Track patient recovery in real-time by processing streaming data

BIOMEDICAL DATA DESIGN

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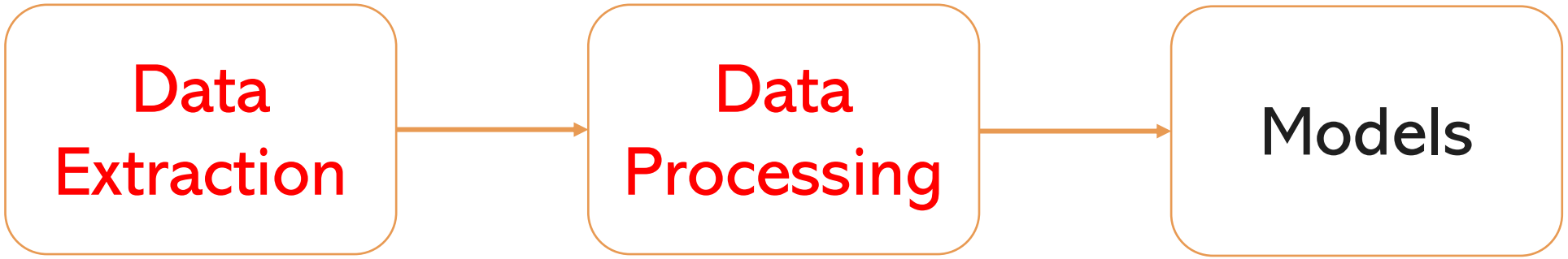
01

Data processing

02 # Our progress



02

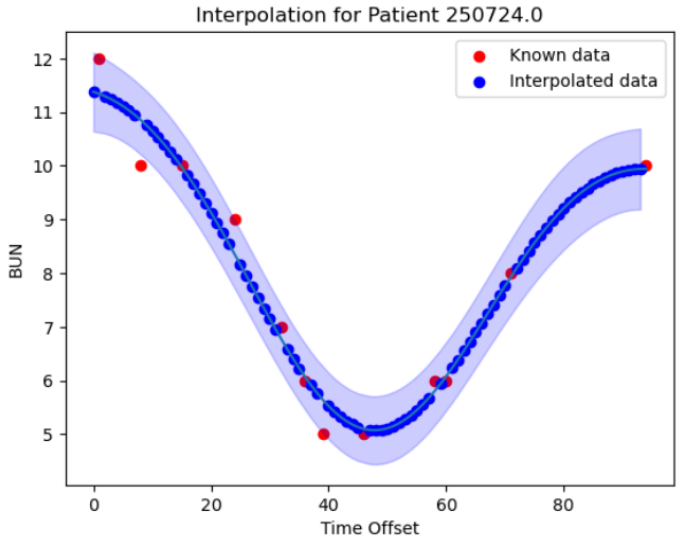
Aligning data

		Glasgow coma score	Nursecharting
Systolic blood pressure（mmHg）	mmHg	Noninvasivesystolic	Avtalperiod
	mmHg	Non-Invasive BP Systolic	Nursecharting
	mmHg	Invasive BP Systolic	Nursecharting
	mmHg	Systemicsystolic	Vitalperiod
		Pasystolic	Vitalperiod
Heart rate		Heart Rate	Nursecharting
Body temperature（⩾39ºC (102.2ºF)）	ºC	temperature	Vitalperiod
	ºC	Temperature(C)	Nursecharting
	ºF	Temperature (F)	Nursecharting
		Temperature Location	Nursecharting
pao2/fio2 ratio（mm Hg/%）	%	FiO2	lab
	mmHg	paO2	lab
		SVO2	Nursecharting
		O2 Saturation	Nursecharting
	%	FiO2	respiratoryCharting
	%	FiO2(%)	respiratoryCharting
Urine output（mL/day）	mL/day	Outputtotal	IntakeOutput
		intakeoutputoffset	IntakeOutput
Serum urea nitrogen level（mg/dL）	mg/dL	BUN	lab
White blood cells count（x 10^3/mm^3）	K/mcL	WBC x 1000	lab
Serum bicarbonate level（mEq/L）	mmol/L	bicarbonate	lab
Sodium level（mEq/L or mmol/L）	mmol/L	sodium	lab
Potassium level（mEq/L）	mmol/L	potassium	lab
Bilirubin level（mg/dL）	mg/dL	total bilirubin	lab

