

A Personalized Predictive Framework for Multivariate Clinical Time Series via Adaptive Model Selection

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Personalized Prediction Problem

Clinical time series forecasting for **each individual patient**.



MCH: 32.45
MPV: 09.35
RBC: 03.84
.....

Day₁

MCH: 31.94
MPV: 08.73
RBC: 04.21
.....

Day₂

.....

.....

MCH: 34.45
MPV: 09.21
RBC: 03.92
.....

Day_t

?

Day_{t+1}

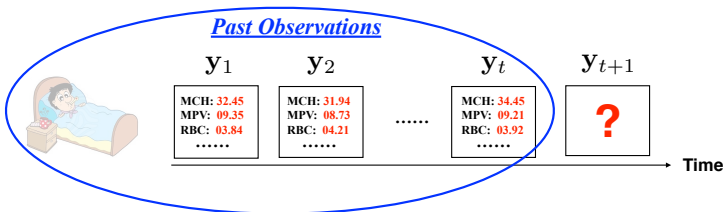
Time



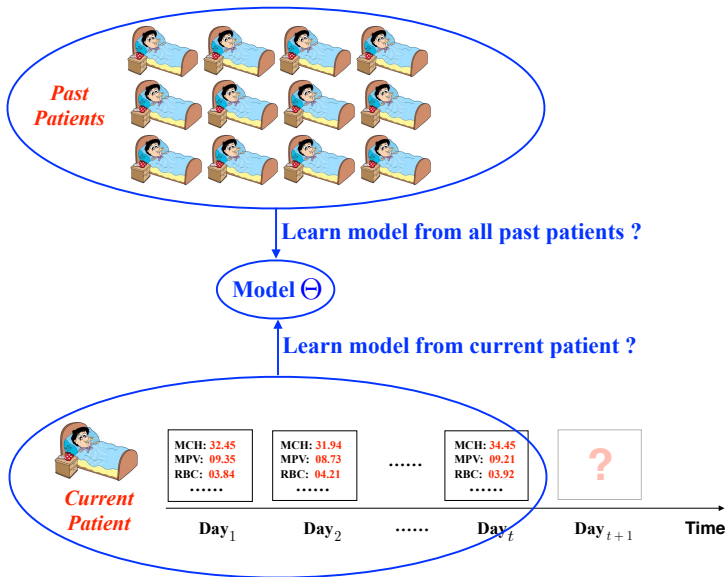
MCH: mean corpuscular hemoglobin (pg/cell)
MPV: mean platelet volume (fL)
RBC: red blood cell (10E12/cell)

How to learn a good forecasting model(Θ) from the past?

Question: How to learn a good personalized forecasting model(Θ) from past observations?



How to learn a good forecasting model(Θ) from the past?



Two Existing Approaches

- **Population-based models**

Problem: patient-specific variations are typically large and population-based models are unable to support accurate predictions for each individual patient.

- **Instance/patient-specific models**

Problem: time series observed for one patient may be too short to learn a high-quality patient-specific model.

Goal

Build a personalized predictive model that relies on the data for **past patient population** but can adapt quickly to new observations made for **the target patient**.

Building Personalized Predictive Models

- **Subpopulation models**
- **Model adaptation**
- **Adaptive model selection**

- **Subpopulation models:** learned from a selected collection of similar examples out of the entire population.

Disadvantages:

- Finding “neighbors” is difficult when **the sequence is very short**.
- Intensive neighbor searching process has to be redone once new observations arrive
- A subpopulation may still be very large and exhibit a lots of patient-specific variations.

- **Subpopulation models**
- **Model adaptation:** adjusting the population-based model to fit better the specific instance.

Disadvantages:

- Designing and deriving adaptation is difficult and varies from model to model. (For example, deriving exact posterior in Bayesian setting.)
- A larger number of instance-specific features or observations are required to conduct adaptation.

Building Personalized Predictive Models

- **Subpopulation models**
- **Model adaptation**
- **Adaptive model selection:** combining a pool of predictive models which are built either from the entire population or a subpopulation of instances.

Disadvantages:

- Error feedback over longer periods of time are required to optimize the combination weights.
- Recent errors are smoothed out by the errors made in the early stage of the process.

We develop a personalized clinical time series prediction frameworks that better mimic patient specific temporal behaviors and variations.

- **Personalized prediction via adaptive model selection:** selecting the appropriate model at each time stamp for each patient.

