

Mathematical Modelling of Myeloproliferative Neoplasms and Hematopoietic Stem Cells

An overview of our recent work and a look to the future

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► Who am I?

- ▶ Who am I?
 - ▶ Postdoc at the PandemiX Research Center, working on COVID-19 and historical epidemics.



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- Ph.D. at Roskilde University: Mathematical modelling of blood cancers, with Johnny and Morten.



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- ▶ This talk:

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► This talk:

- Illustration of how mathematical modelling could contribute to clinical practice in the future.

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► This talk:

- Illustration of how mathematical modelling could contribute to clinical practice in the future.
- Focus on general aspects of mathematical modelling rather than mathematical details.

- **Myeloproliferative Neoplasms (MPNs):** Group of diseases characterized by overproduction of blood cells.

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- **Myeloproliferative Neoplasms (MPNs):** Group of diseases characterized by overproduction of blood cells. Believed to arise from mutations occurring in hematopoietic stem cells (HSC)

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- ▶ **Myeloproliferative Neoplasms (MPNs):** Group of diseases characterized by overproduction of blood cells. Believed to arise from mutations occurring in hematopoietic stem cells (HSC)
- ▶ **Clinicians from Zealand University Hospital:** MPN-patients treated with pegylated interferon- α obtain long-term normalization of cell-counts.

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- ▶ **Data:** Clinical trial with patients treated with interferon- α .

Our purpose and goal

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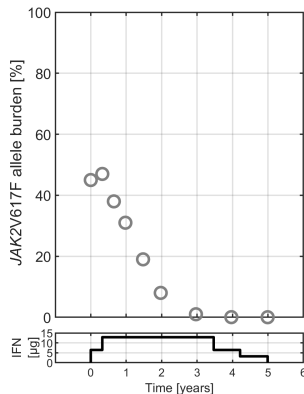
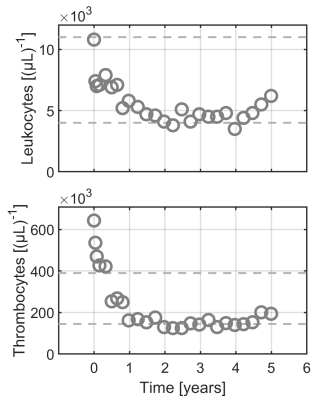
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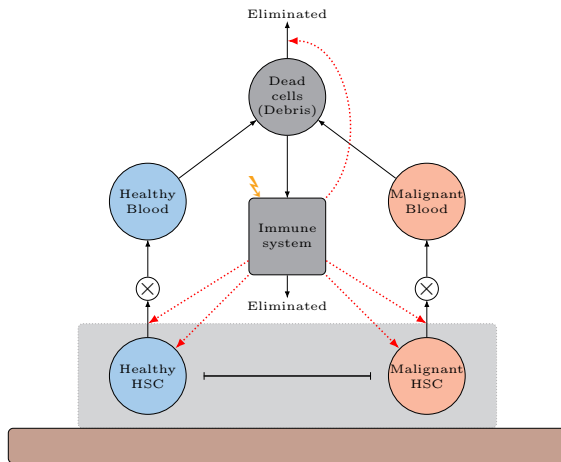
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- ▶ **Myeloproliferative Neoplasms (MPNs):** Group of diseases characterized by overproduction of blood cells. Believed to arise from mutations occurring in hematopoietic stem cells (HSC)
- ▶ **Clinicians from Zealand University Hospital:** MPN-patients treated with pegylated interferon- α obtain long-term normalization of cell-counts.
- ▶ **Data:** Clinical trial with patients treated with interferon- α .
- ▶ **Goal:** Can the effects of interferon- α be accurately described by a mathematical model?

