

An integrated approach for monitoring and control of refolding kinetics by combining PAT and modelling

Himmelfahrtstagung 2021 – Novel downstream technologies and integrated bioprocesses

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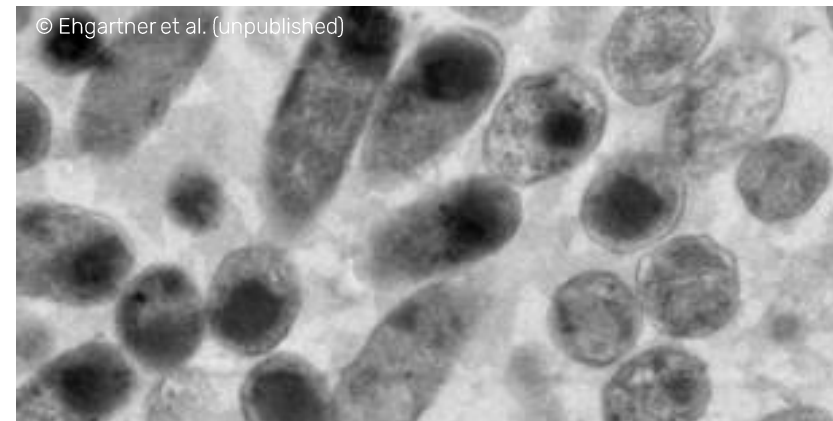


The Challenge

E. coli is commonly used for the production of biopharmaceuticals.



- + Cheap substrates
- + Fast growth
- + High product titers
- + Ease in genetic manipulation



- Extensive DSP
- Inclusion body formation

Inclusion Bodies

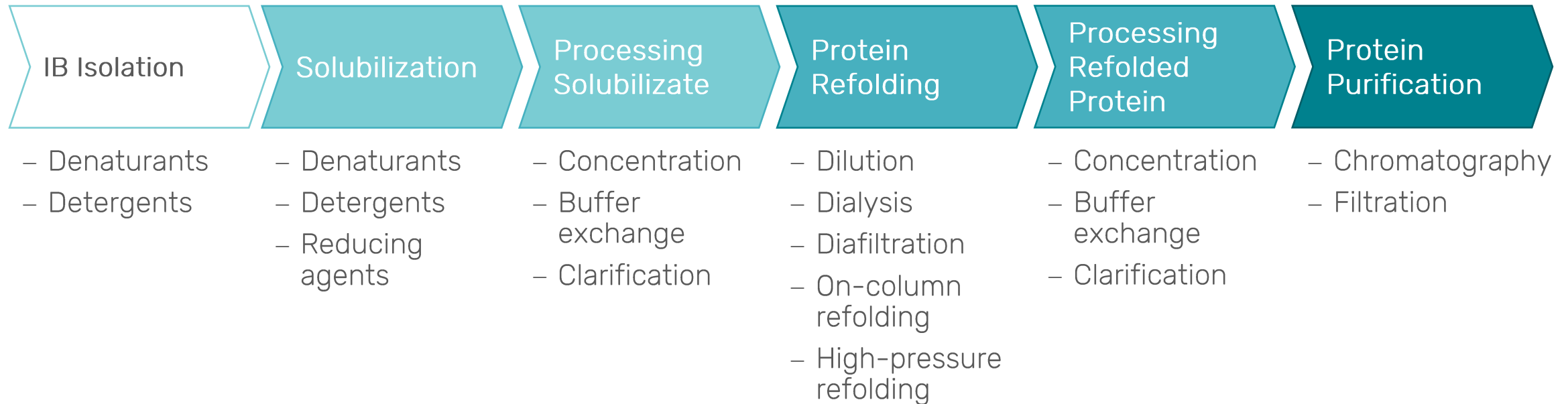
Benefits & Industrial Relevance

Product	Therapeutic Indication	Manufacturer
Betaseron (interferon beta 1b)	Multiple Sclerosis	Bayer
Humalog (lispro)	Diabetes	Eli Lilly
Humulin (rh insulin)	Diabetes	Eli Lilly
Lantus (long-acting insulin glargine)	Diabetes	Aventis
Neulasta (pegfilgrastim)	Neutropenia	Amgen
Neupogen (filgrastim)	Neutropenia	Roche
Pegasys (peginterferon 2a)	Hepatitis	Genentech
Pegintron (peginterferon 2b)	Hepatitis	Merck & Co.