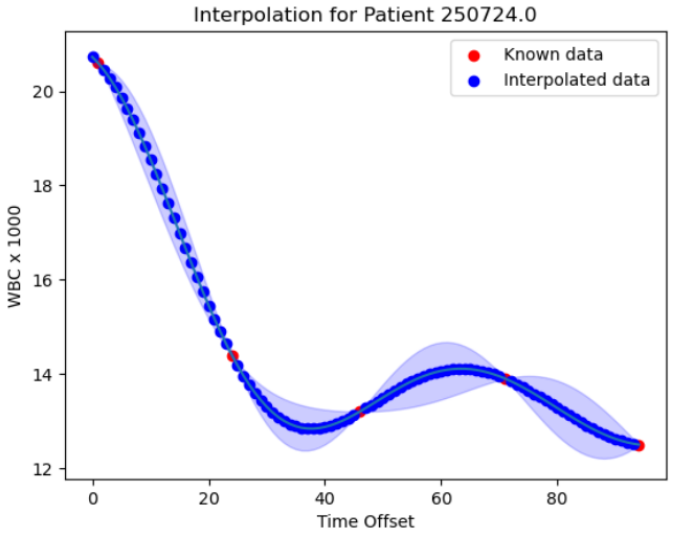
```
def align_data(patient_batch, patient_offset, data, kernel='C(1.0) * RBF(10) + WhiteKernel(noise_level=1, noise_level_bounds=(1e-10, 1e5))'):
    """
    Summary: align data and interpolate missing values

    Args:
        patient_batch: the list of wanted patient id, used to split data
        patient_offset: the dataframe of patient offset data, including patientunitstayid, unitdischargeoffset
        data: the dataframe of data, including patientunitstayid, observationoffset, value
        kernel: the self-defined kernel function for Gaussian Process Regressor

    Returns:
        data_full: the dataframe of aligned and interpolated data, including patientunitstayid, observationoffset, value
        data_full_index: the series of the index of the first occurrence of each patient
    """
```

