Deep latent variable models for longitudinal biomedical data

Harri Lähdesmäki

Department of Computer Science Aalto University

March 20, 2023

Research group: Computational systems biology

Research topics:

- 1. Probabilistic machine learning
 - Deep generative models
 - neural ODEs/PDEs/SDEs, GP ODEs
 - Gaussian processes
 - Longitudinal data analysis
- 2. Computational biology and biomedicine
 - Immune cell receptor sequence analysis
 - Sequencing data analysis
 - Biological network modeling
- 3. Applications in molecular biology and biomedicine

Research group:

- 2 postdocs
- 8 PhD students
- 3 research assistants

https://research.cs.aalto.fi/csb/

harri.lahdesmaki@aalto.fi

What is longitudinal data?

Time-series data that consist of

- Multiple subjects
- Each subject measured repeatedly over time

Observations have correlations

- Within a subject
- Across multiple subjects

Longitudinal data typically have

- High number of subjects
- Low number of measurements per subject



What models exist?

Generalized linear mixed models (GLMM)



where $\boldsymbol{\gamma} \sim \mathcal{N}(\mathbf{0},\mathbf{C})$ and $\boldsymbol{\epsilon} \sim \mathcal{N}(\mathbf{0},\sigma_n^2 l)$

Interpretable, fast, powerful, good software support

What models exist?

Generalized linear mixed models (GLMM)



where $\boldsymbol{\gamma} \sim \mathcal{N}(\mathbf{0},\mathbf{C})$ and $\boldsymbol{\epsilon} \sim \mathcal{N}(\mathbf{0},\sigma_n^2 I)$

Interpretable, fast, powerful, good software support

Several other models:

 GAMs, local polynomials, splines, hierarchical Bayesian models, Gaussian processes, Gaussian process ANOVA, etc.

LonGP and lgpr models



ARTICLE

https://doi.org/10.1038/s41467-019-09785-8 OPEN

An additive Gaussian process regression model for interpretable non-parametric analysis of longitudinal data

Lu Cheng^{1,2}, Siddharth Ramchandran¹, Tommi Vatanen⊕^{3,4}, Niina Lietzén⁵, Riitta Lahesmaa⁵, Aki Vehtan¹ & Harri Lähdesmäki¹ Bioinformatics, 2021, 1–8 doi: 10.1093/bioinformatics/btab021 Advance Access Publication Date: 20 January 2021 Original Paper



Genetics and population analysis

Igpr: an interpretable non-parametric method for inferring covariate effects from longitudinal data

Juho Timonen 💿 *, Henrik Mannerström, Aki Vehtari and Harri Lähdesmäki*

Additive Gaussian processes for longitudinal data

For several existing longitudinal models:

1. The model for the unknown function is additive:

 $f(\mathbf{x}) = f^{(1)}(\mathbf{x}) + \ldots + f^{(J)}(\mathbf{x})$

Each f^(j)(x) depends only on a small subset of variables

Additive Gaussian processes for longitudinal data

For several existing longitudinal models:

1. The model for the unknown function is additive:

 $f(\mathbf{x}) = f^{(1)}(\mathbf{x}) + \ldots + f^{(J)}(\mathbf{x})$

Each f^(j)(x) depends only on a small subset of variables

We assume that each additive component has an independent Gaussian process (GP) prior

$$f^{(j)}(\mathbf{x}) \sim GP(0, \alpha_j^2 k_j(\mathbf{x}, \mathbf{x}' \mid \theta^{(j)})),$$

thus

$$f(\mathbf{x}) \sim GP\left(0, \sum_{j=1}^{J} \alpha_j^2 k_j(\mathbf{x}, \mathbf{x}' \mid \theta^{(j)})
ight)$$

Kernel functions for longitudinal data

- Shared effects: the squared exponential (SE) kernel
- Category effects: product of the zero-sum and SE kernels

- Nonstationary shared effects: SE kernel with monotonic nonlinear input warping
- Individual random effects



Kernel functions for disease effect

Function draws, f ~Normal(0, K)



A. Non-stationary kernel $k_{ns}(\cdot)$ for the diseased individuals

Kernel functions for disease effect

Function draws, f ~Normal(0, K)



