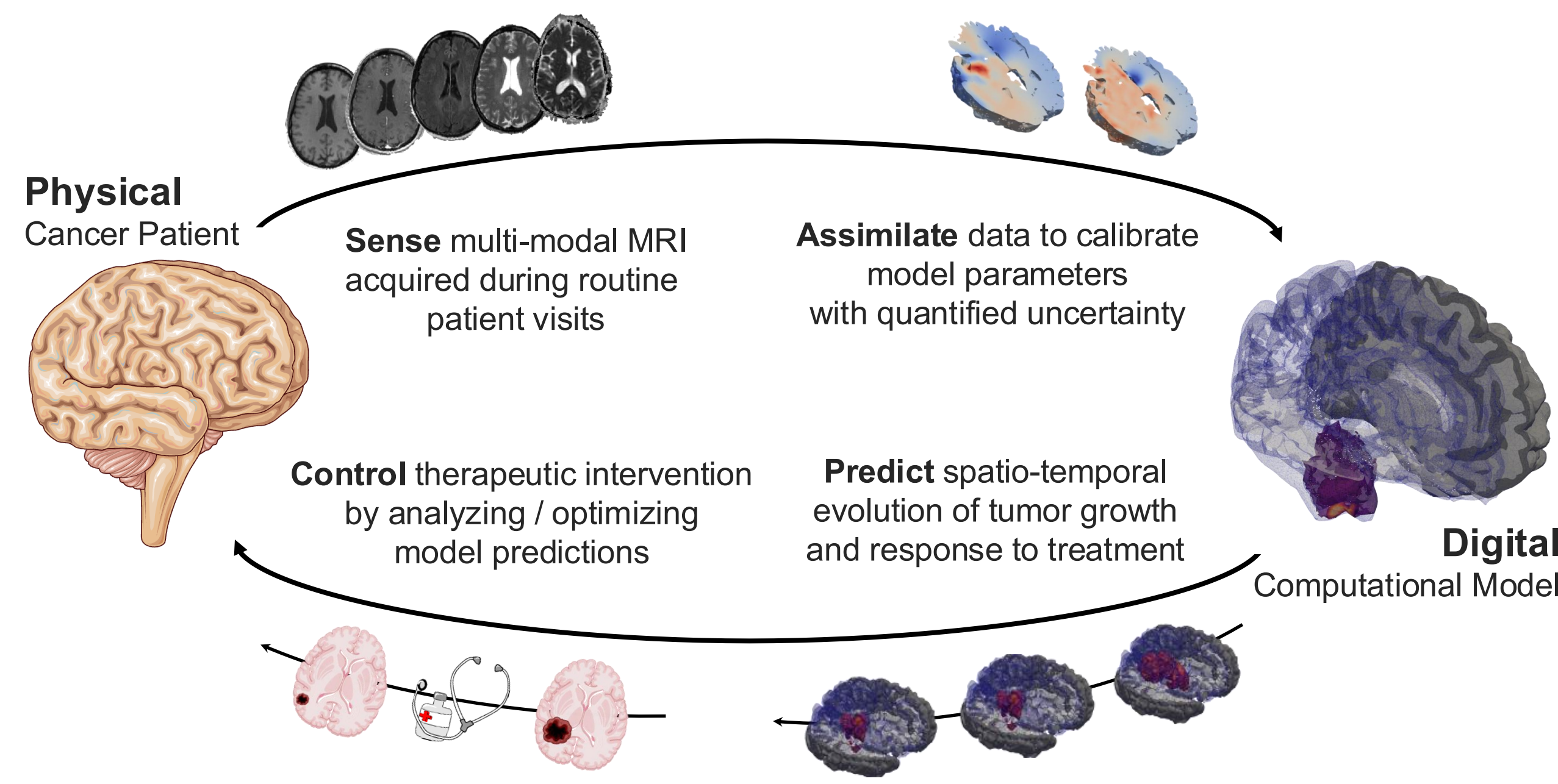


What is a Digital Twin?

“A digital twin is a set of virtual information constructs that mimics the structure, context, and behavior of a natural, engineered, or social system (or system-of-systems), is **dynamically updated** with data from its physical twin, has a **predictive capability**, and **informs decisions** that realize value. The **bidirectional interaction** between the virtual and the physical is central to the digital twin.”

[NASEM, 2023]



Quantifying uncertainty in predictive models is critical for **establishing trust** and enabling **risk-informed decision making**. In contrast to one-size-fits-all approaches that mitigate risk at the population level, **digital twins enable personalized modeling** thereby potentially improving individual outcomes and requires **patient-specific modeling and optimization**.