02

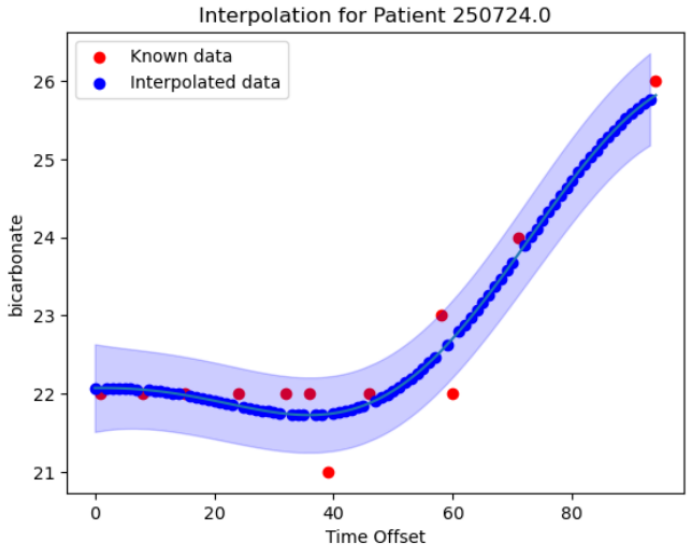
Aligning data



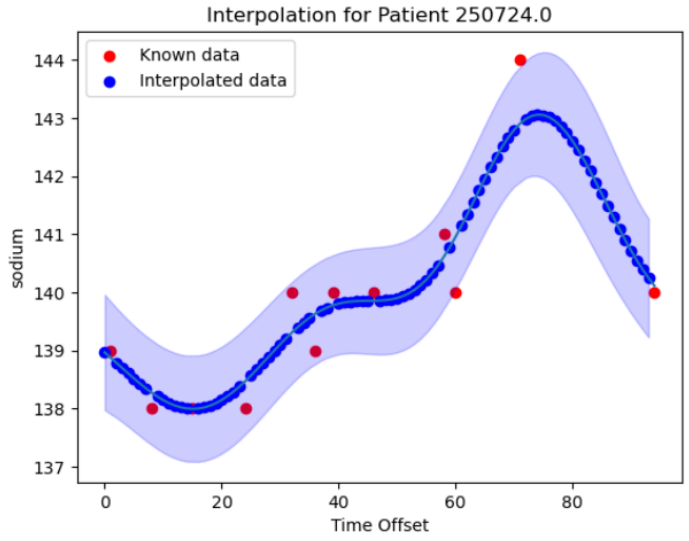
BUN



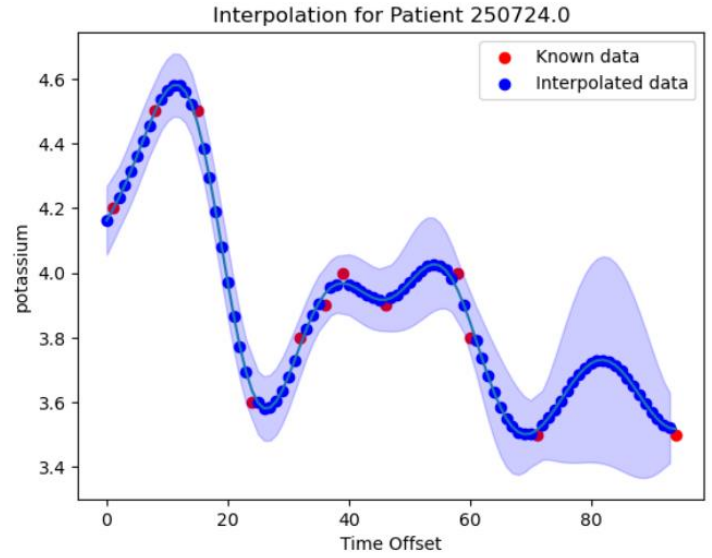
WBC



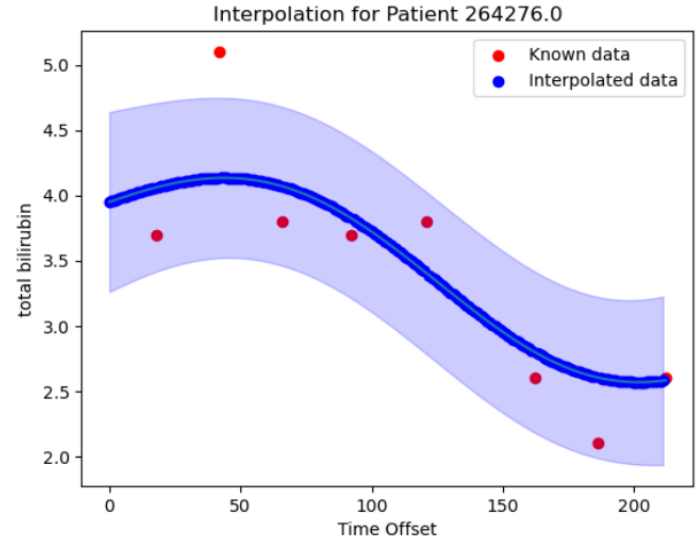