A. Non-stationary kernel $k_{ns}(\cdot)$ for the diseased individuals

B. Variance masking: zero variance prior to disease onset

$$k_{\rm vm}(x,x'\mid a,\ell) = f_{\rm vm}^a(x) \cdot f_{\rm vm}^a(x') \cdot k_{\rm ns}(x,x'\mid a,\ell)$$



Kernel functions for disease effect

Function draws, f ~Normal(0, K)



A. Non-stationary kernel $k_{ns}(\cdot)$ for the diseased individuals

B. Variance masking: zero variance prior to disease onset

$$k_{\rm vm}(x, x' \mid a, \ell) = f_{\rm vm}^a(x) \cdot f_{\rm vm}^a(x') \cdot k_{\rm ns}(x, x' \mid a, \ell)$$

C. Heteregeneous vm kernel: different disease effect magnitude $\beta = [\beta_1, \dots, \beta_Q]$ for each case individual

$$\sqrt{\beta_q \beta_{q'}} \cdot k_{vm}(x_{disAge}, x'_{disAge} \mid a, \ell_{disAge})$$





Bayesian inference and covariate relevance

Robust prior specifications

- ▶ θ_{kernel} : all kernel (hyper)parameters
- ▶ θ_{obs} : params. of the observation model
- θ_{other} : other parameters (input uncertainty etc.)

Bayesian inference and covariate relevance

Robust prior specifications

- ▶ θ_{kernel} : all kernel (hyper)parameters
- $heta_{obs}$: params. of the observation model
- θ_{other} : other parameters (input uncertainty etc.)

Dynamic HMC sampler (Stan) to obtain posterior samples $\{\theta^{(s)}\}_{s=1}^{S}$ and $\{\mathbf{f}^{(j,s)}\}_{s=1}^{S}$

Sample the full model that includes all covariates / additive kernels

Bayesian inference and covariate relevance

Robust prior specifications

- ▶ θ_{kernel} : all kernel (hyper)parameters
- $heta_{obs}$: params. of the observation model
- θ_{other} : other parameters (input uncertainty etc.)

Dynamic HMC sampler (Stan) to obtain posterior samples $\{\theta^{(s)}\}_{s=1}^{S}$ and $\{\mathbf{f}^{(j,s)}\}_{s=1}^{S}$

Sample the full model that includes all covariates / additive kernels

Covariate relevance assessment: decomposition of variance

Longitudinal plasma proteomics from a T1D case-control study



Longitudinal plasma proteomics from a T1D case-control study



Comparison against LMM



Detection of heterogeneous effects



Detection of heterogeneous effects



Scalability

Scalable mixed-domain Gaussian processes

Juho Timonen¹ and Harri Lähdesmäki¹

¹Aalto University, Department of Computer Science

Software



L-VAE model

Longitudinal Variational Autoencoder

 $\begin{array}{ccc} {\rm Siddharth} \ {\rm Ramchandran}^1 & {\rm Gleb} \ {\rm Tikhonov}^1 & {\rm Kalle} \ {\rm Kujanp\ddot{a}}^1 \\ {\rm Miika} \ {\rm Koskinen}^{2,3} & {\rm Harri} \ {\rm L\ddot{a}hdesm\ddot{a}ki}^1 \end{array}$

Deep latent variable models

Generative models of the form

 $egin{aligned} \mathbf{z} &\sim p_{ heta}(\mathbf{z}) \ \mathbf{y} &\sim \operatorname{Expfam}(\mathbf{y} \mid d_{\psi}(\mathbf{z})) \end{aligned}$

Amortized variational inference with $q_{\phi}(\mathbf{z} \mid \mathbf{y})$ (auto-encoding variational Bayes)

When ϕ and ψ are neural nets, the model is called the variational autoencoder (VAE)



https://ijdykeman.github.io/ml/2016/12/21/cvae.html

Conditional deep latent variable models

Conditional generative models of the form

$$egin{aligned} \mathbf{z} &\sim p_{ heta}(\mathbf{z} \mid \mathbf{x}) \ \mathbf{y} &\sim \operatorname{Expfam}(\mathbf{y} \mid d_{\psi}(\mathbf{z}, \mathbf{x})) \end{aligned}$$

and amortized variational inference with $q_{\phi}(\mathbf{z} \mid \mathbf{y}, \mathbf{x})$