Personalized Prediction via Adaptive Model Selection

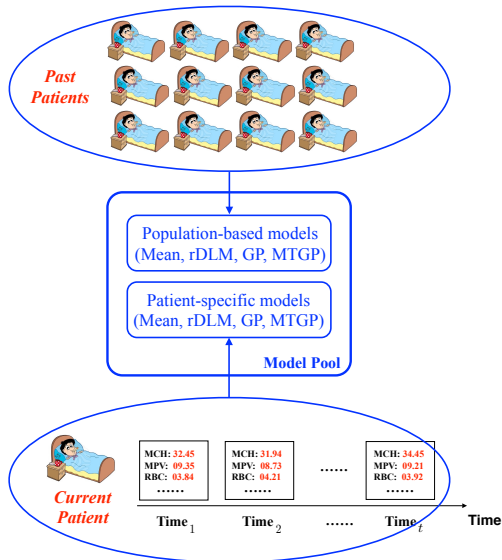
Intuition: predictions at different times may be driven by the different types of prediction models.

Our Approach: online model switching.

Learning: Build a pool of population-based and patient-specific prediction models.

Prediction: Select the appropriate model by the weighted sum of prediction errors (or deviations) of each model on past patient's data.

Learn A Pool of Models

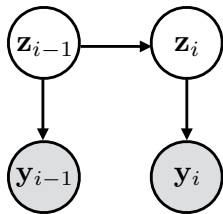


Dynamic Linear Model (DLM)

Dynamic Linear Model

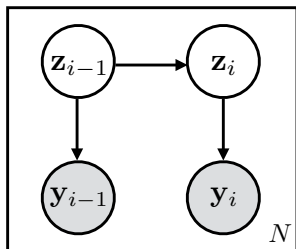
$$\mathbf{y}_i = \mathbf{C}\mathbf{z}_i + \zeta_i; \quad \mathbf{z}_i = \mathbf{A}\mathbf{z}_{i-1} + \epsilon_i$$

$$\epsilon_i \sim \mathcal{N}(0, Q), \zeta_i \sim \mathcal{N}(0, R) \text{ and } \mathbf{z}_1 \sim \mathcal{N}(\boldsymbol{\xi}, \Psi)$$



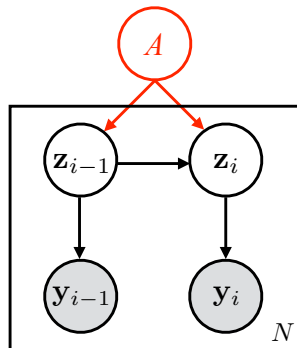
- $\{\mathbf{y}_i\}$ time series of observations.
- $\{\mathbf{z}_i\}$ hidden states driving the dynamics.
- Parameters $\Lambda = \{\mathbf{A}, \mathbf{C}, \mathbf{Q}, \mathbf{R}, \boldsymbol{\xi}, \Psi\}$.

Regularized Dynamic Linear Model (rDLM)



DLM

v.s.



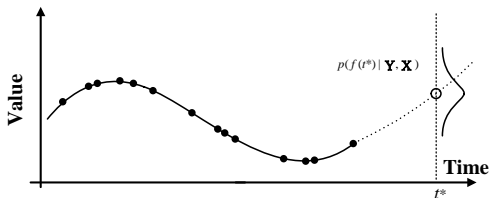
regularized DLM

Achieve low-rank property by introducing priors on A !

Gaussian Processes (GP)

GP can be used to calculate the posterior distribution $p(f(\mathbf{X}^*) | (\mathbf{X}, \mathbf{Y}))$ of f values for inputs \mathbf{X}^* , given a set of observed values \mathbf{Y} for \mathbf{X} .

$$f(\mathbf{X}^*) | (\mathbf{X}, \mathbf{Y}) \sim \mathcal{N}(m(\mathbf{X}^* | (\mathbf{X}, \mathbf{Y})), K^G(\mathbf{X}^* | (\mathbf{X}, \mathbf{Y})))$$



Advantage:

- Non-parametric
- Continuous time
- Capture short-term variability

Multi-task Gaussian Process (MTGP)

The MTGP [Boni 07] is an extension of GP. The covariance matrix of MTGP:

$$\boxed{K^G} + \delta \cdot I$$

Similarities between different time stamps

noise variance

GP

$$\boxed{K^C} \otimes \boxed{K^G} + D \otimes I$$

Similarities between different series

Diagonal matrix with noise variance

MTGP

Online Model Switching

We develop a novel online model switching strategy, i.e., “weighted Follow-the-Leader” (wFTL) which

- quickly adapts to specific patient given short observations.
- is optimized for recent performance.

