

# Methodology: Realistic Estimates of prediction uncertainty from ML

zk: Can we derive composite measures to reduce uncertainty/cope with missingness?

Conformal Prediction looks an exciting approach - how well developed and accepted is this? or is this still a rapidly maturing area for active research?

HH: What is a relevant benchmarking dataset or synthetic dataset to test/validate the proposed methodology for "uncertainty from ML"

HH: Can we narrow-down what specific ML task the R-T partnership is interested in?

CHa : This paper : <https://doi.org/10.1016/j.jannonc.2020.07.013> may give an idea of an application. We would also be interested in doing the same concept with larger-p datasets (genomics, imaging etc)

HH: What expertise is on the panel using Bayesian + ML for uncertainty quantification? Could this person present state-of-the-art? Or case study?

MRB: Prediction uncertainty is likely to be driven by hidden biases in training, test and validation. How can these be minimised and bias detected?

AF: How do we propagate uncertainty downstream? How we deal with uncertainty in heterogenous ML pipelines with different ML models (eg statistical ML, deep learning, etc)

CHa : How do we deal with uncertainty of variables being incorporated downstream into other models?

CHa : How to deal with population (domain) shifts e.g. over time or between regions?

CHa : How do we deal with uncertainty inherent in our data (esp RWD) e.g. abstracted and extracted variables

AF - Standards - distil relevant aspects for the modelling work we undertake in the partnership? e.g., ASME V&V 70 <https://cstools.asme.org/csconnect/CommitteePages.cfm?Committee=103099834&Action=54642>

CHa:What practice? Opportunities to influence Health Authority policy

AF: How do we identify whether epistemic vs aleatoric uncertainty dominates our problem? Best practices?

# Policy: Validation of Prognostic/Predictive Models

**zk: how do we validate early prediction models in preclinical populations?**

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<https://cstools.asme.org/csconnect/CommitteePages.cfm?Committee=103099834&Action=54642>

**CHa :What is best practice? Opportunity to influence Health Authorities?**

**MRB: Validation is probably dependent on Explainability, how can this be maximised? E.g. using Shapley plots to highlight areas for validation**  
<https://www.sciencedirect.com/science/article/pii/S0957417421002736>

**HH: Are there validation case-studies of prognostic/predictive models?**

**benchmark and challenges in predictive models. See for instance MICCAI**  
<https://grand-challenge.org/challenges/> but also  
<https://pubmed.ncbi.nlm.nih.gov/32911207/> and  
<https://pubmed.ncbi.nlm.nih.gov/32911207/>

**HH: Is there a specific case study of interest?**

**HH: What type of data and/or model does the R-T have in mind?**

**MRB: Validation is probably dependent on Explainability, how can this be maximised? E.g. using Shapley plots to highlight areas for validation**  
<https://www.sciencedirect.com/science/article/pii/S0957417421002736>

# Methodology: Multi-Modal Data

GJ: "Deep" matching of patient profiles not just on clinical, but multimodal data. Does a multimodal approach allow us a more complete matching, so eg a hybrid control from RWE is "closer" to the trial population we are comparing to?

GJ: At individual patient level, can we predict risk of future events from currently available modalities earlier and/or more reliably than with single modalities?

GJ: Can we evaluate error propagation throughout the modalities into the final prediction eg of progression?

HH: It might be worth brainstorming together the specific questions to answer with multi-modal data?

HH: We used a tensor data structure in two different multi-modal datasets, I wonder if this is useful for the R-T partnership questions?

AKn: Can multi-modal data help us identify high/low risk patients and patients most likely to respond well to certain therapies?

AKn: Can multi-modal data help us overcome challenges associated with disease heterogeneity?

AKn: Can multi-modal data help us predict recurrence/progression patterns e.g. development of CNS metastases?

AF - Multimodal data never gets all collected at once, but through a sequence of examinations to narrow down diagnostic/prognostic decision uncertainty. What is the optimal multimodal sequence?

AF - how do we build predictors that can make inferences even when some modalities are missing?

MRB: Microarrays, Bulk tissue RNAseq and Single cell can all be used to study the same sample but differ widely in results, can we understand and normalise across such data types?

MRB: Lots of hype around multi-omics has not delivered. Can we perform a meta-analysis of multi-omic studies to define the most productive multi-modal interfaces?

MRB: Can we define/generate gold standard multi-modal data sets for method development?

zk: Can we use multimodal data to identify/profile new disease subtypes?

zk: Can we optimise predictive assays for different disease stages?

Dan: How do we integrate multimodal data so they can reinforce each others' evidence for/against a biological hypothesis (e.g. RNA/protein expression in pathways)?