Model description



(Pedersen et al, 2021)

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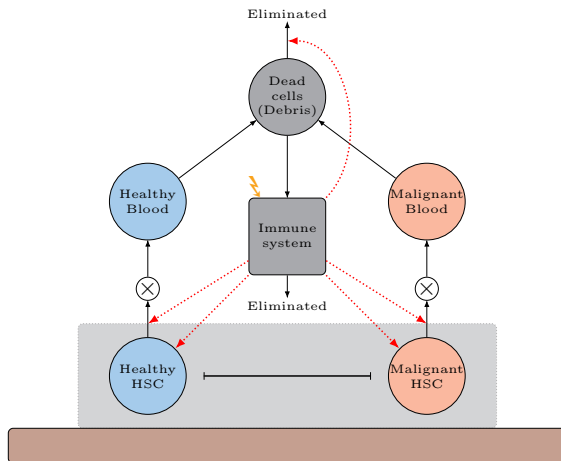
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Model description



(Pedersen et al, 2021)

Based on previous model of Andersen et al (2017), combined with a model of HSC developed together with Thomas Stiehl (Roskilde University & RWTH Aachen).

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- ▶ System of 6 ODEs, with about 16 parameters.

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- ▶ System of 6 ODEs, with about 16 parameters.
- ▶ Most parameters determined from the literature.

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- ▶ System of 6 ODEs, with about 16 parameters.
- ▶ Most parameters determined from the literature.
- ▶ General model behaviour in agreement with clinical intuition.

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 - ▶ Chronic inflammation leads to faster disease progression.

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- ▶ General model behaviour in agreement with clinical intuition.
 - ▶ No mutations \rightarrow long-term health.
 - ▶ Disease progression over a long period (15+ years).
 - ▶ Chronic inflammation leads to faster disease progression.
- ▶ We can perturb specific model-parameters that relate to the biological effect of interferon- α treatment.

Treatment-specific perturbations

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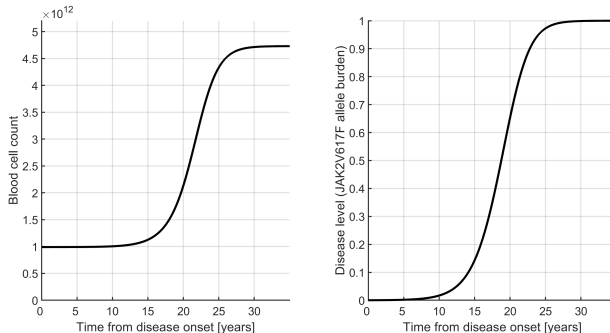
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Typical disease progression in the model.

Treatment-specific perturbations

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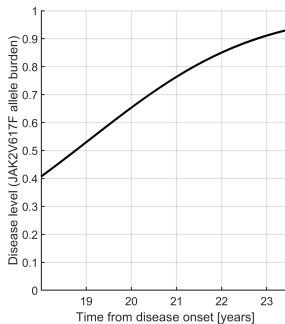
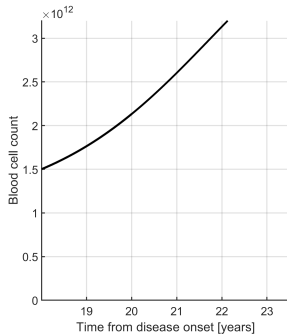
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Zooming in on year 20 after original mutation.

Treatment-specific perturbations

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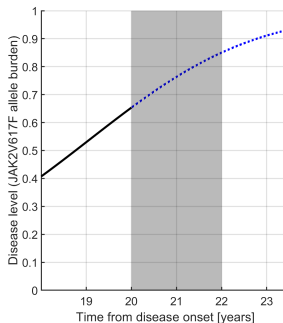
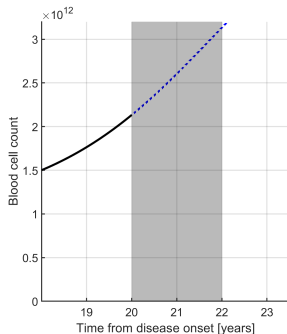
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Considering two years of treatment.