Limitations of VAEs and cVAEs

- 1. The model assumes that the data samples are independent
- 2. Real-world data contains missing values
- 3. Real-world data can be multi-modal



https://ijdykeman.github.io/ml/2016/12/21/cvae.html

Deep latent variable models: Longitudinal, missing and multi-modal data

Multi-output additive GP prior

The L-dimensional latent \mathbf{z} has a vector-valued additive model, conditioned on \mathbf{x}

$$\mathbf{z} = \mathbf{f}^{(1)}(\mathbf{x}) + \mathbf{f}^{(2)}(\mathbf{x}) + \ldots + \mathbf{f}^{(R)}(\mathbf{x}) + \operatorname{diag}(\sigma_{z1}^2, \ldots, \sigma_{zL}^2),$$

where each

$$\mathbf{f}^{(r)}(\mathbf{x}) \sim \textit{GP}(\mathbf{0}, \mathbf{K}^{(r)}(\mathbf{x}, \mathbf{x}'| heta))$$

with a matrix-valued ($L \times L$) cross-covariance function $\mathbf{K}^{(r)}(\mathbf{x}, \mathbf{x}' | \theta)$

Multi-output additive GP prior

The L-dimensional latent \mathbf{z} has a vector-valued additive model, conditioned on \mathbf{x}

$$\mathbf{z} = \mathbf{f}^{(1)}(\mathbf{x}) + \mathbf{f}^{(2)}(\mathbf{x}) + \ldots + \mathbf{f}^{(R)}(\mathbf{x}) + \operatorname{diag}(\sigma_{z1}^2, \ldots, \sigma_{zL}^2),$$

where each

$$\mathbf{f}^{(r)}(\mathbf{x})\sim \mathit{GP}(\mathbf{0},\mathbf{K}^{(r)}(\mathbf{x},\mathbf{x}'| heta))$$

with a matrix-valued (L \times L) cross-covariance function $\mathbf{K}^{(r)}(\mathbf{x},\mathbf{x}'|\theta)$

Thus

$$\mathbf{z} \sim GP\left(\mathbf{0}, \sum_{r=1}^{R} \mathbf{K}^{(r)}(\mathbf{x}, \mathbf{x}'| \theta) + \operatorname{diag}(\sigma_{z1}^{2}, \dots, \sigma_{zL}^{2})
ight)$$

Kernel functions for longitudinal data

- Shared effects: the exponentiated quadratic (EQ) kernel
- Nonstationary shared effects: EQ kernel with monotonic nonlinear input warping

- Category effects: product of the zero-sum and EQ kernels
- Individual random components



High-dimensional, correlated data

Data:

$$Y = [\mathbf{y}_1, \dots, \mathbf{y}_N]^T = [Y_1^T, \dots, Y_P^T]^T$$
$$X = [\mathbf{x}_1, \dots, \mathbf{x}_N]^T = [X_1^T, \dots, X_P^T]^T$$
$$Z = [\mathbf{z}_1, \dots, \mathbf{z}_N]^T = [\mathbf{\bar{z}}_1, \dots, \mathbf{\bar{z}}_L]$$

D-dimensional data Q-dimensional covariates L-dimensional latent

The generative model: L-VAE

Conditional probability for the full dataset (X, Y)

$$p_{\omega}(Y|X) = \int_{Z} p_{\psi}(Y|Z) p_{\theta}(Z|X) dZ$$
$$= \int_{Z} \left(\prod_{n=1}^{N} \underbrace{p(\mathbf{y}_{n}|d_{\psi}(\mathbf{z}_{n}))}_{\text{likelihoods}} \right) \underbrace{p_{\theta}(Z|X)}_{\text{GP prior}} dZ,$$