Bicarbonate



Sodium

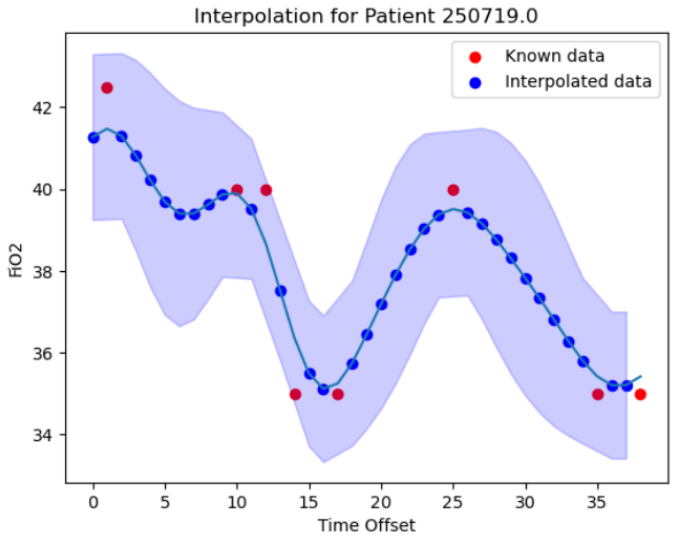


Potassium

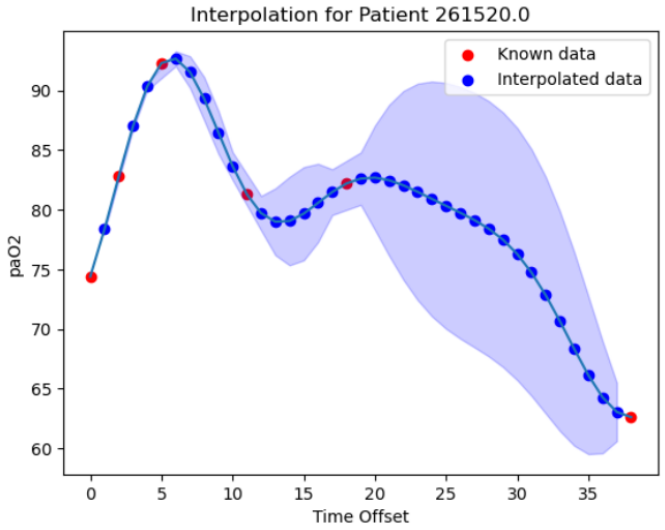


Bilirubin

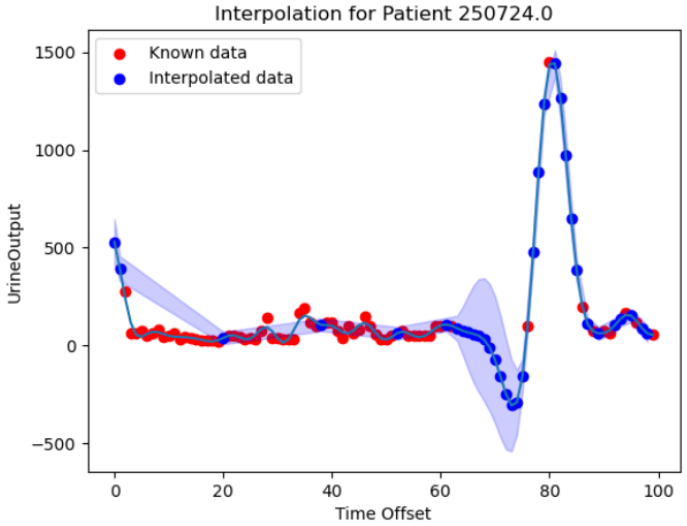