Treatment-specific perturbations

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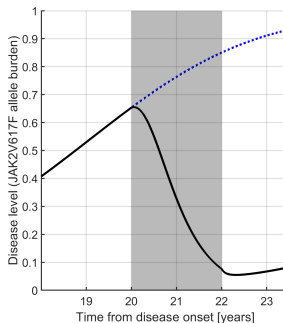
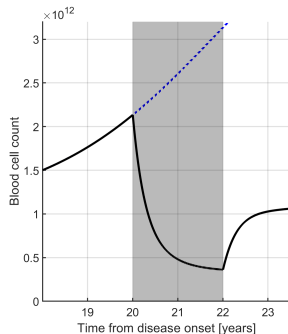
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Considering two years of treatment.
Perturbing model-parameters related to treatment.

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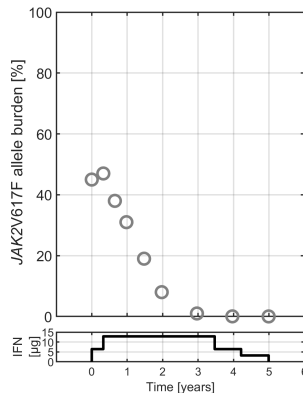
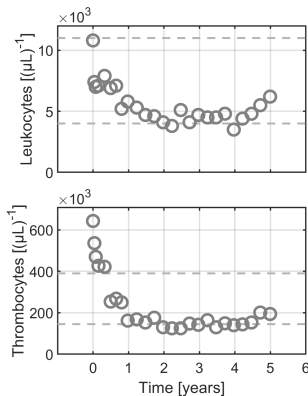
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Raw data

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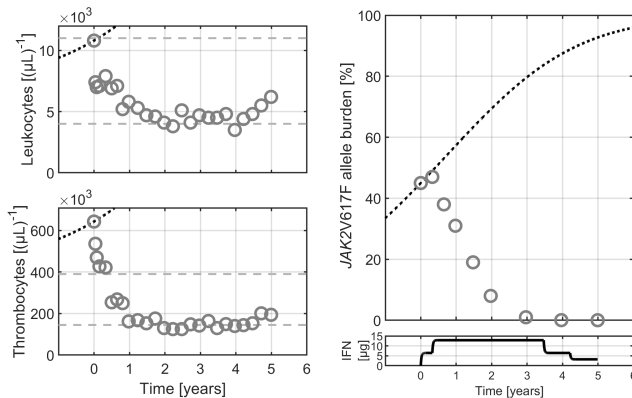
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Adding modelled scenario without treatment,
time-shifted to agree with baseline data
(and PK/PD-modelling of treatment)

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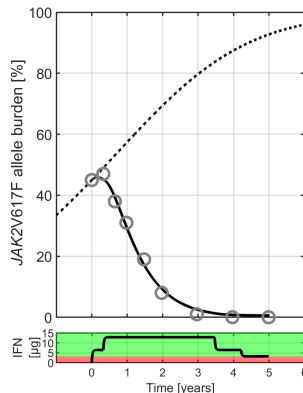
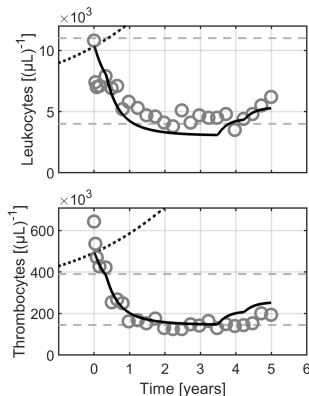
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Dose-dependent fitting of model-parameters

Halting treatment

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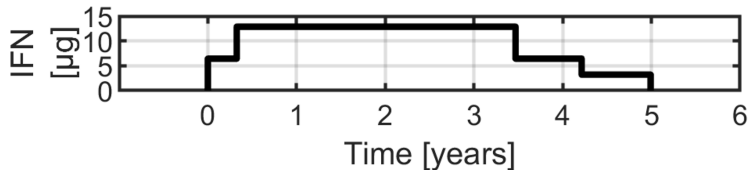
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Actual treatment:

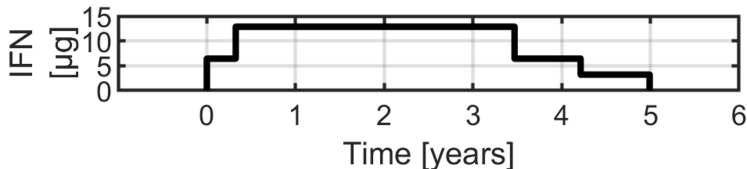


Halting treatment

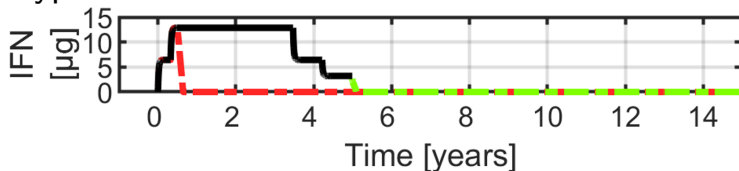
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Actual treatment:



Hypothetical treatment:



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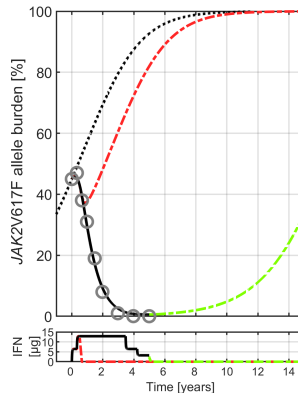
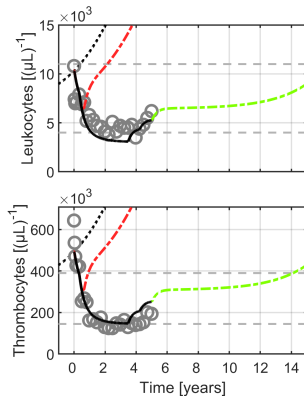
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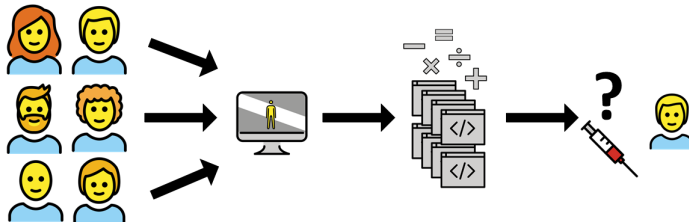
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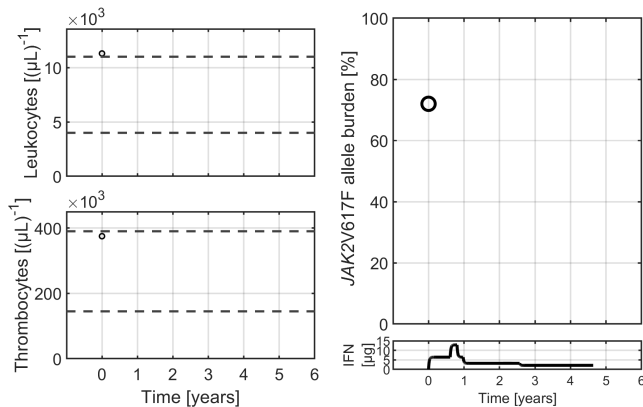
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Baseline data

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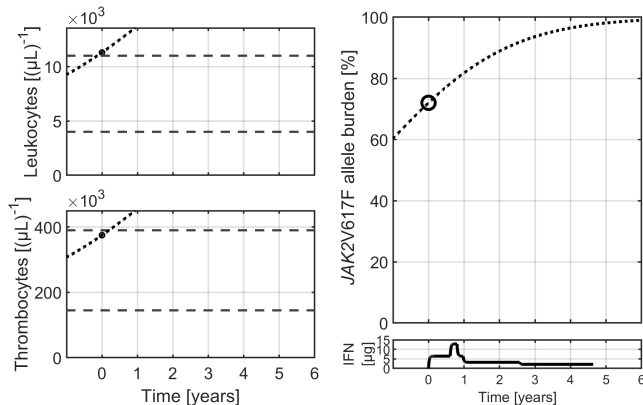
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Estimating stage of disease progression and prediction in absence of treatment.