Auto-encoding variational Bayes for L-VAE

Amortized variational inference:

$$q_{\phi}(Z|Y) = \prod_{n=1}^{N} \mathcal{N}\left(\mathsf{z}_{n} | \boldsymbol{\mu}_{\phi}(\mathbf{y}_{n}), \mathsf{diag}(\boldsymbol{\sigma}_{\phi}^{2}(\mathbf{y}_{n}))
ight)$$

where μ_{ϕ} and σ_{ϕ}^2 are neural networks

Auto-encoding variational Bayes for L-VAE

Amortized variational inference:

$$q_{\phi}(Z|Y) = \prod_{n=1}^{N} \mathcal{N}\left(\mathsf{z}_{n} | \boldsymbol{\mu}_{\phi}(\mathsf{y}_{n}), \mathsf{diag}(\boldsymbol{\sigma}_{\phi}^{2}(\mathsf{y}_{n}))
ight)$$

where μ_{ϕ} and σ_{ϕ}^2 are neural networks

ELBO objective:

$$\log p_{\omega}(Y|X) \geq \mathcal{L}(\phi, \psi, \theta; Y, X) \triangleq \underbrace{\mathbb{E}_{q_{\phi}(Z|Y)} \left[\log p_{\psi}(Y|Z)\right]}_{\text{easy}} - \underbrace{D_{\mathrm{KL}}(q_{\phi}(Z|Y)||p_{\theta}(Z|X))}_{\text{closed form, but slow}}$$

Auto-encoding variational Bayes for L-VAE

Amortized variational inference:

$$q_{\phi}(Z|Y) = \prod_{n=1}^{N} \mathcal{N}\left(\mathsf{z}_{n} | \boldsymbol{\mu}_{\phi}(\mathsf{y}_{n}), \mathsf{diag}(\boldsymbol{\sigma}_{\phi}^{2}(\mathsf{y}_{n}))
ight)$$

where μ_{ϕ} and σ^2_{ϕ} are neural networks

ELBO objective:

$$\mathsf{og}\, p_{\omega}(Y|X) \geq \mathcal{L}(\phi, \psi, \theta; Y, X) \triangleq \underbrace{\mathbb{E}_{q_{\phi}(Z|Y)}\left[\mathsf{log}\, p_{\psi}(Y|Z)\right]}_{\mathsf{easy}} - \underbrace{D_{\mathrm{KL}}(q_{\phi}(Z|Y)||p_{\theta}(Z|X))}_{\mathsf{closed form, but slow}}$$

A novel and provably tighter evidence lower bound for longitudinal GPs (→ upper bound for the KL)

A novel mini-batch compatible KL upper bound

Autoencoder view of L-VAE



The Health MNIST experiment



- Simulated longitudinal data using MNIST dataset
- Train: P = 1000 unique instances (N = 20000)
- Q = 6 covariates: id, age, diseasePresence, diseaseAge, sex, and location
- Test: 100 additional instances: given time points [-10,...,-6], predict [-5,...,9]

The Health MNIST experiment



- Simulated longitudinal data using MNIST dataset
- Train: P = 1000 unique instances (N = 20000)
- Q = 6 covariates: id, age, diseasePresence, diseaseAge, sex, and location
- Test: 100 additional instances: given time points [-10,...,-6], predict [-5,...,9]

Table 2: MSE from performing future predictions (i.e., from time [-5, 9]) on the Health MNIST dataset. The values are the means and respective standard errors.

Model	Latent dimension	MSE
GPPVAE	64	0.057 ± 0.003
GP-VAE	64	0.059 ± 0.002
VRNN	64	0.049 ± 0.004
BRITS	N/A	0.047 ± 0.004
GRUI-GAN	64	0.053 ± 0.007
L-VAE	8	0.038 ± 0.003
L-VAE	16	0.033 ± 0.0018
L-VAE	32	0.025 ± 0.0015

The Physionet 2012 experiment

- Predict in-hospital mortality of ICU patients
- Train: P = 3997 individuals (N = 191856)
- Test: P = 3993 individuals
- D = 35 features: glucose level, blood pressure, temperature, ...
- Q = 9 covariates: id, time, ICUtype, height, weight, age, sex, mortality, mortalityTime