02 Aligning data



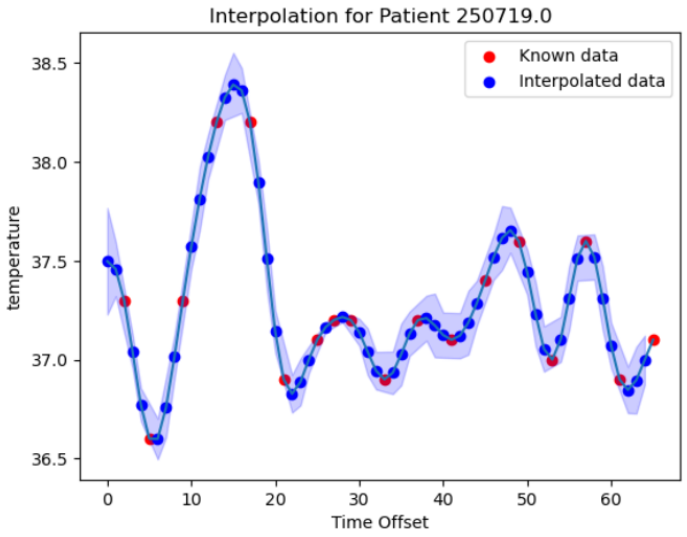
FiO2



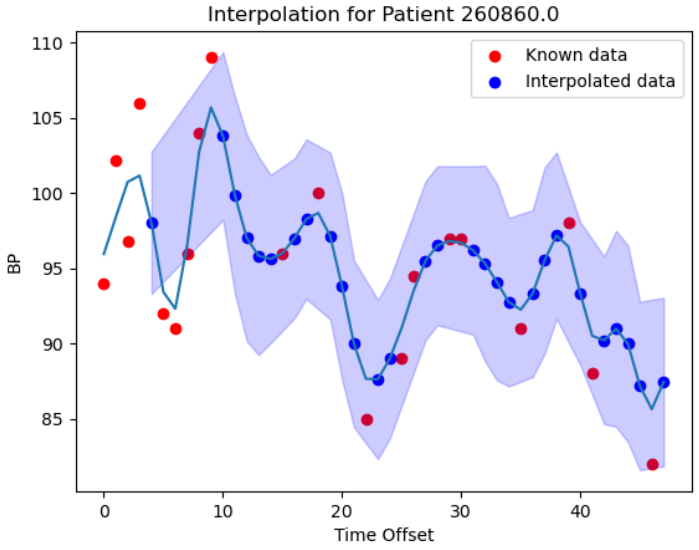
PaO2



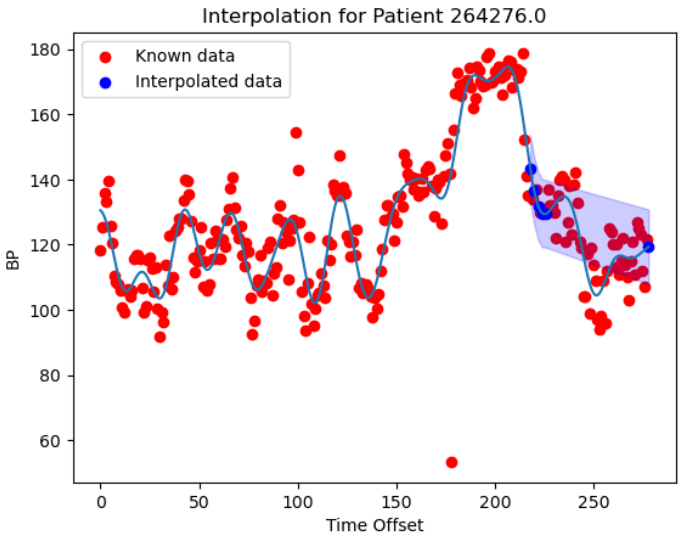
Urine