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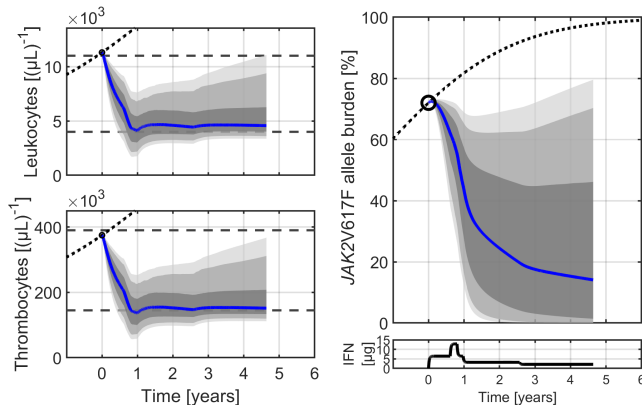
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Simulation 1000 virtual patients with same treatment-plan.

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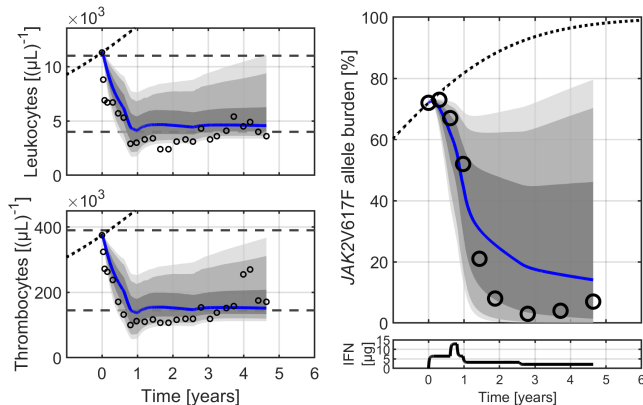
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Comparing to actual patient data

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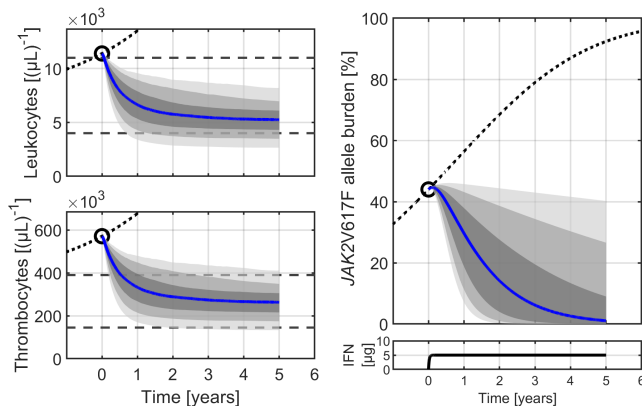
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Completely hypothetical patient: Baseline data from mean of cohort.

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- ▶ Mathematical modelling can relate mechanistic understanding of treatment to clinical measures.

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- ▶ Mathematical modelling can relate mechanistic understanding of treatment to clinical measures.
- ▶ Individual patients' response to treatment can be captured by the model.

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- ▶ Mathematical modelling can relate mechanistic understanding of treatment to clinical measures.
- ▶ Individual patients' response to treatment can be captured by the model.
- ▶ Combining the response of multiple patients could make forecasting possible.