The Physionet 2012 experiment

- Predict in-hospital mortality of ICU patients
- ▶ Train: *P* = 3997 individuals (*N* = 191856)
- Test: P = 3993 individuals
- D = 35 features: glucose level, blood pressure, temperature, ...
- Q = 9 covariates: id, time, ICUtype, height, weight, age, sex, mortality, mortalityTime
- Model-based prediction for mortality

$$P_1 = \frac{\exp(L_1)}{\exp(L_0) + \exp(L_1)},$$

where
$$L_i = \mathcal{L}(\phi, \psi, heta; Y_*, X_*, \mathsf{mortality} = i)$$
 for $i = \{0, 1\}$



Randomized clinical trial (RCT) analysis

- Predict appearance of adverse effects (AE) in RCTs (colon cancer treatment)
- ▶ *P* = 480 subjects (*N* = 6605)
- > D = 30 features: lab measurements and vitals
- Q = 24 covariates: demographics, adverse effects, medication

Randomized clinical trial (RCT) analysis

- Predict appearance of adverse effects (AE) in RCTs (colon cancer treatment)
- ▶ *P* = 480 subjects (*N* = 6605)
- \blacktriangleright D = 30 features: lab measurements and vitals
- Q = 24 covariates: demographics, adverse effects, medication
- Model-based prediction for adverse effects

$$P_1 = \frac{\exp(L_1)}{\exp(L_0) + \exp(L_1)},$$

where $L_i = \mathcal{L}(\phi, \psi, \theta; Y_*, X_*, AE = i)$ for $i = \{0, 1\}$

Adverse effect (AE)	AUC
Skin appendage conditions	0.970
General system disorders nec	0.945
Gastrointestinal signs and symp.	0.900
Gastrointestinal mot. & def.cond.	0.871
White blood cell disorders	0.901
Oral soft tissue conditions	0.966
Neurological disorders nec	0.908
Respiratory disorders nec	0.978
Appetite and GND	0.915
Infections - pathogen unspec.	0.873

Deep latent variable models: Longitudinal, missing and multi-modal data

Learning conditional VAEs with missing covariates

Many real-world datasets contain missing values

- Missingness in features y
- Missingness in covariates x

Learning conditional VAEs with missing covariates

Many real-world datasets contain missing values

- Missingness in features y
- Missingness in covariates x

Goal: learn conditional VAE models from partially observed datasets that contain missing values also in the auxiliary covariates **x**

For each data sample (x, y) any subset of the covariates x and observed variables y may be missing completely at random (MCAR)

$$\begin{aligned} \mathbf{x} &= (\mathbf{x}^o, \mathbf{x}^u) & \mathbf{y} &= (\mathbf{y}^o, \mathbf{y}^u) \\ X &= (X^o, X^u) & Y &= (Y^o, Y^u) \end{aligned}$$

The model

Augment the generative model with a prior distribution for **x**, $p_{\lambda}(\mathbf{x})$

 $p_{\omega}(\mathbf{y},\mathbf{z},\mathbf{x})=p_{\psi}(\mathbf{y}\mid\mathbf{z})p_{ heta}(\mathbf{z}\mid\mathbf{x})p_{\lambda}(\mathbf{x})$

Covariates ${\bf x}$ contain both discrete and continuous variables

• Amortised variational approximation for \mathbf{x}^u

 Maximize the ELBO while simultaneously marginalising uncertainty associated with the missing covariates

The model

Augment the generative model with a prior distribution for $\mathbf{x}, \ p_\lambda(\mathbf{x})$

$$p_{\omega}(\mathbf{y}, \mathbf{z}, \mathbf{x}) = p_{\psi}(\mathbf{y} \mid \mathbf{z}) p_{ heta}(\mathbf{z} \mid \mathbf{x}) p_{\lambda}(\mathbf{x})$$

Covariates ${\bf x}$ contain both discrete and continuous variables

- Amortised variational approximation for \mathbf{x}^{u}
- Maximize the ELBO while simultaneously marginalising uncertainty associated with the missing covariates

