

Results of the Bayesian Calibration

GliomaSolver

INPUT

The Bayesian calibration was performed for

- the input data provided in the folder
 - `/home/tudorm/GliomaSolver/InputData/`
- Using 2048 samples.

RESULTS

The results include:

1. **The calibrated model parameters** reported in Table 1 and Table 2.
2. **The posterior probability distribution (PDF)**
 - With manifold shown in Figure 1.
 - And samples stored in `Results/Details/posterior.txt`
3. **The most probable tumor cell density**, given by the maximum a posteriori (MAP) estimate is:
 - Saved in `Results/MAP.nii`
 - With a preview shown in Figure 2.

Calibrated parameters

- The calibrated parameters are reported in:
 - Table 1: for the tumor growth model
 - Table 2: for image related parameters
- Reported is MAP, mean and standard deviation (std) of the marginal distribution.
- The units are
 - Dw [cm^2/day]; ρ [$1/day$]; T [day];
 - (icx, icy, icz) is reported in dimension-less units.

Table 1: The calibrated parameters of the tumor growth model:

| | Dw | ρ | T | icx | icy | icz |
|------|------------|-----------|----------|----------|----------|----------|
| MAP | 0.00088888 | 0.0289972 | 185.674 | 0.244556 | 0.640598 | 0.645072 |
| mean | 0.0009 | 0.0290 | 185.6788 | 0.2446 | 0.6401 | 0.6452 |
| std | 0.0000 | 0.0000 | 0.0257 | 0.0003 | 0.0006 | 0.0001 |

Table 2: The calibrated parameters of the image model:

| | σ | b | $ucT1$ | $ucFLAIR$ | σ - α |
|------|----------|---------|----------|-----------|---------------------|
| MAP | 0.190255 | 0.61777 | 0.600046 | 0.322598 | 0.0776379 |
| mean | 0.1914 | 0.6181 | 0.6002 | 0.3223 | 0.0776 |
| MAP | 0.0008 | 0.0007 | 0.0002 | 0.0006 | 0.0000 |

Posterior probability distribution

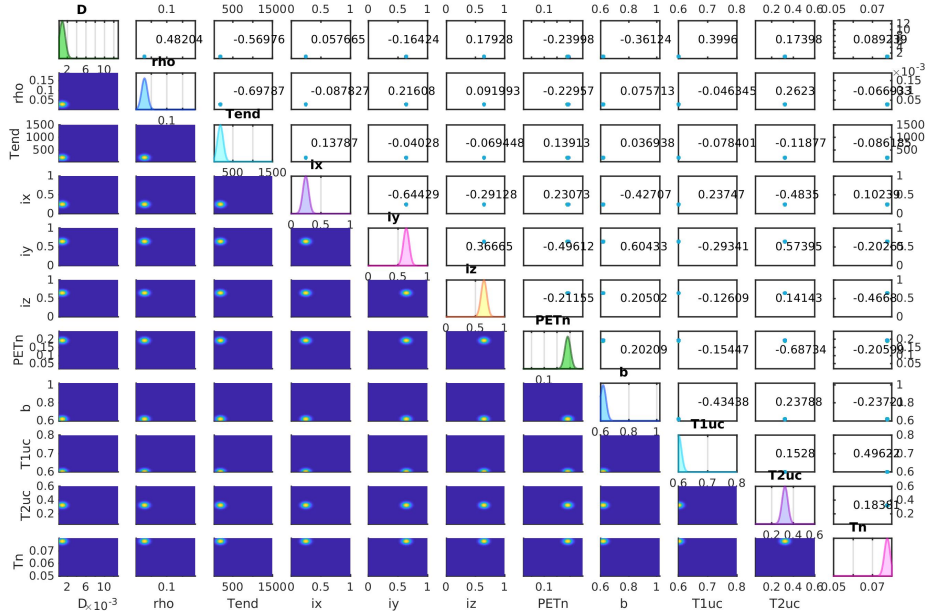


Figure 1: The results of the Bayesian calibration. **Above the diagonal:** Projection of the TCMCMC samples of the posterior distribution in 2D parameter space. The colors indicate likelihood values of the samples. The number in each plot shows the Pearson correlation coefficient between the parameter pairs. **Diagonal:** Marginal distributions obtained with Gaussian kernel estimates. **Below the diagonal:** Projected densities in 2D parameter space constructed by 2D Gaussian kernel estimates.

