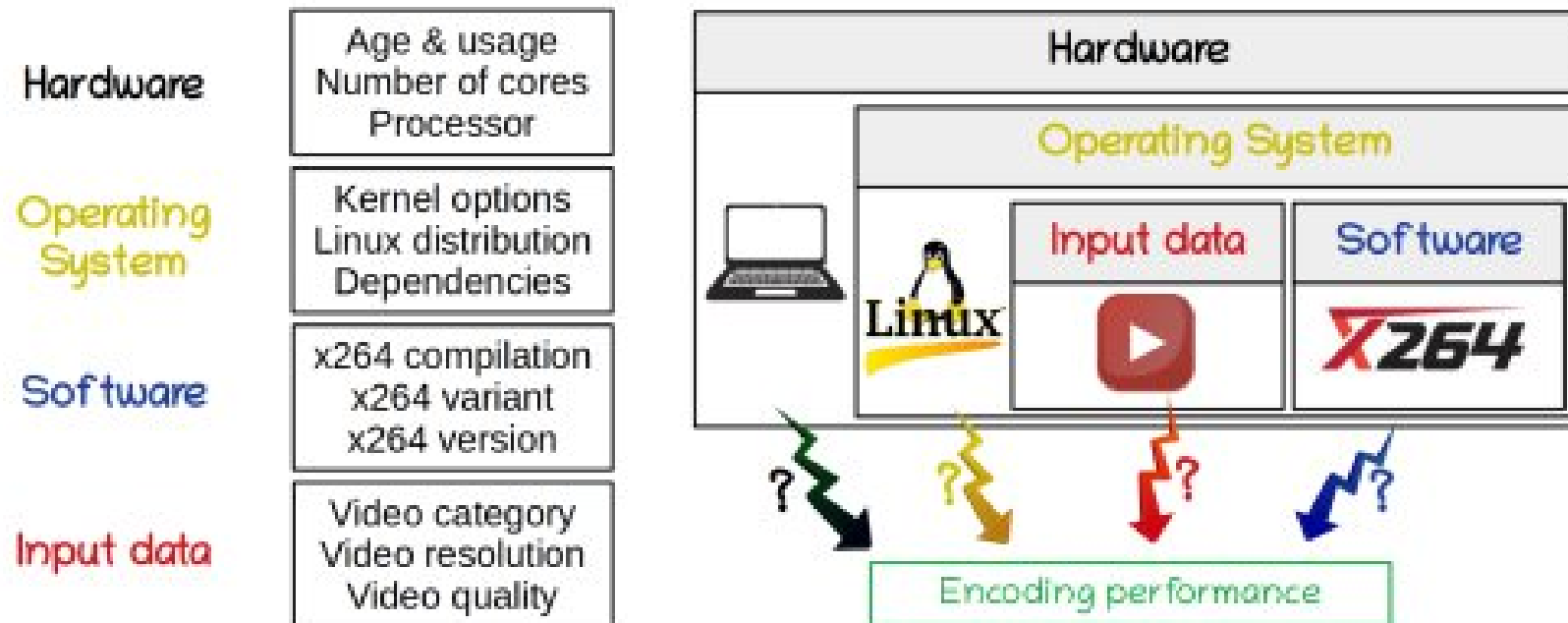


Figure 3.1 – Deep Variability of x264

What we already know

- Use of different Hardware can induce variation in results

G. Vila, E. Medernach, I. Gonzalez Pepe, A. Bonnet, Y. Chatelain, M. Sdika, T. Glatard, and S. Camarasu Pop, "The impact of hardware variability on applications packaged with docker and guix: a case study in neuroimaging," in Proceedings of the 2nd ACM Conference on Reproducibility and Replicability, ser. ACM REP '24.

- Software configuration can lead to discrepancies in fMRI prepped data

Y. Chatelain, L. Tetrel, C. J. Markiewicz, M. Goncalves, G. Kiar, O. Esteban, P. Bellec, and T. Glatard, "A numerical variability approach to results stability tests and its application to neuroimaging," IEEE Trans. Comput., vol. 74, no. 1, p. 200–209, Jan. 2025.

- Software versions can lead to divergence between series of runs in brain **structural** analysis workflows

A. Sokołowski, N. Bhagwat, D. Kirbizakis, Y. Chatelain, M. Dugr'e, J.-B. Poline, M. Sharp, and T. Glatard, "The impact of freesurfer versions on structural neuroimaging analyses of parkinson's disease," bioRxiv, pp. 2024–11, 2024.