The ELBO with missing covariate

$$\begin{split} &\log p_{\omega}(Y^{\mathrm{o}}|X^{\mathrm{o}}) \geq \mathcal{L}(\phi,\psi,\theta,\lambda;Y^{\mathrm{o}},X^{\mathrm{o}}) \\ &\triangleq \mathbb{E}_{q}[\log p_{\psi}(Y^{\mathrm{o}}|Z)] \\ &- \underbrace{\mathrm{KL}[q_{\phi}(Z,X^{\mathrm{u}}|Y^{\mathrm{o}},X^{\mathrm{o}})||p_{\theta,\lambda}(Z,X^{\mathrm{u}}|X^{\mathrm{o}})]}_{D_{\mathrm{KL}}} \end{split}$$

where

$$egin{aligned} D_{ ext{KL}} &= \mathbb{E}_{q}\left[ext{KL}[q_{\phi}(Z|Y^{ ext{o}},X^{ ext{o}})|| p_{ heta}(Z|X^{ ext{u}},X^{ ext{o}})]
ight] \ &+ ext{KL}[q_{\phi}(X^{ ext{u}}|X^{ ext{o}})|| p_{\lambda}(X^{ ext{u}})] \end{aligned}$$

Mini-batch compatible scalable computation

VAE model overview



Time-series MNIST dataset

Manipulated digits from the MNIST dataset

- digit rotation
- shift along diagonal
- image intensity
- ► [time]

... <t



$\ensuremath{\mathsf{NLL}}$ for test predictions

N (- 4) - J	Dataset	Missing %				
Method		5%	10%	$\mathbf{20\%}$	30%	40%
Temporal L-VAE with mean impute	Dataset 3	0.19 ± 0.008	0.27 ± 0.008	0.39 ± 0.02	0.42 ± 0.01	0.56 ± 0.03
Temporal L-VAE with KNN impute	Dataset 3	0.17 ± 0.005	0.25 ± 0.009	0.35 ± 0.01	0.47 ± 0.02	0.58 ± 0.03
Temporal L-VAE with HI-VAE impute	Dataset 3	0.14 ± 0.004	0.21 ± 0.007	0.29 ± 0.009	0.42 ± 0.01	0.51 ± 0.03
Temporal L-VAE with our method †	Dataset 3	0.12 ± 0.003	0.18 ± 0.002	0.23 ± 0.004	0.35 ± 0.02	0.46 ± 0.03
Temporal L-VAE with our method	Dataset 3	0.12 ± 0.002	0.19 ± 0.003	0.25 ± 0.006	0.38 ± 0.01	0.44 ± 0.02
Temporal L-VAE with oracle	Dataset 3	0.11 ± 0.001	0.16 ± 0.003	0.21 ± 0.007	0.28 ± 0.008	0.37 ± 0.01

MSE in test set covariate imputation

Method	Dataset	Missing %				
		5%	10%	$\mathbf{20\%}$	$\mathbf{30\%}$	40%
Mean impute	Dataset 3	0.75	0.77	0.95	0.97	1.25
KNN impute	Dataset 3	0.71	0.74	1.025	1.012	1.35
Temporal L-VAE with our method	Dataset 3	0.21 ± 0.02	0.22 ± 0.04	0.29 ± 0.06	0.35 ± 0.04	0.68 ± 0.06

Randomized clinical trial (RCT) analysis

Longitudinal data from a RCT (prostate cancer treatment) observed over a period of ${\sim}2$ years

- ▶ 184 patients, 1287 data samples
- D = 28 lab measurements as well as vital signs (Y)
- Q = 23 patient-specific auxiliary covariates
 (X)

Randomized clinical trial (RCT) analysis

Longitudinal data from a RCT (prostate cancer treatment) observed over a period of ${\sim}2$ years

- ▶ 184 patients, 1287 data samples
- D = 28 lab measurements as well as vital signs (Y)
- Q = 23 patient-specific auxiliary covariates
 (X)

Evaluate NLL for test set predictions



A Parkinson's Progression Markers Initiative Dataset (Marek et al., 2011)

Longitudinal data from a observational studies

- Approx. 5 year follow-up study
- ▶ 545 patients: 371 PD, 174 healthy
- ► Total 3135 measurements
- ► D = 42 features in Y: cognitive tests, DaTSCAN, cerebrospinal fluid results, bio-specimen, etc. with ~ 4.8% missing values
- Q = 7 auxiliary covariates (X) with missingness between 2% and 32%

A Parkinson's Progression Markers Initiative Dataset (Marek et al., 2011)