- Ease of isolation
- High product yield and purity
- Mechanic stability
- Expression of toxic proteins

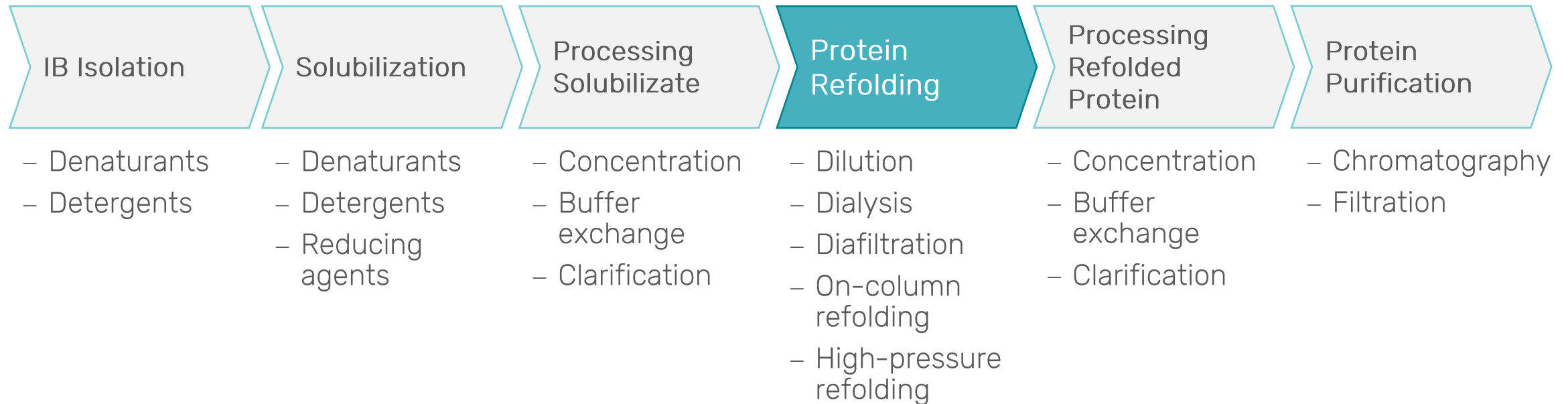
Inclusion Bodies

Downstream Processing



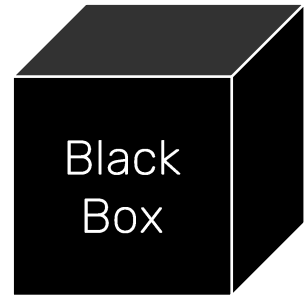
Inclusion Bodies

Downstream Processing



Improving low recovery yields by optimizing the refolding process mode