Experimentation over NARPS

- What kind of Exps. are we talking about ?
 - Fix version of SPM (SPM12) with different revisions/releases
 - Matlab (comes with SPM)
 - 100 subjects
 - All 9 RQs
- => Were able to re-run (only) 2 pipelines from 2 different teams (U26C and 2T6S)

NARPS open pipelines : https://github.com/Inria-Empenn/narps_open_pipelines

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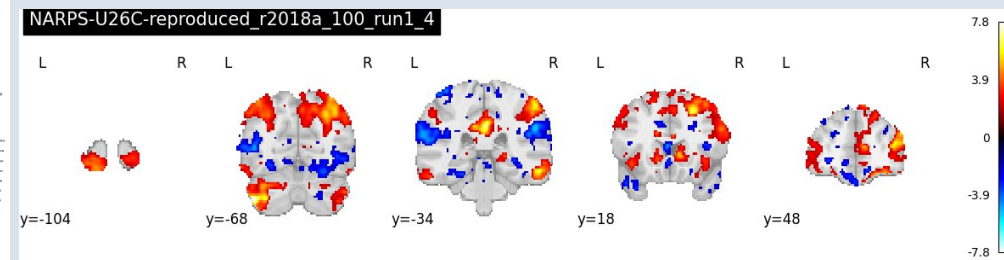
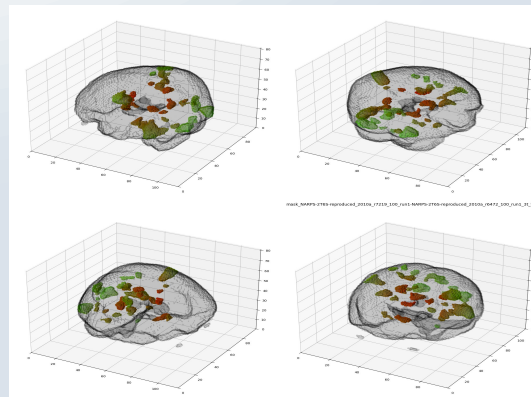
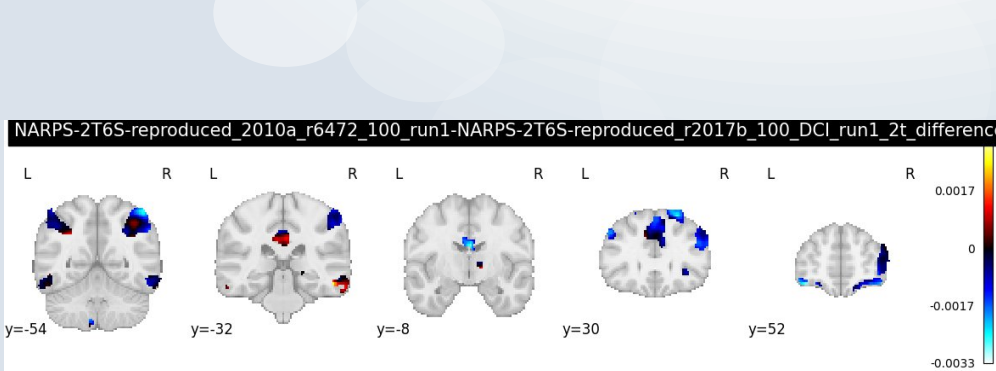
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- Hundreds of GB of data generated
- Ad-hoc code for statistical (matrices) analysis and dataviz

Differences in Results

- **Minor statistical discrepancies on preproc. AND final data:**
 - $\sim[6E-5 ; 1E-3]$ between comparable runs
 - Meaningful data usually ranges in $[-8 ; 8]$

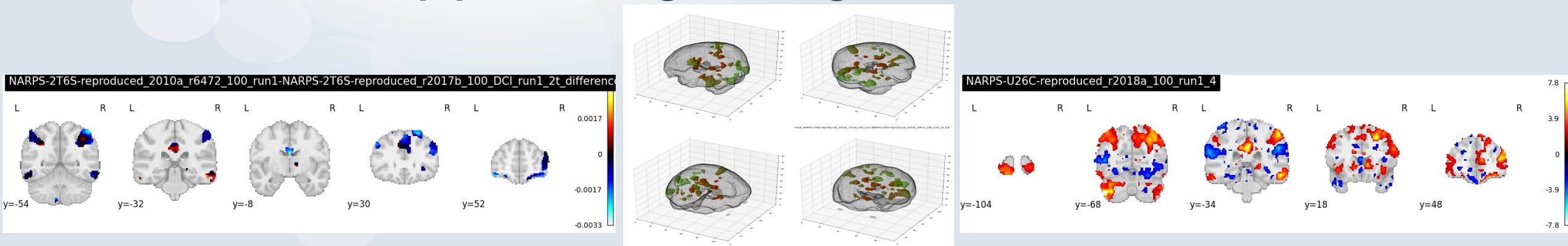
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- **Minor visual differences in outcome data, most of it bound to statistical differences :**
 - We had to emphasize statistical differences a lot to be able to filter them out
- **Nothing Major came out of it BUT the complexity of the software environment, pipeline usage, configuration, and fMRI silos.**