Temperature



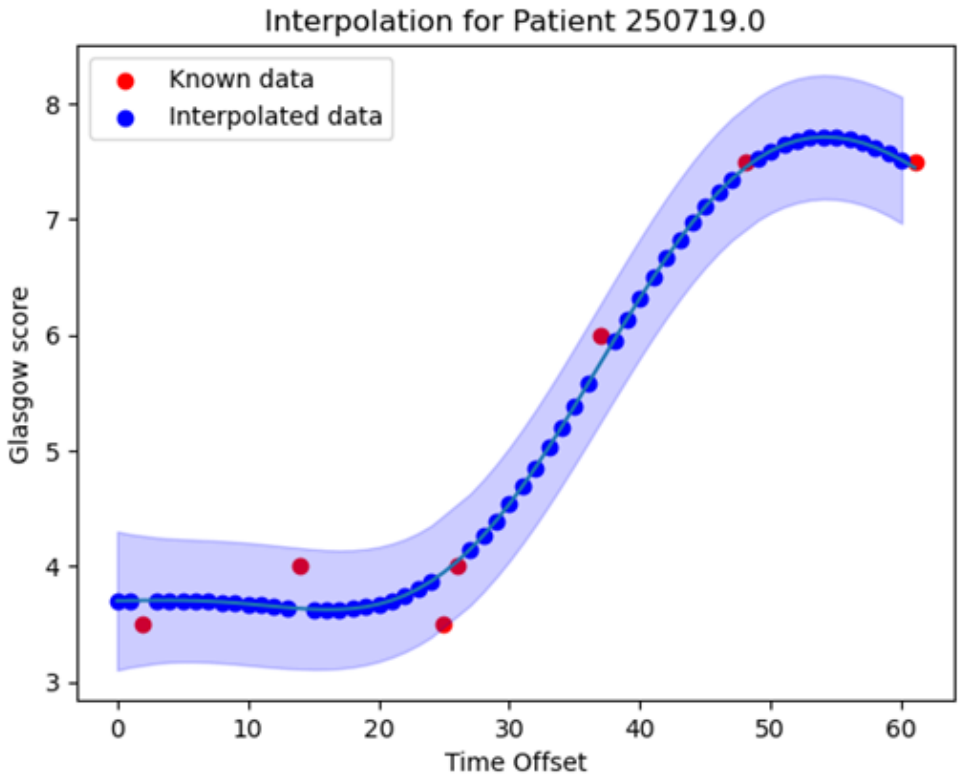
Blood pressure



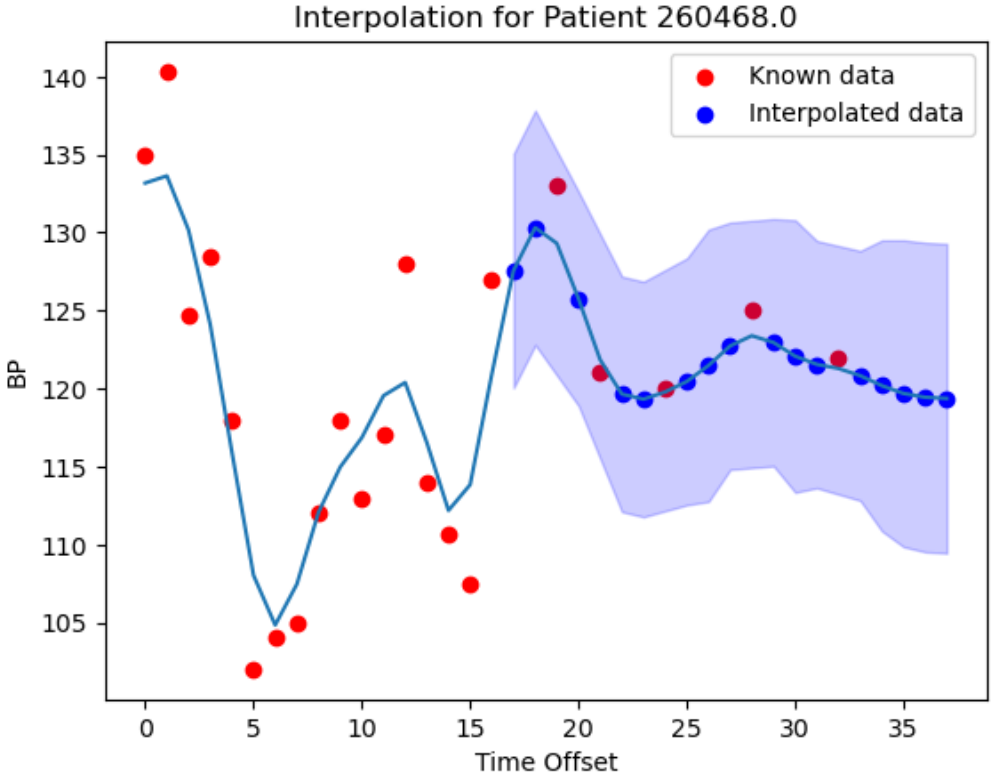
Blood pressure

02

Aligning data

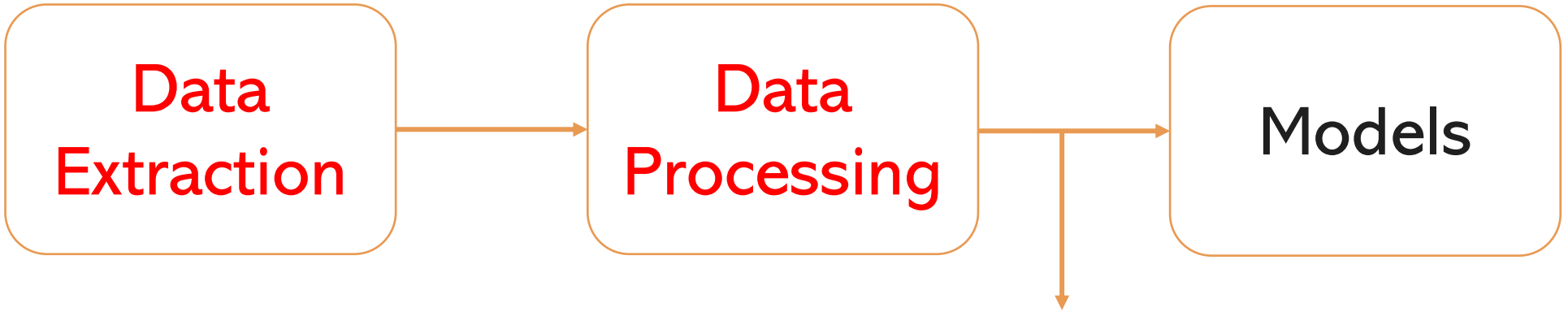