Key Idea: Improving decision making for the individual will improve outcomes at the population level.

Scalable Bayesian Inference for Patient-Specific Modeling

Realizing digital twins in biomedicine requires **scalable** and **efficient** methods to **integrate patient data** with **mechanistic models** of disease progression. We develop an end-to-end data-to-decisions methodology that integrates **MRI data** with mechanistic models of tumor growth to **forecast progression**. The methodology is demonstrated on a **virtual patient** and **validated on clinical data** showing relevance to real cases.

We model **tumor invasion** into healthy tissue and **proliferation** of exiting tumor with a semi-linear parabolic partial differential equation model.

$$\frac{\partial u}{\partial t} - \underbrace{\nabla \cdot (D(x)\nabla u)}_{\text{infiltration}} - \underbrace{\kappa(x)u(1-u)}_{\text{proliferation}} = \underbrace{f(u)}_{\text{treatment}} \quad \text{in } \Omega \times (t_0, t_f)$$

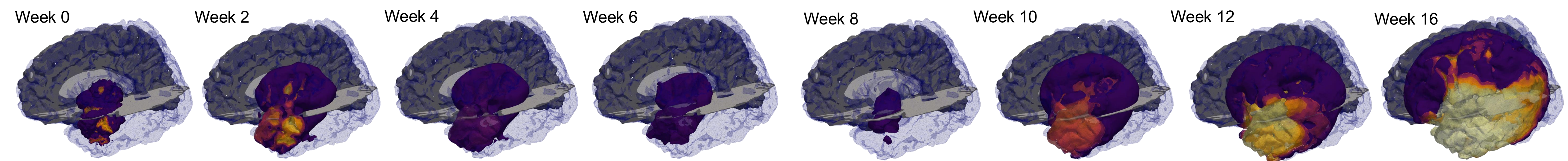
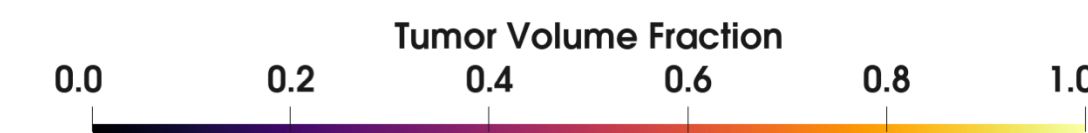
We pose model calibration as a **Bayesian inverse problem** where we seek the **posterior** distribution. Due to the high computational cost associated in the PDE setting, we leverage the **Laplace approximation** to the posterior.

Forward model $\mathcal{F}(m) = \mathcal{B}(u(m)), \text{ s.t. } \underbrace{r(u(m), m)}_{\text{residual form of PDE}} = 0$

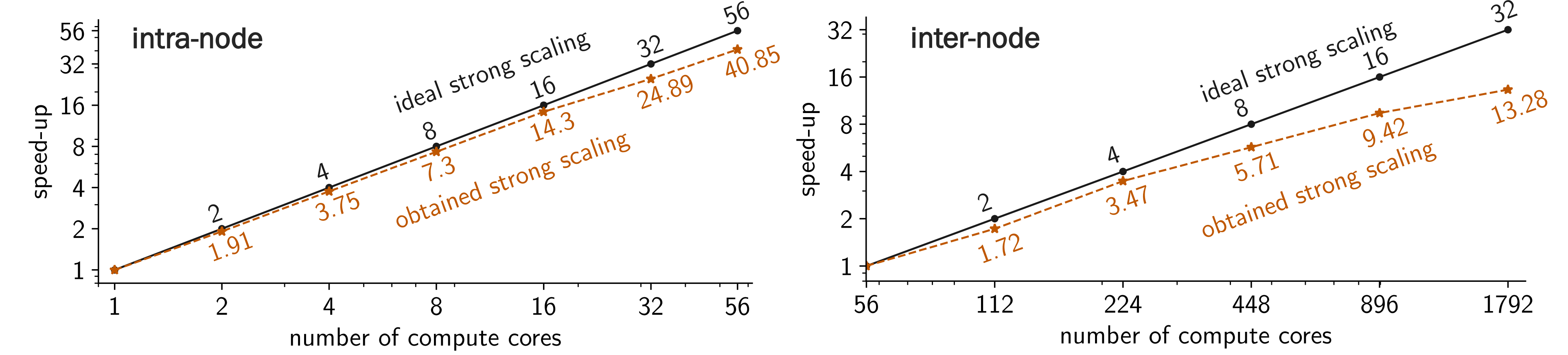
Posterior $d\nu_{\text{post}} \propto \exp \left\{ \underbrace{-\frac{1}{2} \|\mathcal{F}(m) - d\|_{\Gamma^{-1}}^2}_{\text{misfit}} - \underbrace{\frac{1}{2} \|m - m_{\text{pr}}\|_{C_{\text{prior}}^{-1}}^2}_{\text{prior}} \right\}$