Experimentation challenges

- Heavy software environment (many dependencies, discrete pieces of software, configuration and versions)
- Huge dataset and storage needs

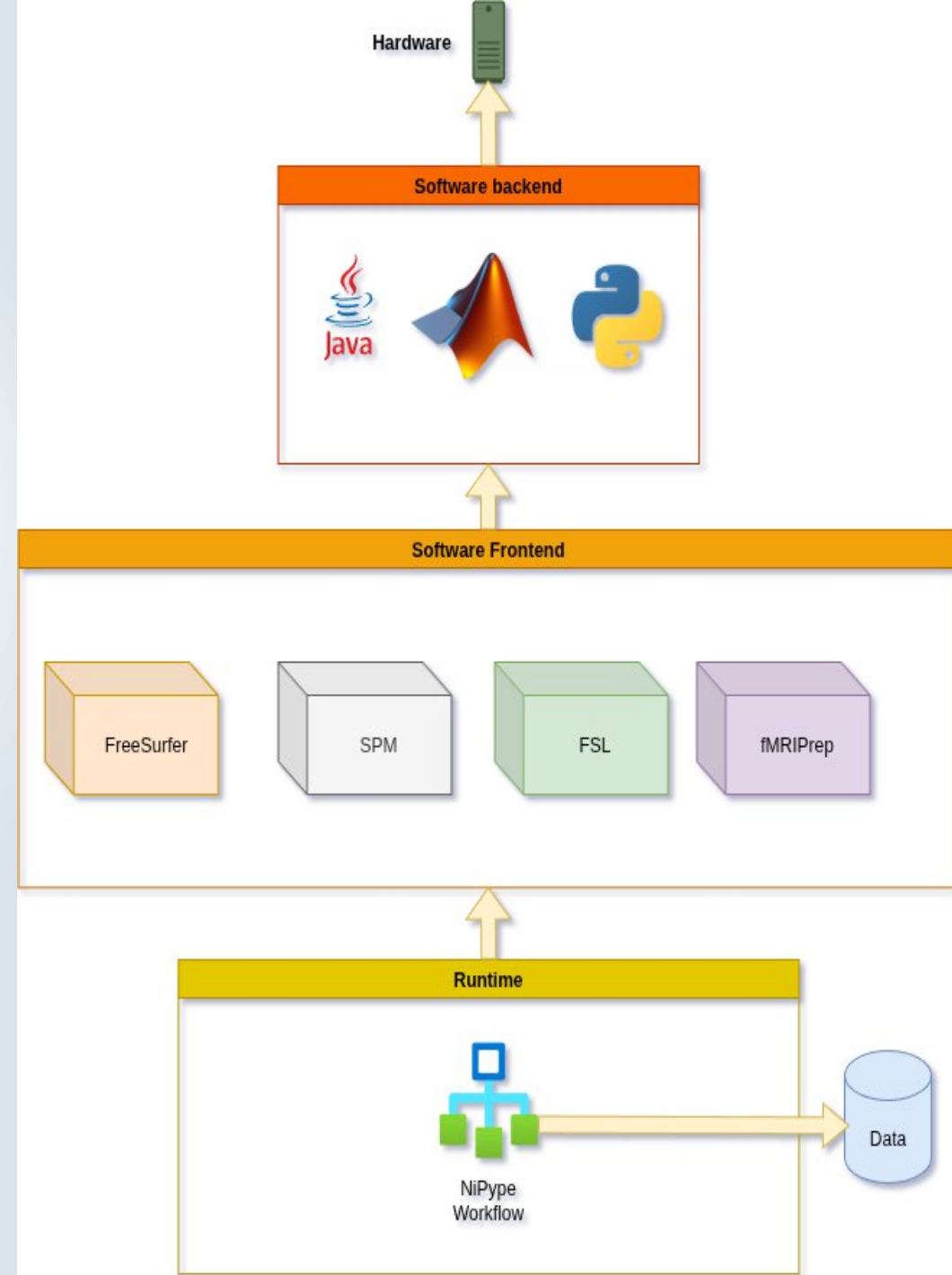