CHa : How much value does multi-modal data add in addressing these questions? How much additional information does it need to add to overcoming the added complexity?

# Methodology: Prognostic/Predictive Modelling (Health Status Metric)

**HH: What type of models are best suited to prognostic predictive modelling (compare different methodologies)**

**HH: What is a suitable validation/testing/benchmarking system for prognostic/predictive modelling?**

**AKn: Similar questions to those posed on board #3**

**AF - indeed, do not understand how this differs from board 3.**

# Tackling difficult issues in Computational Pathology

zk: Can predictive models help us understand disease pathology/make causative inferences?

HH: Can we create an end-to-end pipeline that highlights the different computational/methodological/data research questions?

HH: the difficult issues are likely dependent on the system of interest. Can the R-T partnership pin down a concrete problem/dataset?

MRB: Most computational pathology originates from the NHS. There are considerable barriers, including research environments and GDPR. Can technical solutions address this?

MRB: Pathology imaging depends on robust image patching, however public domain tools, like clam (<http://clam.mahmoodlab.org/>) struggle with some image/tissue types. Are other solutions available?

MRB: Can we develop portable, standardised pipelines for pathology image analysis?

Dan: How can we integrate different modalities (e.g. H&E, IHC, spatial-omics) from the same patient?

Dan: Pathologists integrate info across scales, whereas end-to-end ML approaches typically work at one scale (pixel level). Would multi-scale approaches be advantageous? (e.g. U-Net)

Dan: How important is color calibration/normalization to computational pathology?

Dan: How do we best integrate clinical variables (e.g. age, sex, cancer staging) with spatial data in deep learning architectures?



# Early life predictions, following life trajectories

AKn: Are we thinking here about enhancing screening/surveillance approaches that currently exist?

AF - how do we update early life predictions as a patient's record gets "enhanced" with additional evidence/examinations? How we develop systems open not only to new data, but also to new modalities?

zk: how early can we predict? do the predictors/combinations of features change at different stages of disease?

zk: can we predict change in individual trajectories rather than clinical labels to reduce misdiagnosis?

HH: I have little experience in this domain, so I look forward to learning more about these questions.

MRB: Some promise with deep diffusion processes (DDP) to model the temporal relationships between disease onset expressed as a dynamic graph.  
<http://proceedings.mlr.press/v108/qian20a/qian20a.pdf>

MRB: EHR time course can be studied as a point process, using methods to Balance likelihood of already observed events with prediction of future events. See Work of Turing Fellow Mihaela van der Schaar,

# Methodology: Knowledge Graphs

AP - How do we incorporate "prior mechanistic" information in prediction models. This is interesting justification of why you may want to do this  
<https://www.nature.com/articles/s42256-019-0077-5>

MRB: Lots of AI SMEs are using Knowledge graphs, how do these compare to other methodologies, what are the benefits and weaknesses?

What concrete question does the R-T partnership hope to answer with KG? This will then determine what are the nodes and edges of the KG.

MRB: Do open source knowledge graph frameworks exist?

# Detecting Confounders/Matching populations

HH: I have little experience with this topic. I look forward to learning more and contributing once the questions are more concrete.

zk: how do confounders impact model generalisation across populations?

MRB: Do clinical trial methodologies like propensity score matching have a broad application in better matching populations for ML?



# Creating virtual populations

**AF - How do we quantify the coverage of a virtual population wrt to the target real population in typical RWE settings?**

**AF - How do we create generative virtual populations of digital twins based on large multimodal datasets of datasets?**

**MRB: Obvious opportunities to consider digital twins here? Can we use digital twins to maximise treatment arms of clinical trials?**

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Suits a 6-12 month pilot project e.g could be done by Turing partner universities

Would be suitable to start a major research project in this area e.g may be suitable for our workshop/funding call model

'Deep' matching of patient profiles on multi-modal data (not just clinical). Does this approach allow us more complete matching e.g a hybrid control from RWE is 'closer' to the trial population we are comparing to?

Lower priority for Partnership/Roche

Would developing multi-scale approaches/models be advantageous (e.g in pathology?)

How do we incorporate 'prior mechanistic' information into machine learning models?

Medium priority for Partnership/Roche

How do we update predictive models over time as data evolves?

Can we use multi-modal data to address questions such as predicting recurrent regression patterns, identifying high or low risk patients?

What methods should be used to validate/benchmark/compare predictive models?

How do we deal with uncertainty in predictive modelling, in the data, predictions themselves, in downstream tasks?

Can machine learning models help decipher disease mechanisms?

How do we best integrate clinical variables (e.g age, sex, cancer staging) with spatial data in deep-learning architectures?

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\* these may be related

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# Heather Harrington

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# Markus Bundschus

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# Michael Barnes

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