The model being pick at time t^* is selected by

$$\mathcal{M}_* = \arg \min_m \sum_{i=1}^q w_i * e_i^m.$$

The diagram shows the equation $\mathcal{M}_* = \arg \min_m \sum_{i=1}^q w_i * e_i^m$ with several annotations. A red arrow labeled "past time index" points to the subscript i in w_i . Another red arrow labeled "model index" points to the superscript m in e_i^m . Below the equation, two blue arrows point downwards from the terms w_i and e_i^m to the labels "weight" and "error" respectively.

$$\mathcal{M}_* = \arg \min_m \sum_{i=1}^q \underbrace{w_i}_{\text{weight}} * \underbrace{e_i^m}_{\text{error}}$$

“weighted Follow-the-Leader” (wFTL): $\mathcal{M}_* = \arg \min_m \sum_{i=1}^q w_i * e_i^m$

Intuition: errors made far away should be less penalized compared to the most recent errors.

- **Square exponential kernel:** $K_{se}(t_i, t^*) = \exp \left(- \frac{(t_i - t^*)^2}{\gamma} \right)$
- **Mean reverting kernel:** $K_{mr}(t_i, t^*) = \exp \left(- \frac{|t_i - t^*|}{\gamma} \right)$

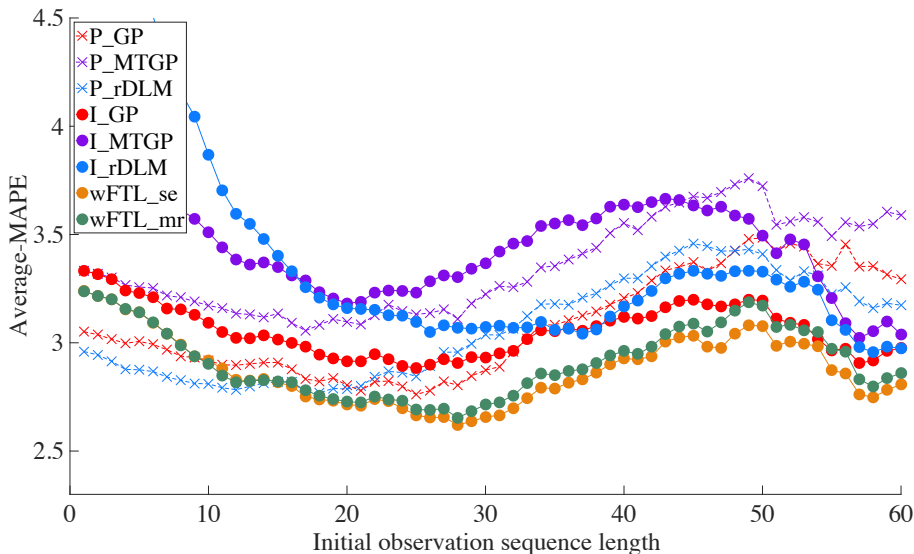
where t_i is the all the past time stamps, $i = 1, 2, \dots, q$ and γ is the bandwidth parameter.

- Clinical data: 500 patients who had their *Complete Blood Count* (CBC) tests in PCP database [Haus 10].
- Evaluation metric: Mean Absolute Percentage Error (MAPE)

$$\text{Average-MAPE} = \frac{\sum_{l=1}^N \sum_{j=1}^n \sum_{i=1}^{T_l} |1 - \hat{y}_{j,i}^l / y_{j,i}^l|}{n \sum_{l=1}^N T_l} \times 100\%$$

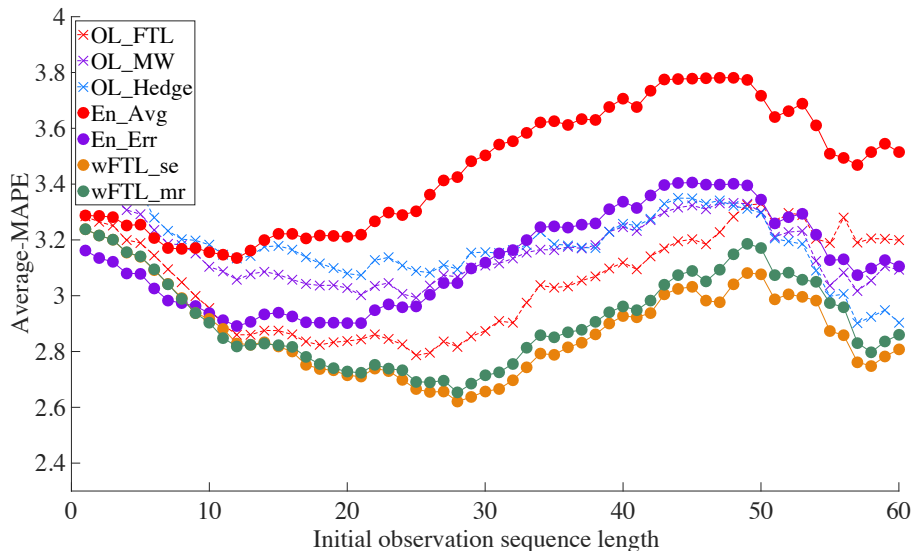
- Prediction task: per (patient(l), time stamp(t))