Laplace approximation $\nu_{\text{post}}^{\mathcal{L}} \sim \mathcal{N}(m_{\text{MAP}}, \mathcal{H}_{\text{MAP}}^{-1})$

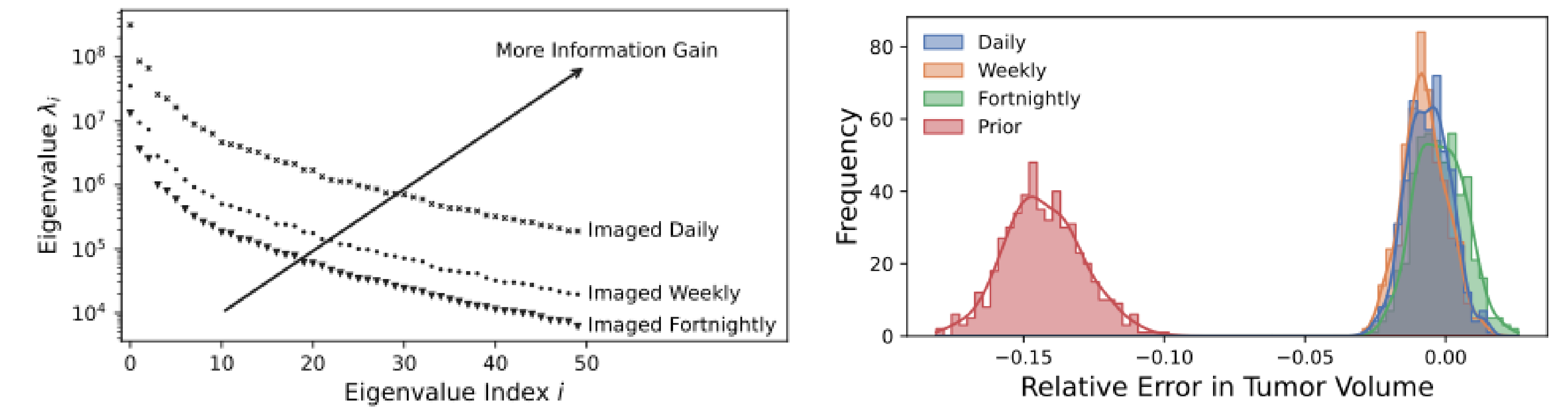
Synthetic data is generated *in silico* from a **real geometry** and initial tumor condition to **verify model calibration** with **known dynamics**.



High-performance computing enables simulation and insight on **clinically relevant timelines**. We achieve suitable **strong scaling** intra-node and competitive scaling inter-node.