Longitudinal data from a observational studies

- Approx. 5 year follow-up study
- 545 patients: 371 PD, 174 healthy
- Total 3135 measurements
- ► D = 42 features in Y: cognitive tests, DaTSCAN, cerebrospinal fluid results, bio-specimen, etc. with ~ 4.8% missing values
- Q = 7 auxiliary covariates (X) with missingness between 2% and 32%

Evaluate NLL for test set predictions



Deep latent variable models: Longitudinal, missing and multi-modal data Biomedical data sets are often multi-modal



L-VAE model for multi-modal / heterogeneous data (HL-VAE)

We utilize ideas from (Nazabel et al., 2020) for modeling heterogeneous data



L-VAE model for multi-modal / heterogeneous data (HL-VAE)

We utilize ideas from (Nazabel et al., 2020) for modeling heterogeneous data





A Parkinson's Progression Markers Initiative Dataset (Marek et al., 2011)

- Approx. 5 year follow-up study
- ▶ 545 patients: 371 PD, 174 healthy
- Total 3135 measurements
- ▶ D = 80 dimensional measurements (Y)
- Q = 7 auxiliary covariates (X)

	Configuration
Gaussian Distribution	8
LogNormal Distribution	12
Poisson Distr.	12
Ordinal	12
Categorical	36

A Parkinson's Progression Markers Initiative Dataset (Marek et al., 2011)

Approx. 5 year follow-up study			
545 patients: 371 PD, 174 healthy			
Total 3135 measurements			
• $D = 80$ dimensional measurements (Y)			
• $Q = 7$ auxiliary covariates (X)			
Gaussian Distribution LogNormal Distribution Poisson Distr.	Configuration 8 12 12		
Ordinal Categorical	12 36		

Non Categorical					
Dataset	L-VAE \downarrow	HL-VAE↓			
Future Predic					
10% Missing	0.099 ± 0.003	0.086 ± 0.002			
20% Missing	0.097 ± 0.001	0.086 ± 0.003			
30% Missing	0.1 ± 0.001	0.091 ± 0.002			
40% Missing	0.102 ± 0.001	0.088 ± 0.004			
50% Missing	0.105 ± 0.002	0.094 ± 0.002			
Test Predictio	on				
10% Missing	0.093 ± 0.004	0.079 ± 0.003			
20% Missing	0.091 ± 0.002	0.080 ± 0.003			
30% Missing	0.094 ± 0.002	0.087 ± 0.003			
40% Missing	0.095 ± 0.001	0.085 ± 0.001			
50% Missing	0.099 ± 0.001	$\textbf{0.091} \pm \textbf{0.003}$			

Acknowledgements

Aalto Univ.

Lu Cheng Kalle Kujanpää Otto I önnroth Henrik Mannerström Mine Ögretir Dimitris Papatheodorou Siddharth Ramchandran **Gleb Tikhonov** Juho Timonen Tommi Vatanen Aki Vehtari

Univ. of Helsinki Miika Koskinen

Univ. of Turku Niina Lietzen Riitta Lahesmaa

Bayer Pharmaceuticals Pekka Tiikkainen Jussi Leinonen

Funding Academy of Finland Bayer Pharmaceuticals

References

- Cheng L, Ramchandran S, Vatanen T, Lietzen N, Lahesmaa R, Vehtari A and Lähdesmäki H, An additive Gaussian process regression model for interpretable non-parametric analysis of longitudinal data, *Nature Communications*, Vol. 10, No. 1798, 2019.
- Timonen J, Mannerström H, Vehtari A, Lähdesmäki H, lgpr: An interpretable nonparametric method for inferring covariate effects from longitudinal data, *Bioinformatics*, Vol. 37, No. 13, pp. 1860-1867, 2021.
- Ramchandran S, Tikhonov G, Kujanpää K, Koskinen M, Lähdesmäki H, Longitudinal variational autoencoder, AISTATS, 2021.
- Ramchandran S, Tikhonov G, Lönnroth O, Tiikkainen P, Lähdesmäki H Learning conditional variational autoencoders with missing covariates, https://arxiv.org/abs/2203.01218
- Ögretir M, Ramchandran S, Papatheodorou D, Lähdesmäki H A variational autoencoder for heterogeneous longitudinal data, https://arxiv.org/abs/2204.09369