Using low-rank tensor formats to enable computations of cancer progression models in large state spaces

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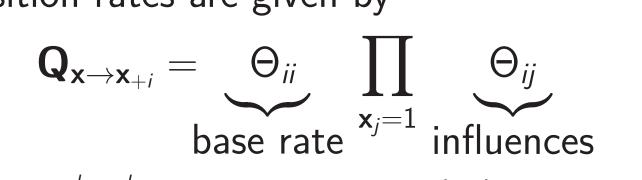
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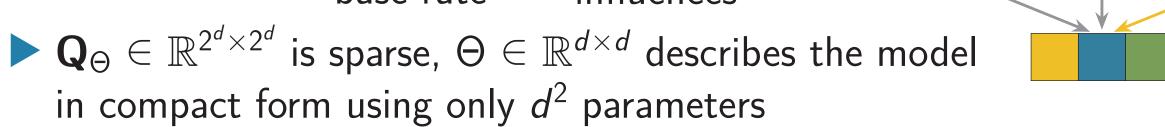
Summary

- \triangleright Comprehensive cancer progression models should include a large number d of genomic events
- Mutual Hazard Networks model the progression process using only d^2 parameters [1]
 - Computational complexity of a straightforward implementation still scales exponentially in d
 - Calculations using $\gtrsim 25$ events are computationally infeasible [2]
- Tensor Trains allow for cost-effective storage and calculations for high-dimensional tensors
 - This method reduces the computational complexity from exponential to polynomial in d

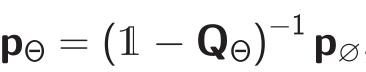
Mutual Hazard Network (MHN) model

- MHN models tumor progression as a continuous-time Markov chain on the 2^d -dimensional state space of possibly active events [1]
- Events can only occur one at a time
- Transition rates are given by





 \blacktriangleright Time marginal probability distribution from Θ :





 \triangleright Optimal Θ matrices are found by optimizing the time-marginalized Kullback-Leibler divergence from the given data distribution $\mathbf{p}_{\mathcal{D}}$:

$$S_{\mathsf{KL}}(\mathbf{p}_{\Theta}) = \sum (\mathbf{p}_{\mathcal{D}})_{\mathsf{x}} \log ((\mathbf{p}_{\Theta})_{\mathsf{x}})$$

Gradients can be calculated analytically:

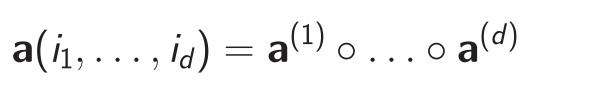
$$\frac{\partial S_{\mathsf{KL}}}{\partial \Theta_{ij}} = \underbrace{\frac{\partial S_{\mathsf{KL}}}{\partial (\mathbf{p}_{\Theta})_{\mathsf{x}}} (\mathbb{1} - \mathbf{Q}_{\Theta})_{\mathsf{xy}}^{-1}}_{\mathbf{q}_{\mathsf{y}}} \left(\frac{\partial \mathbf{Q}_{\Theta}}{\partial \Theta_{ij}}\right)_{\mathsf{yz}} (\mathbf{p}_{\Theta})_{\mathsf{x}}^{\mathsf{y}}$$

Score and gradient calculation time is dominated by solution time of two linear equations:

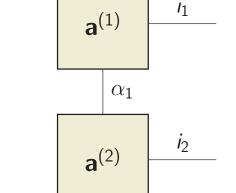
 $(\mathbb{1} - \mathbf{Q}_{\Theta}) \mathbf{p}_{\Theta} = \mathbf{p}_{\varnothing} \qquad (\mathbb{1} - \mathbf{Q}_{\Theta})^{\mathsf{T}} \mathbf{q} = \frac{\partial S_{\mathsf{KL}}}{\partial \mathbf{p}_{\Theta}}$

Tensor Train (TT) representation

lackbrack d-dimensional tensors $\mathbf{a} \in \mathbb{C}^{n_1 \times ... \times n_d}$ can be written as a product of d Tensor Train cores $\mathbf{a}^{(k)} \in \mathbb{C}^{r_{k-1} \times n_k \times r_k}$:



X o Y denotes contraction of last index of X with first index of Y



 $\Theta_{22}\Theta_{23}$

 $\Theta_{11}\Theta_{12}\Theta_{13}$

Similar for operators $\mathbf{A} \in \mathbb{C}^{(m_1 \times ... \times m_d) \times (n_1 \times ... \times n_d)}$: TT cores $\mathbf{A}^{(k)} \in \mathbb{C}^{r_{k-1} \times m_k \times n_k \times r_k}$

- \triangleright Storage cost goes from exponential to linear in d, but additional dependency on TT ranks r_k is introduced
- Many arithmetic operations can be performed directly in the TT format, reducing the computational complexity [3]:
 - Superposition $\lambda \mathbf{a} + \nu \mathbf{b}$: $\mathcal{O}(dn(r_{\mathbf{a}} + r_{\mathbf{b}})^2)$ $n := \max(n_k)$ $n := \max(n_k)$ > Inner product $\langle \mathbf{a}, \mathbf{b} \rangle$: $\mathcal{O}(dnr_{\mathbf{a}}r_{\mathbf{b}}(r_{\mathbf{a}} + r_{\mathbf{b}}))$ $m := \max(m_k)$
 - Operator-by-Tensor product \mathbf{Ab} : $\mathcal{O}(dmn(r_{\mathbf{A}}r_{\mathbf{b}})^2)$ $r_{\mathbf{X}} := \max((r_{\mathbf{X}})_k)$

\blacktriangleright Linear equations $\mathbf{A}\mathbf{x} = \mathbf{b}$ can also be solved efficiently directly in this format

References

- [1] R. Schill, S. Solbrig, T. Wettig, and R. Spang, Modelling cancer progression using Mutual Hazard Networks, Bioinformatics 36 (January, 2020) 241.
- [2] P. Georg, L. Grasedyck, M. Klever, R. Schill, R. Spang, and T. Wettig, Low-rank tensor methods for Markov chains with applications to tumor progression models, Journal of Mathematical Biology 86 (December, 2022).
- [3] P. Georg, Tensor Train Decomposition for solving high-dimensional Mutual Hazard Networks, PhD thesis, Universität Regensburg, October, 2022.