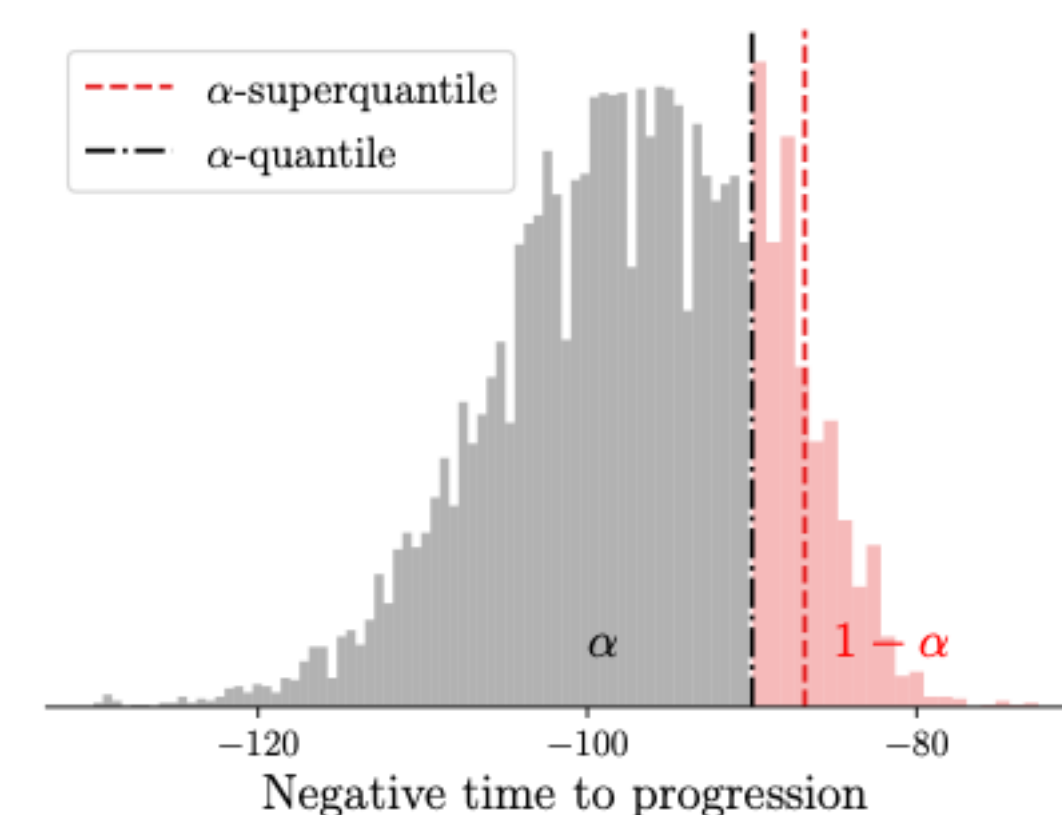
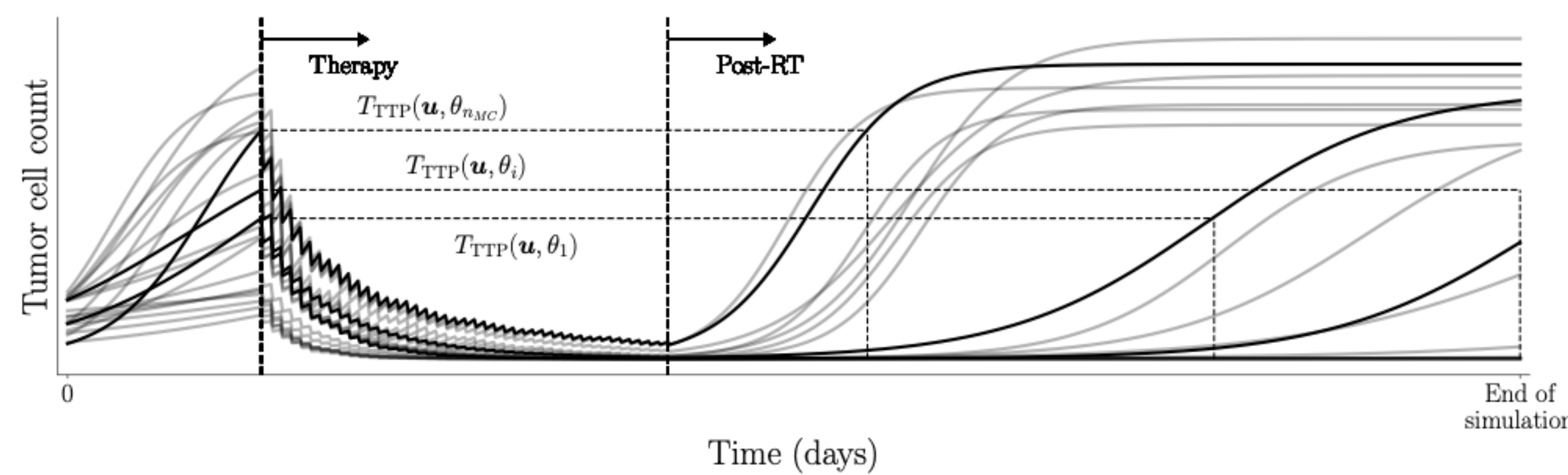
Model calibration is performed for **various imaging schedules** assessing the **impact of additional imaging on prediction quality**. The spectrum of prior-preconditioned Hessian quantifies **information gain**. Posterior predictive distributions for relative error in tumor volume reveals **balance between model performance and data quantity**.



Optimizing Patient-Specific Radiotherapy Schedules

Patient-specific **therapy planning** should account for uncertainties in the underlying biology. Bayesian approaches provide a mathematically rigorous foundation to quantify uncertainty which are in turn used to solve a **risk-based formulation**. Optimized treatment is tailored to the individual to **reduce toxicity and tumor burden**.

Proposed dose schedules are assessed by computing **statistical estimates** of the **time-to-progression (TTP)** from the posterior predictive distribution.