Glasgow



Heartrate

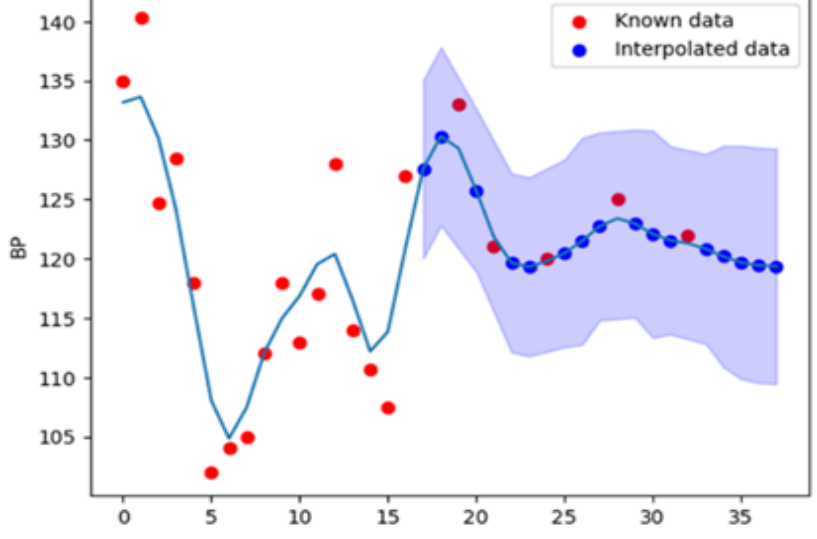
02 **Our progress**



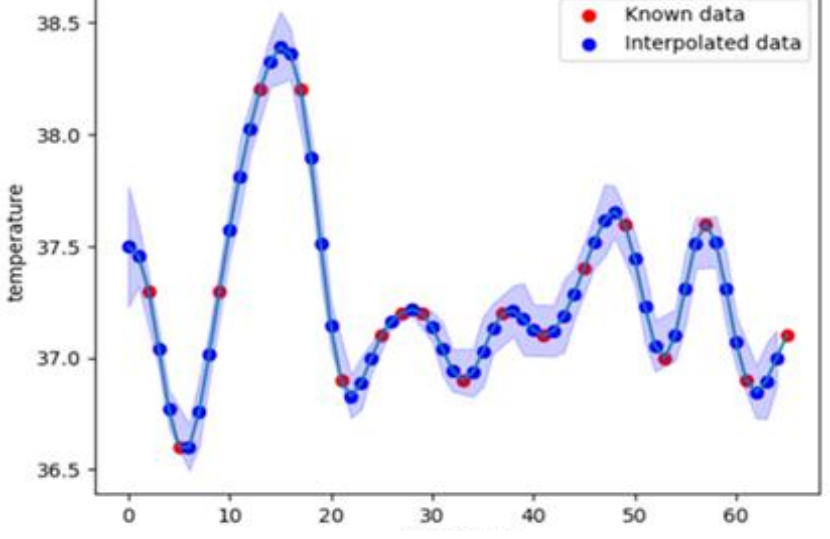
Find out the data interface of the models