Tensor Trains for MHN

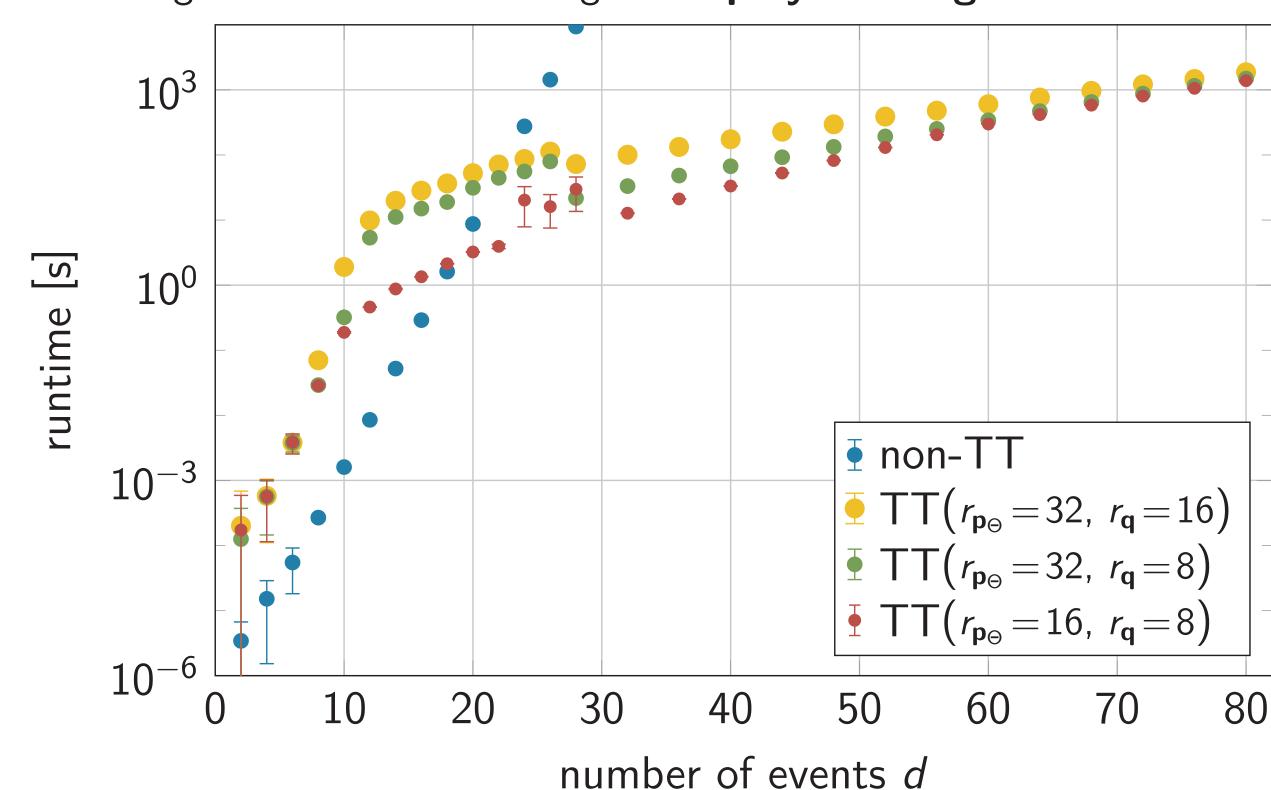
- ightharpoonup Events are binary $\rightarrow n_k = 2$ for all mode sizes
- $ightharpoonup \mathbf{Q}_{\Theta}$ can naturally be written as a Tensor Train [1]:

$$\mathbf{Q}_{\Theta} = \sum_{i=1}^{d} \left(\bigotimes_{j=1}^{i-1} \left(\underbrace{\begin{array}{c} 1 & 0 \\ 0 & \Theta_{ij} \end{array}}_{\in \mathbb{R}^{1 \times 2 \times 2 \times 1}} \otimes \left(\underbrace{\begin{array}{c} -\Theta_{ii} & 0 \\ \Theta_{ii} & 0 \end{array}}_{\in \mathbb{R}^{1 \times 2 \times 2 \times 1}} \otimes \left(\underbrace{\begin{array}{c} 1 & 0 \\ 0 & \Theta_{ij} \end{array}}_{j=i+1} \left(\underbrace{\begin{array}{c} 1 & 0 \\ 0 & \Theta_{ij} \end{array}}_{\in \mathbb{R}^{1 \times 2 \times 2 \times 1}} \right) \right)$$

- \mathbf{Q}_{Θ} is a sum of d rank-1 Tensor Trains
- \triangleright All TT-ranks of \mathbf{Q}_{Θ} equal d
- \mathbf{p}_{\varnothing} is a canonical unit Tensor Train, with all TT-ranks equal to 1
- \mathbf{p}_{Θ} and \mathbf{q} can be calculated in the TT format (max. TT ranks $r_{\mathbf{p}_{\Theta}}$ and $r_{\mathbf{q}}$)
- \blacktriangleright For gradients, each nonzero entry in $\mathbf{p}_{\mathcal{D}}$ has to be treated individually
- One linear equation has to be solved for each nonzero entry (usually $\sim \! 1000)$
- This can be parallelized trivially