Current Strategies and Challenges



Limited process knowledge available

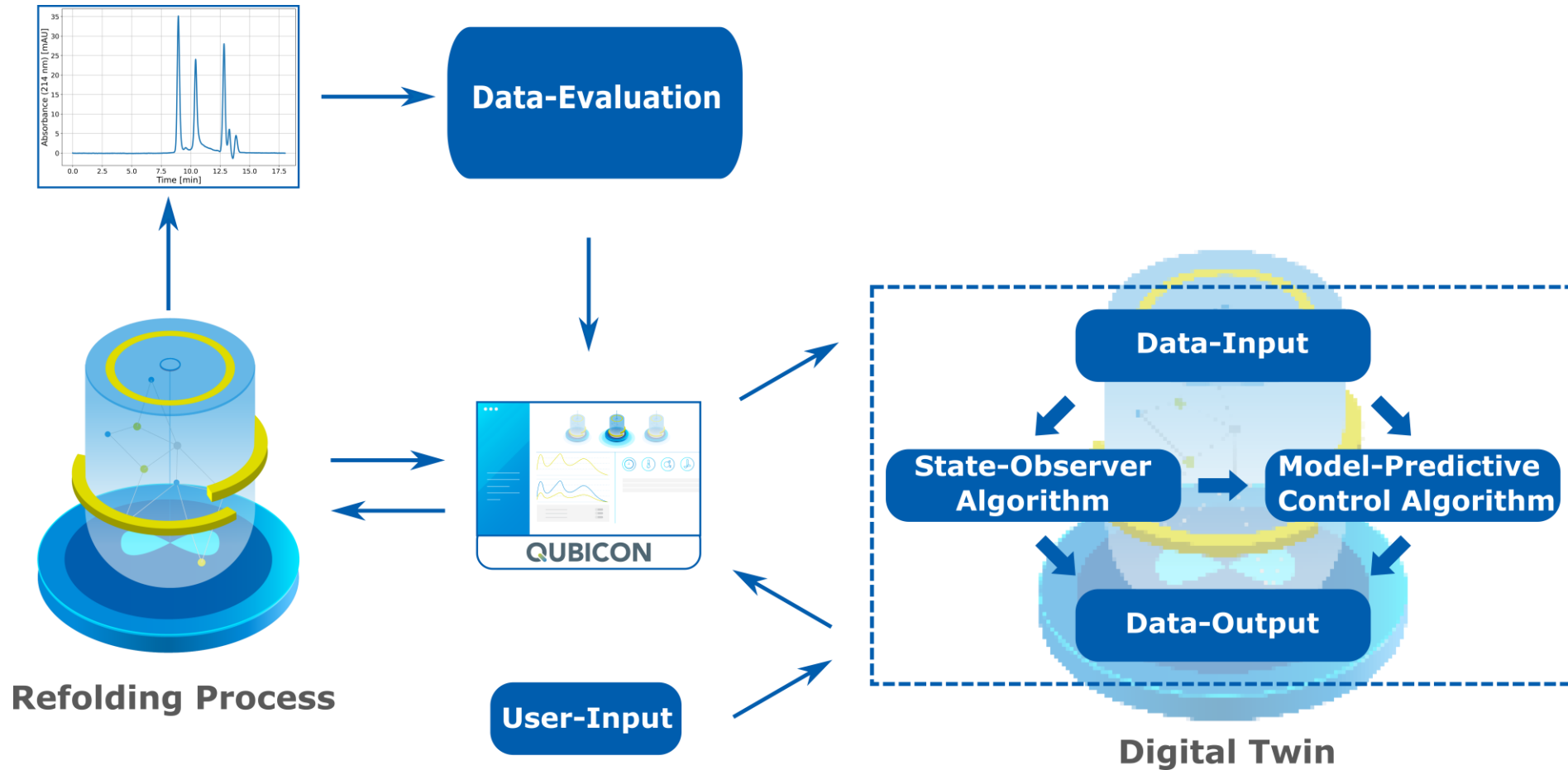
- Empirical
- Product specific
- Uneconomical
- High variability
- Low yields

- + Knowledge-based
- + Transferable
- + Robust control
- + RT optimization
- + High yields