Process data from the complete dataset and save it in a format callable by the model

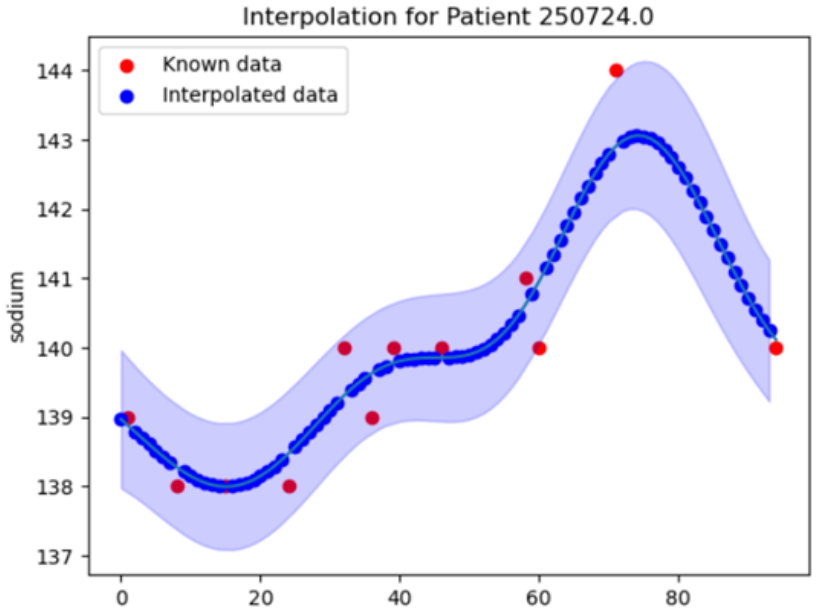
Thank you


Known data
Interpolated data
BP

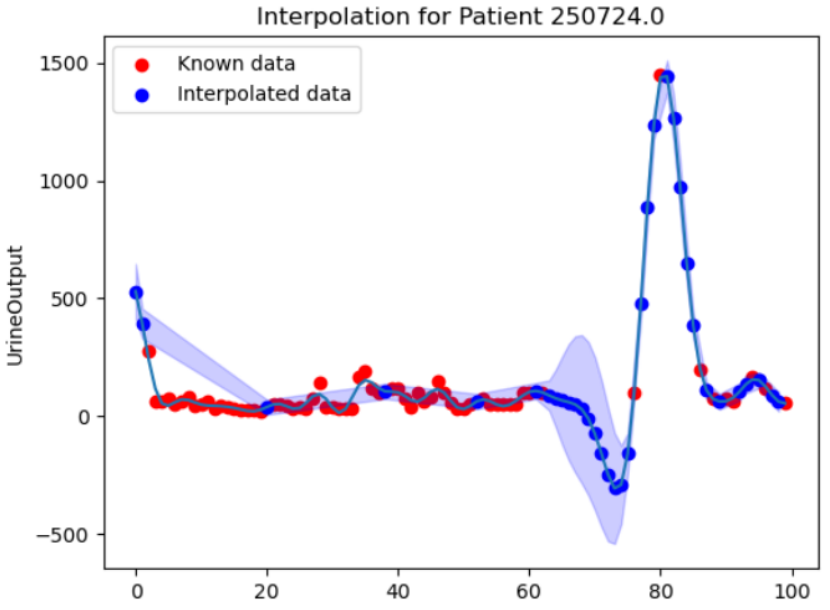
(a)


Known data
Interpolated data
temperature

(b)


Interpolation for Patient 250724.0
Known data
Interpolated data
sodium

(c)


Interpolation for Patient 250724.0
Known data
Interpolated data
UrineOutput

(d)

- func convert_to_float
- func create_index
- func patient_id_age
- func heart_rate
- func temp
- func blood_pressure
- func glasgow
- func urine
- func pao2fio2
- func lab_result
- func normal_heartrate
- func normal_temperature
- func percentage_to_float
- func align_data