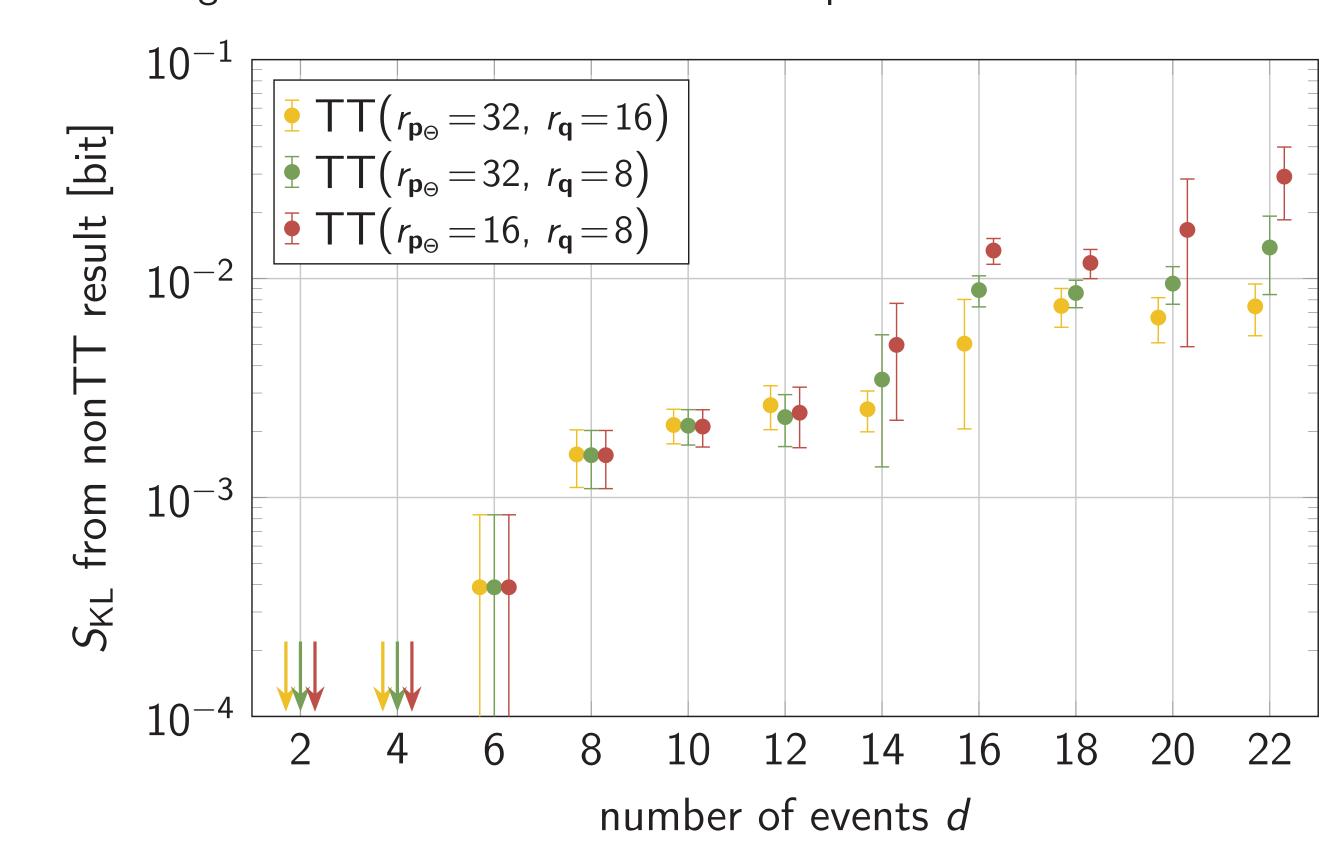
Results: Runtime speedup

- Runtime for one score and gradient calculation
- $ightharpoonup \mathbf{p}_{\mathcal{D}}$ constructed from 1000 random samples, $\Theta = \text{independence model}$
- Runtime grows with $\sim d^{5.4}$ for large $d \Rightarrow$ polynomial growth!



Results: Accuracy of the TT solution

 \triangleright KL-divergence from non-TT result after full optimization of Θ



Code availablility

- C++ library for TT-calculations pRC: gitlab.com/pjgeorg/pRC
- ► Application-specific C++ library cMHN that utilizes pRC for MHN-calculations: soon to be open-source

Future improvements

- ► Reduce runtime by accelerating solution of linear equations in TT format
- Include formation of metastases in the model