Tumor Cell Density

References

Please cite

- Lipkova et al.: *Personalized Radiotherapy Planning for Glioma Using Multimodal Bayesian Model Calibration*, preprint arXiv:1807.00499, (2018)
- Rossinelli D, et al.: *Mrag-i2d: Multi-resolution adapted grids for remeshed vortex methods on multicore architectures*. Journal of Computational Physics 288:1–18, (2015).
- P. E. Hadjidoukas et al.: **“Pi4u: A high performance computing framework for bayesian uncertainty quantification of complex models,”* Journal of Computational Physics, 2015.

SEE ALSO

The GliomaSolver source code and all documentation may be downloaded from <http://COMING-SOON/>.

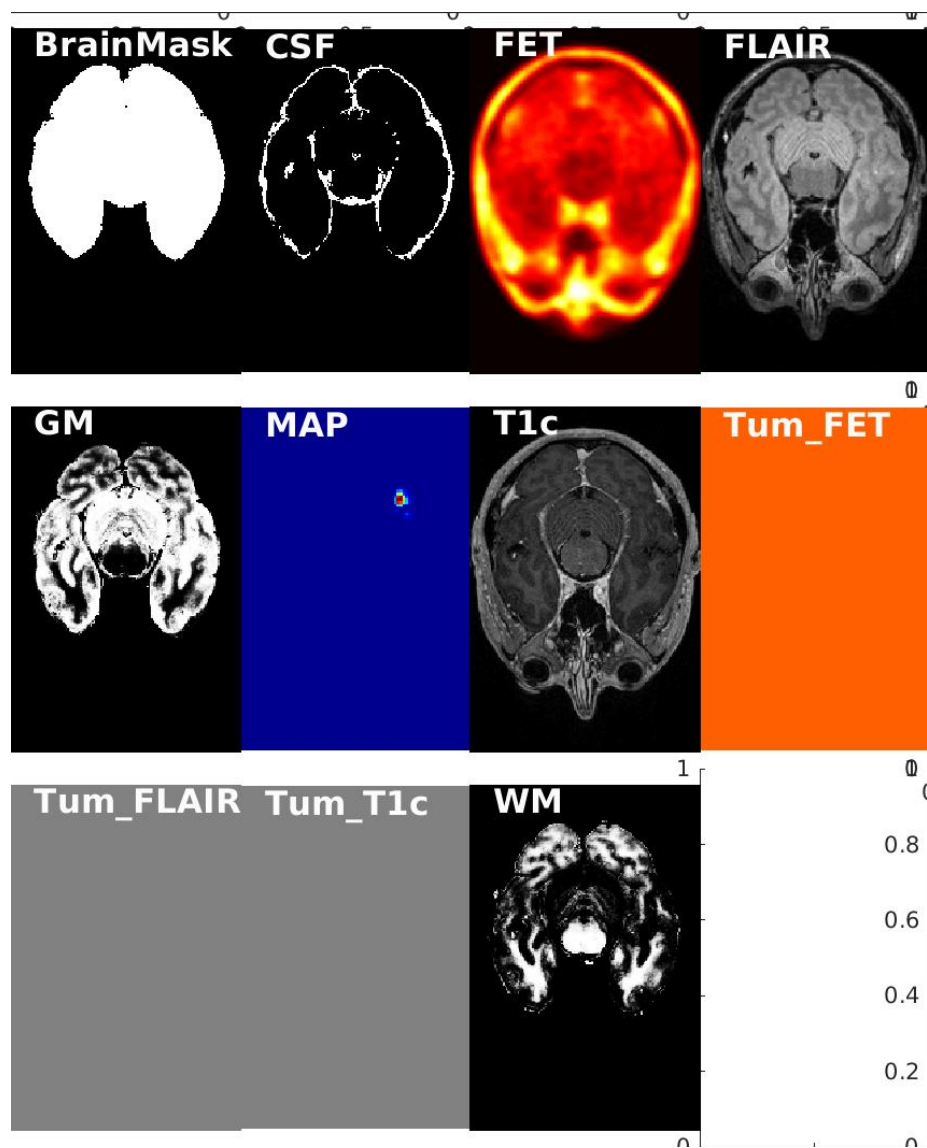


Figure 2: Overview of the input modalities and the inferred MAP tumor cell density. Shown is a middle slice across the MAP tumor cell density.