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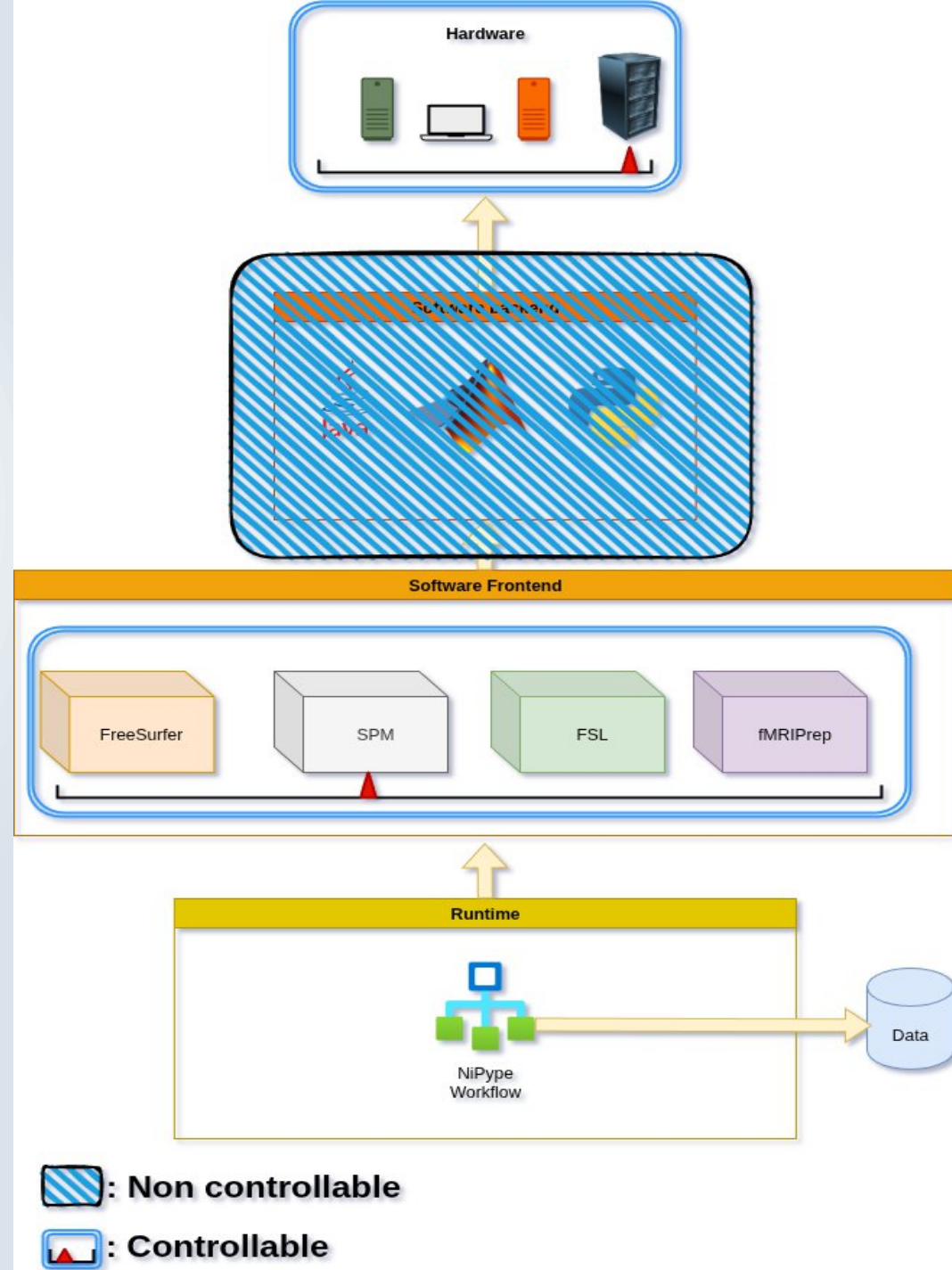
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- **Complexity of (re)implementation of pipelines**