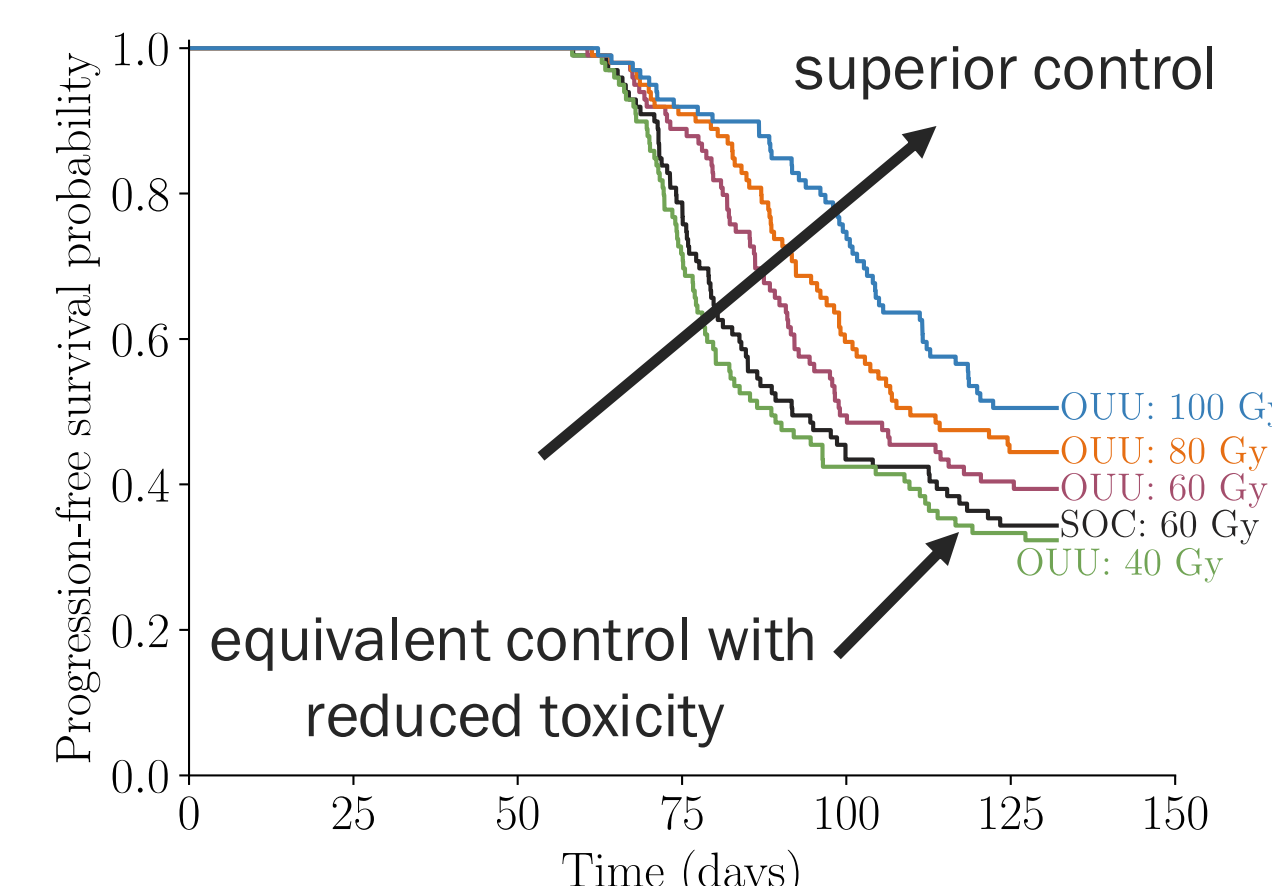


We maximize **time to progression (TTP)** in a risk-based formulation regularized to promote sparsity and **reduce toxicity** in the adapted plan, and subject to a **dosage constraint**.

$$z^* = \arg \min_{z \in \mathcal{Z}_{\text{ad}}} \rho(Q(u); z) + \lambda \|z\|_1$$

$$\text{s.t. } \sum_i z_i \leq z_{\text{max}}$$

Statistical analysis of the **survival curves** demonstrates that optimal scheduling is **significantly better** for the same amount of applied radiation. Statistically **equivalent control** can be achieved with **reduced toxicity**.



Personalized Computational Representation

Personalized modeling starts at the level of computational domains **tailored to the individual**, capturing patient-specific anatomical features. Anatomic segmentation and mesh generation for **patient-specific geometry, cellularity estimation, and longitudinal registration**. Tumor volume fraction is estimated by combining tumor segmentations with cellularity estimates from apparent diffusion coefficient (ADC) images.