Population-based V.S. Patient-specific Models

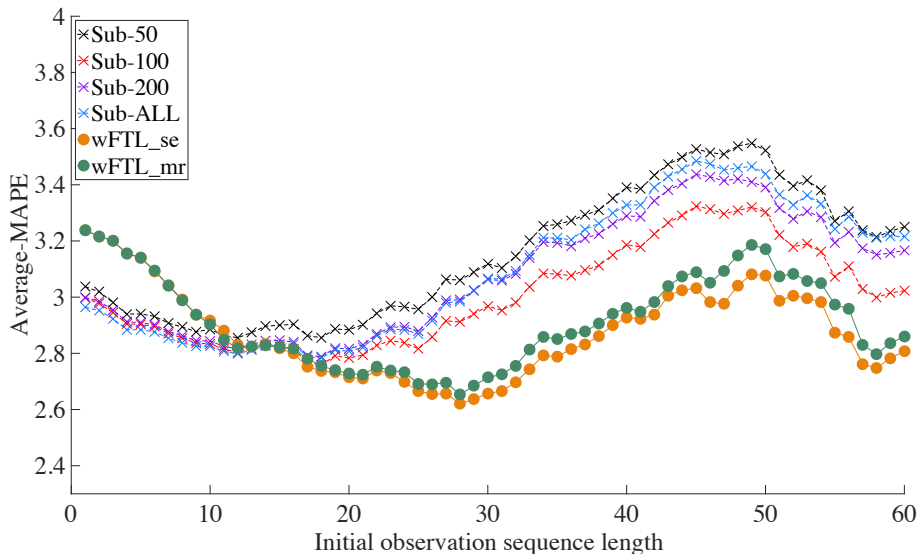


- Subpopulation methods
 - *Sub-k*: For each patient at each time stamp, top k similar patients are selected and are used to train the rDLM model.
- Model adaptation
 - *rDLM+reGP* [Liu 15]
 - *rDLM+reMTGP* [Liu 15]
- Adaptive model selection
 - Ensemble methods
 - *En_Avg*: uniformly averaging
 - *En_Err*: exponential weight method
 - Online learning
 - *OL_FTL*: Follow-the-Leader
 - *OL_MW*: Multiplicative weights algorithm $w_m^+ = w_m(1 - \eta e_m)$
 - *OL_Hedge*: Hedge algorithm $w_m^+ = w_m \exp(-\eta e_m)$

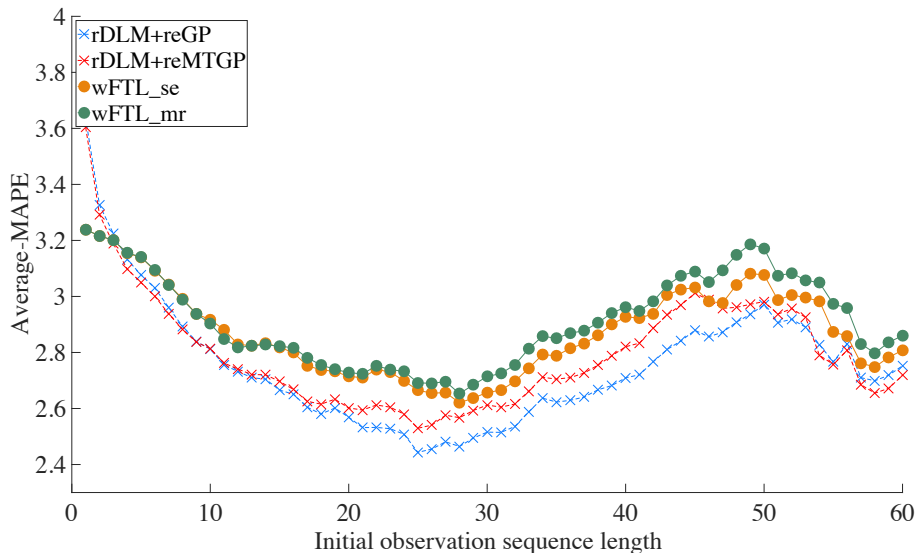
Comparison of Results for Ensemble and Online Methods



Comparison of Results for Subpopulation Methods



Comparison of Results for Model Adaptation Approaches



- Build a pool of population-based and patient-specific models.
- Develop a novel online model switching strategy, i.e., “weighted Follow-the-Leader”
- Experiment with real-world clinical data.

Reference I



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Thank You
Q & A