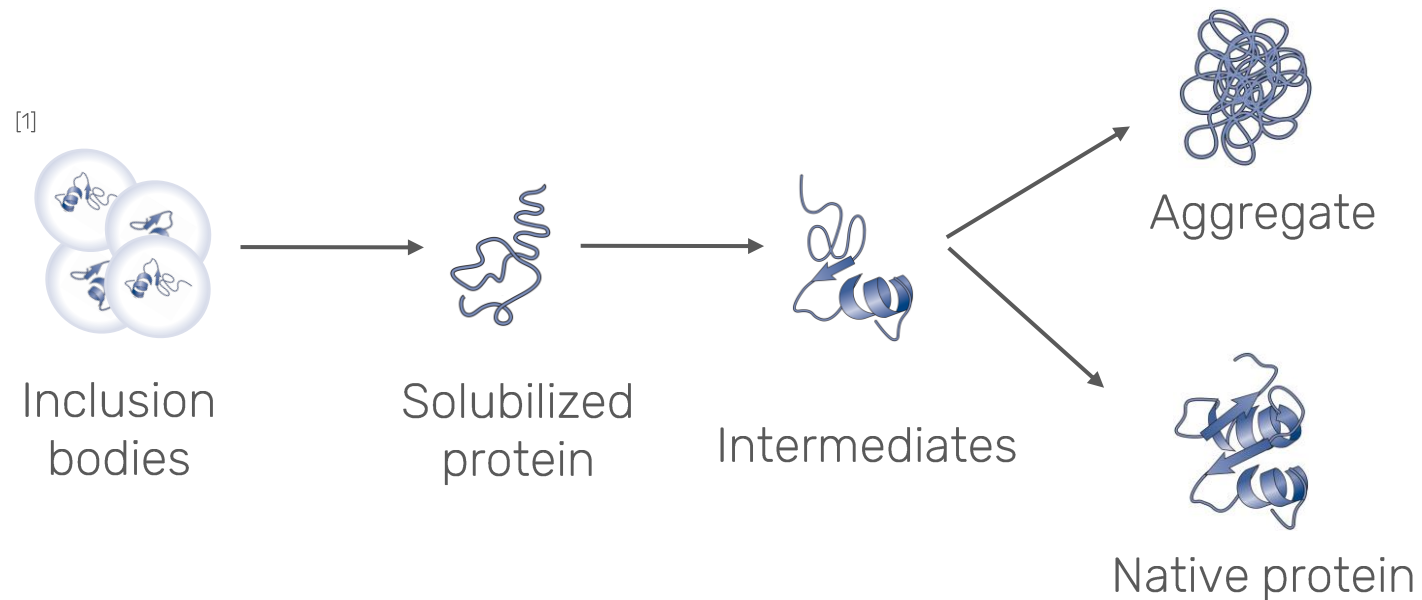
Transferable process knowledge available

Platform Refolding Process

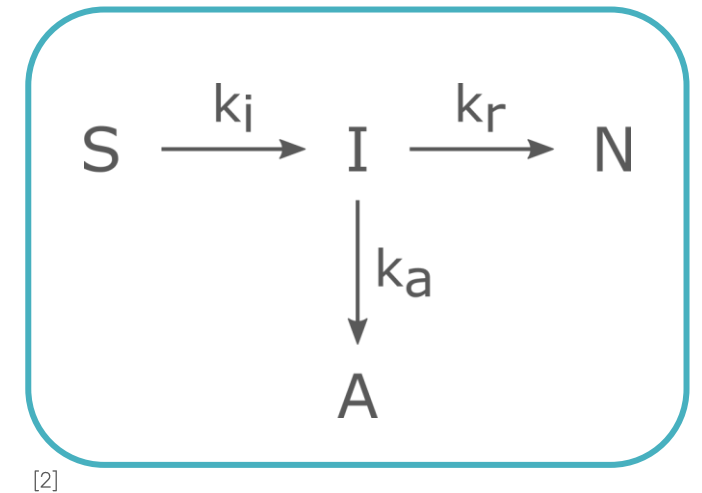
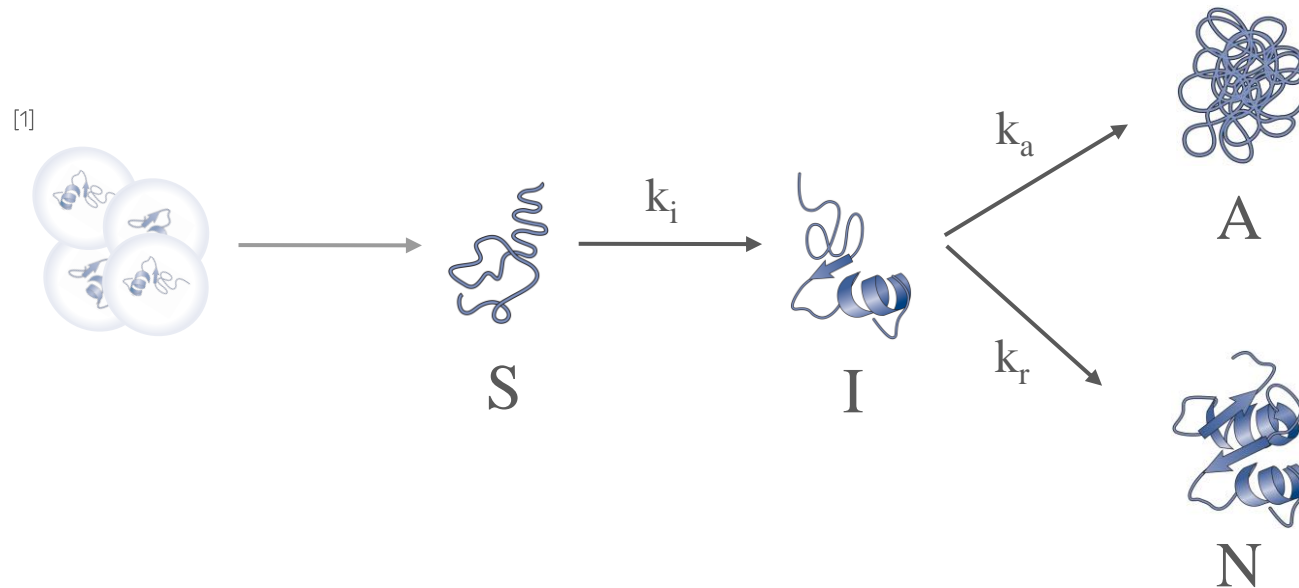