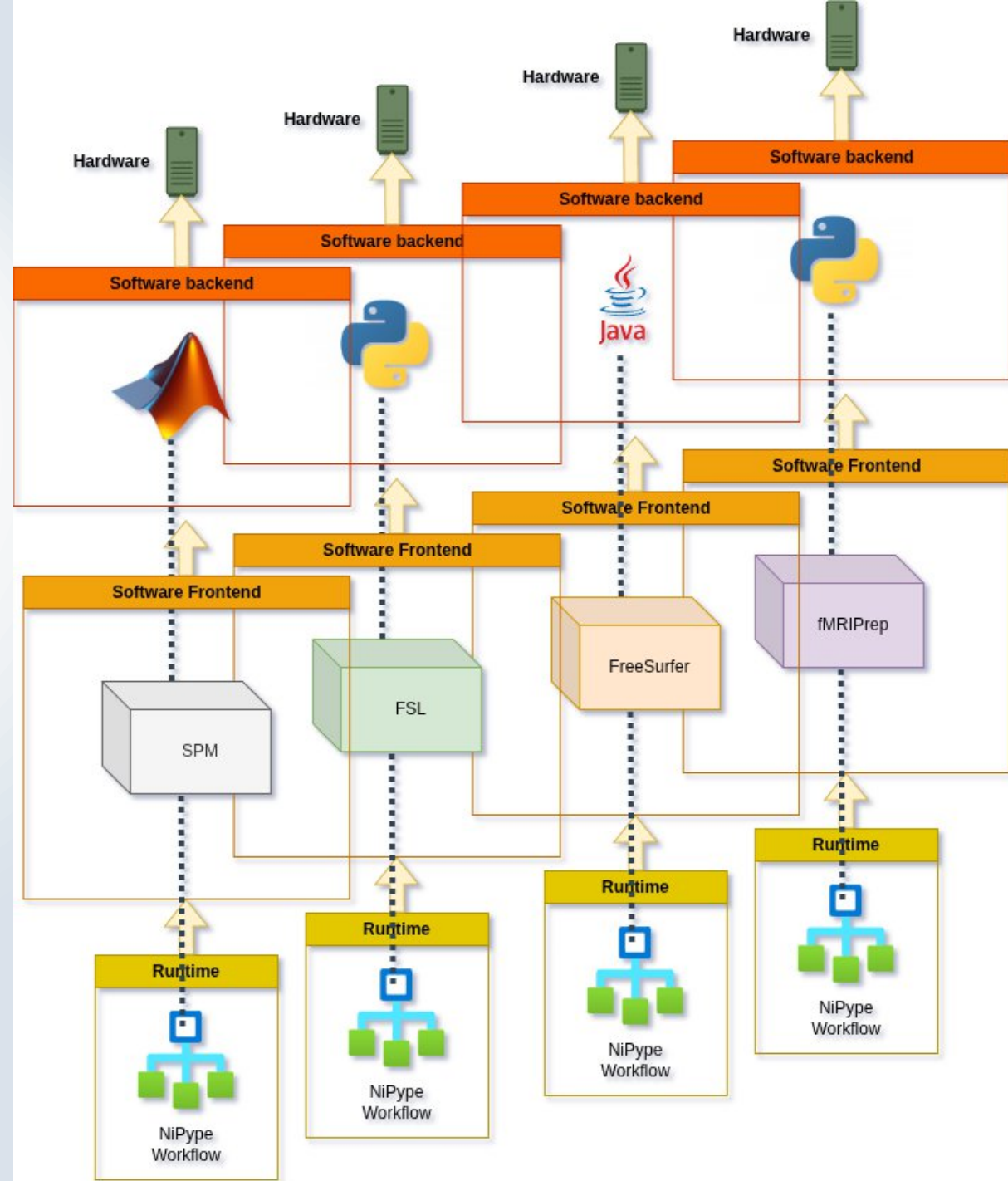
Pipelines structure



Pipelines control



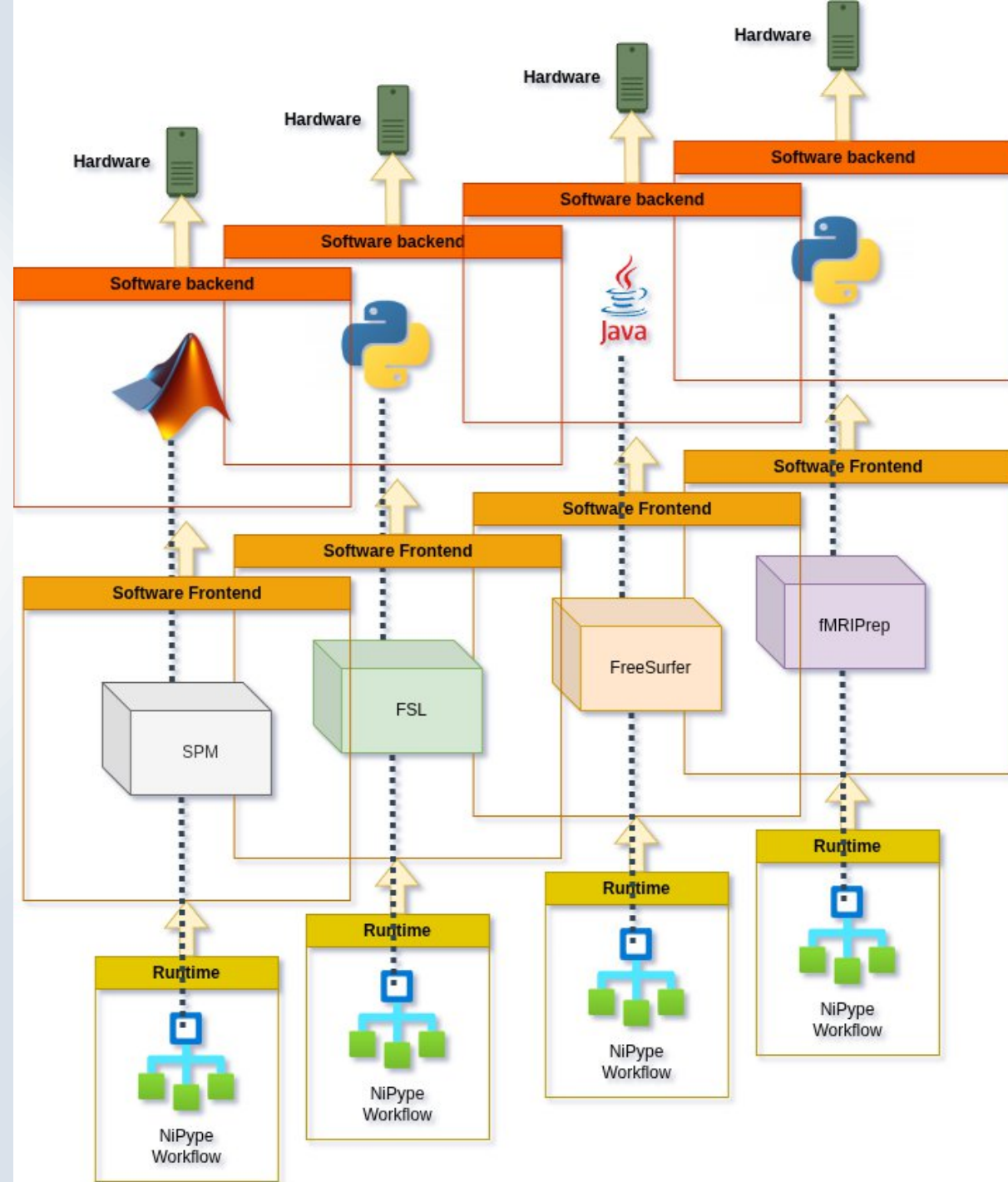
Pipelines issues



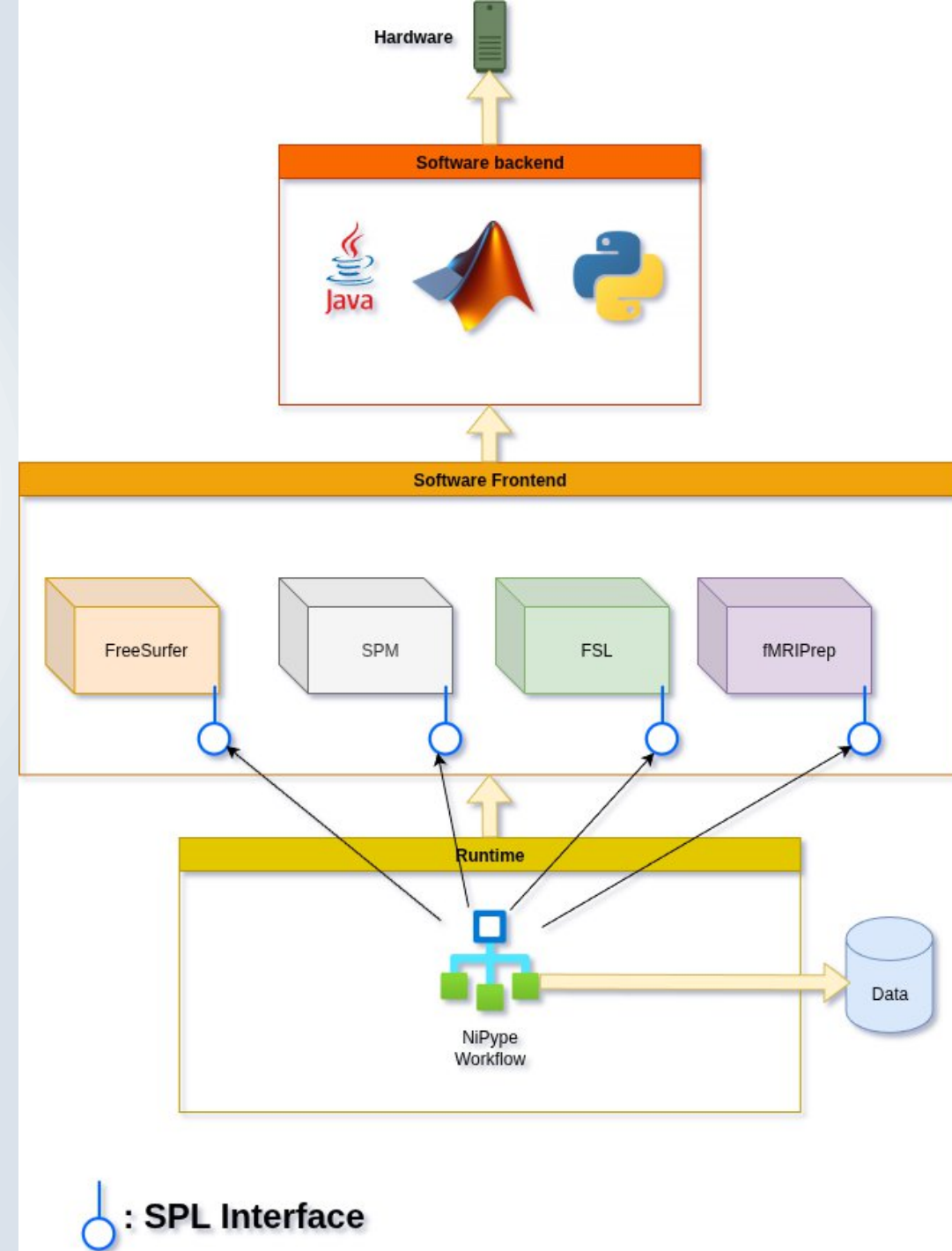