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- ▶ Mathematical modelling can relate mechanistic understanding of treatment to clinical measures.
- ▶ Individual patients' response to treatment can be captured by the model.
- ▶ Combining the response of multiple patients could make forecasting possible.
- ▶ However, further validation is required before predictions can be used in the clinic.

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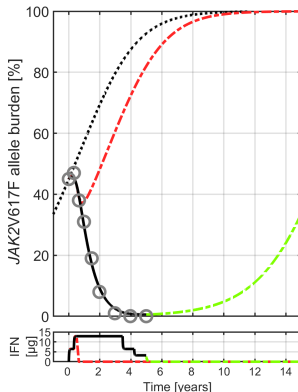
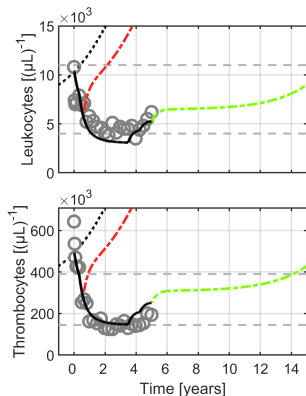
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- Highly complex diseases affecting the entire body can be modelled successfully.

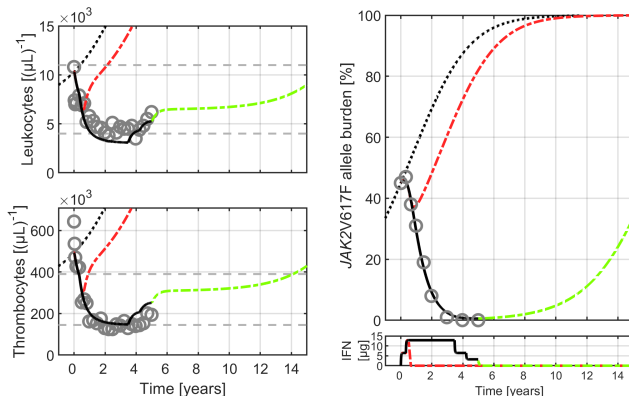
Comments on the future

- ▶ Highly complex diseases affecting the entire body can be modelled successfully.
- ▶ Mathematical models as expert-assistance tool.



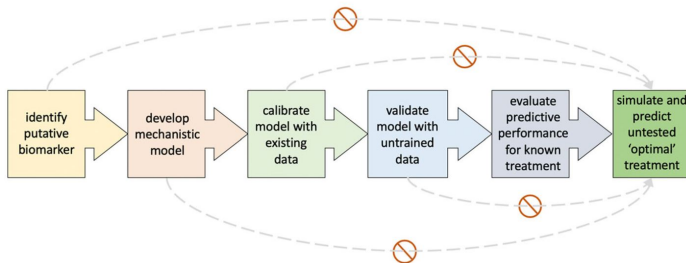
Comments on the future

- ▶ Highly complex diseases affecting the entire body can be modelled successfully.
- ▶ Mathematical models as expert-assistance tool.
- ▶ And as a tool for patient-communication.



Comments on the future

- ▶ Highly complex diseases affecting the entire body can be modelled successfully.
- ▶ Mathematical models as expert-assistance tool.
- ▶ And as a tool for patient-communication.
- ▶ Promising for the future of oncology and heamatology, but careful and thoughtful validation is important.



(Brady & Enderling, 2019)

Thank you for your attention.

Any questions?



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- ▶ Pedersen RK, et al (2021), Dose-dependent mathematical modeling of interferon- α -treatment for personalized treatment of myeloproliferative neoplasms. *Comp. Sys. Onco.*; 1:e1030. <https://doi.org/10.1002/cso2.1030>
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Flowchart for prediction of "optimal" treatment from

- ▶ Brady, R., & Enderling, H. (2019). Mathematical Models of Cancer: When to Predict Novel Therapies, and When Not to. *Bulletin of Mathematical Biology*, 81(10), 3722-3731. <https://doi.org/10.1007/s11538-019-00640-x>