Pipelines issues

Problems :

1. No inter-operability
2. Code duplication
3. Errors spreading
4. No OOB comparison between tools
5. No standard tooling
6. Maintenance
7. Interfacing for middleware like NiPype
8. NO TESTING



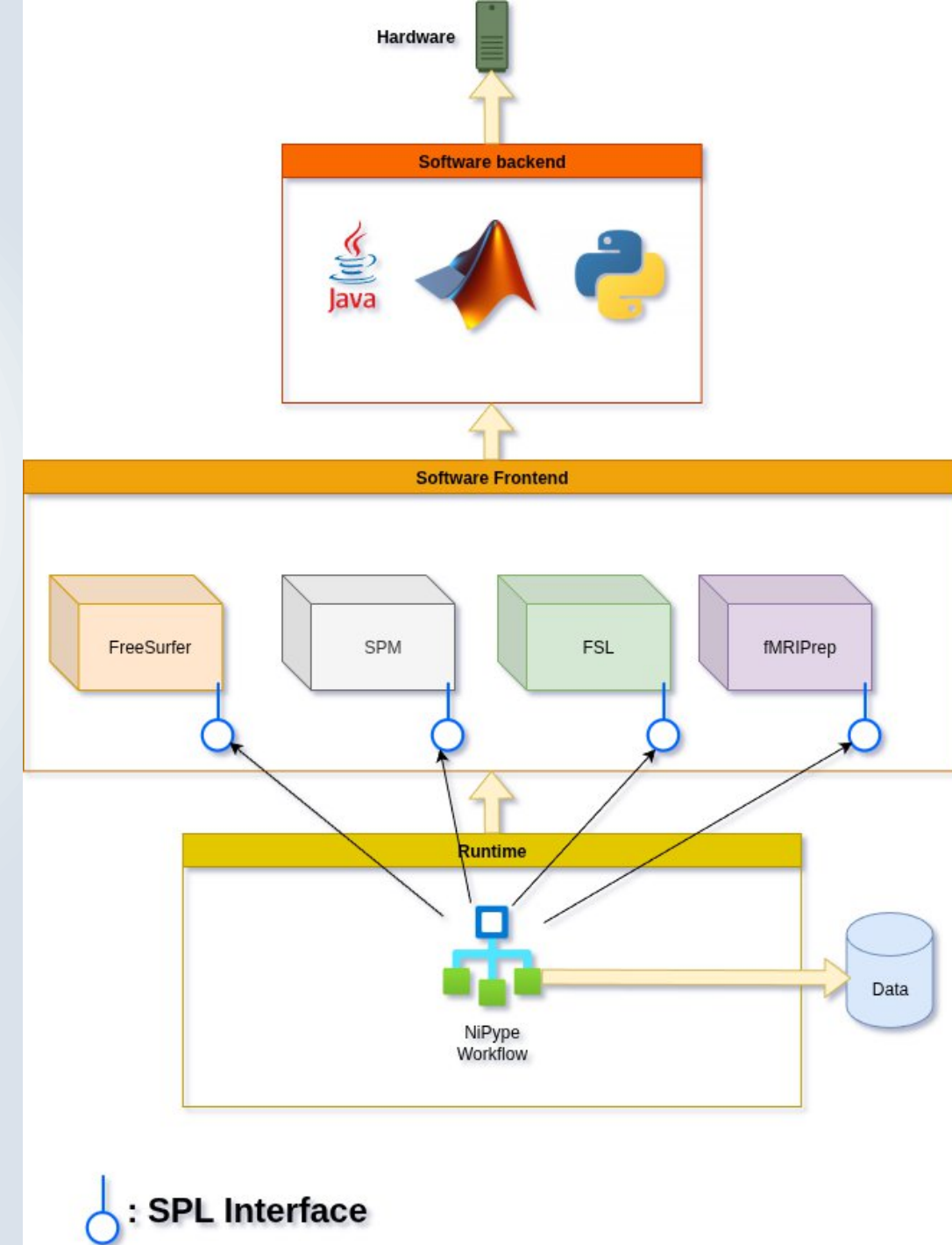
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Advantages:

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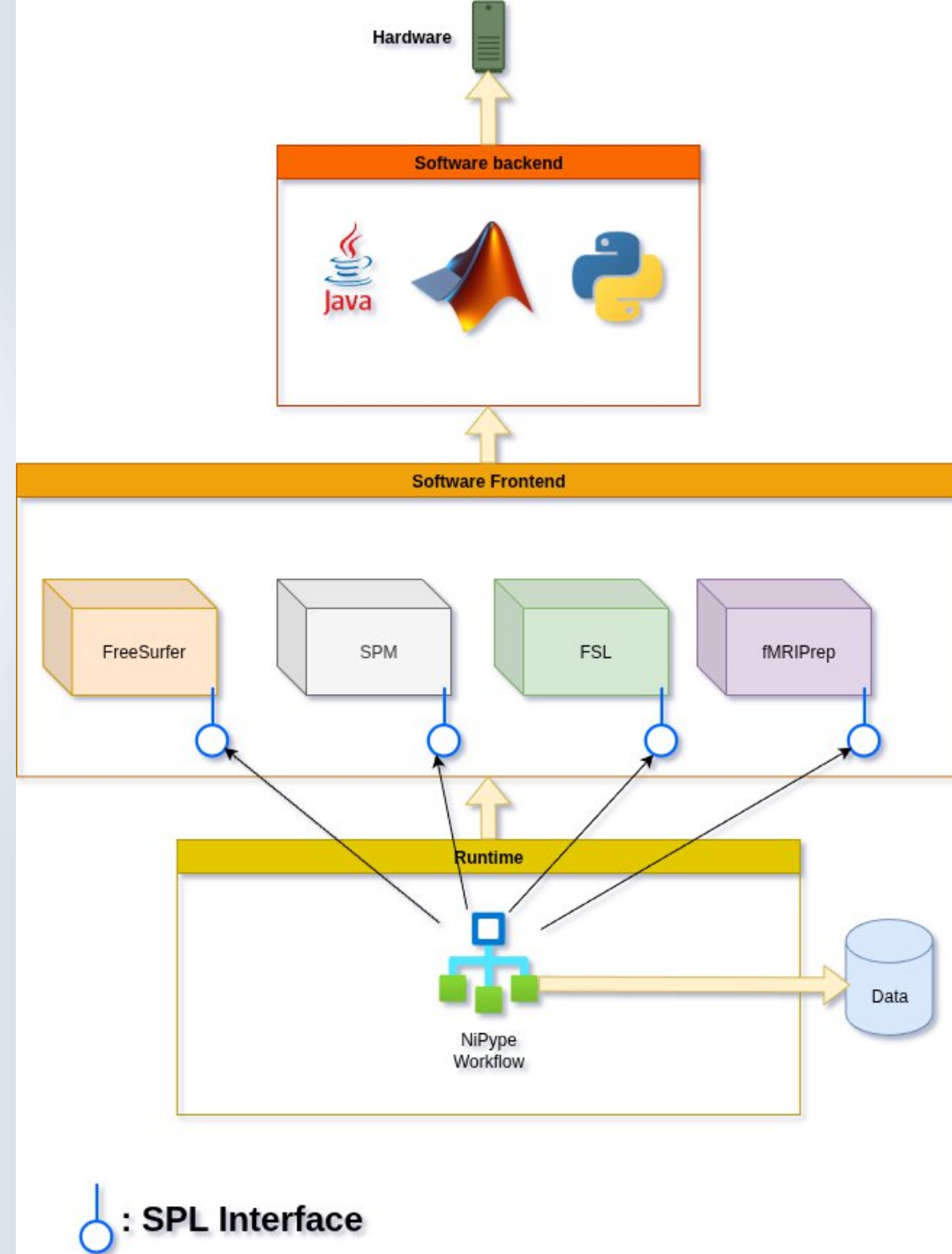
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Caveats:

1. Huge step over for stakeholders
2. Stakeholders must reunite and agree on a standard interface
3. Possibly time and money demanding
4. Many stakeholders are OS community based



Wrap-up

- Medical Imaging analysis is hard to perform
- Lot of variability (material, software, pipeline, etc.)
- Why not propose an SPL approach ?
 - An interface => select the pipeline to run
 - Ease for reproducing
 - Ease for comparison
 - More resilient
 - ...
- We are not there yet...
 - No inter-operability
 - Heavy maintenance
 - No standard tooling
 - ...

Should it lead to a paper ?