Enhanced Control of Refolding

Protein Refolding Models



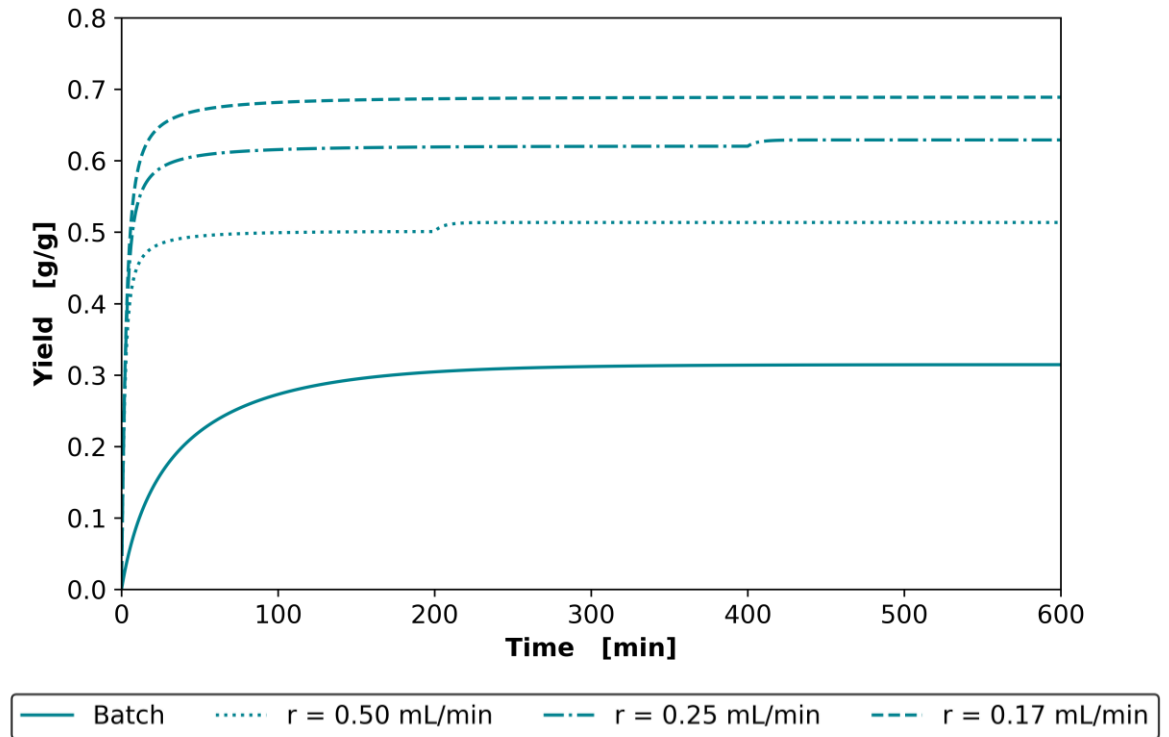
Protein Refolding Models



Adaption of model to complex proteins to develop a generic tool library

Protein Refolding Process

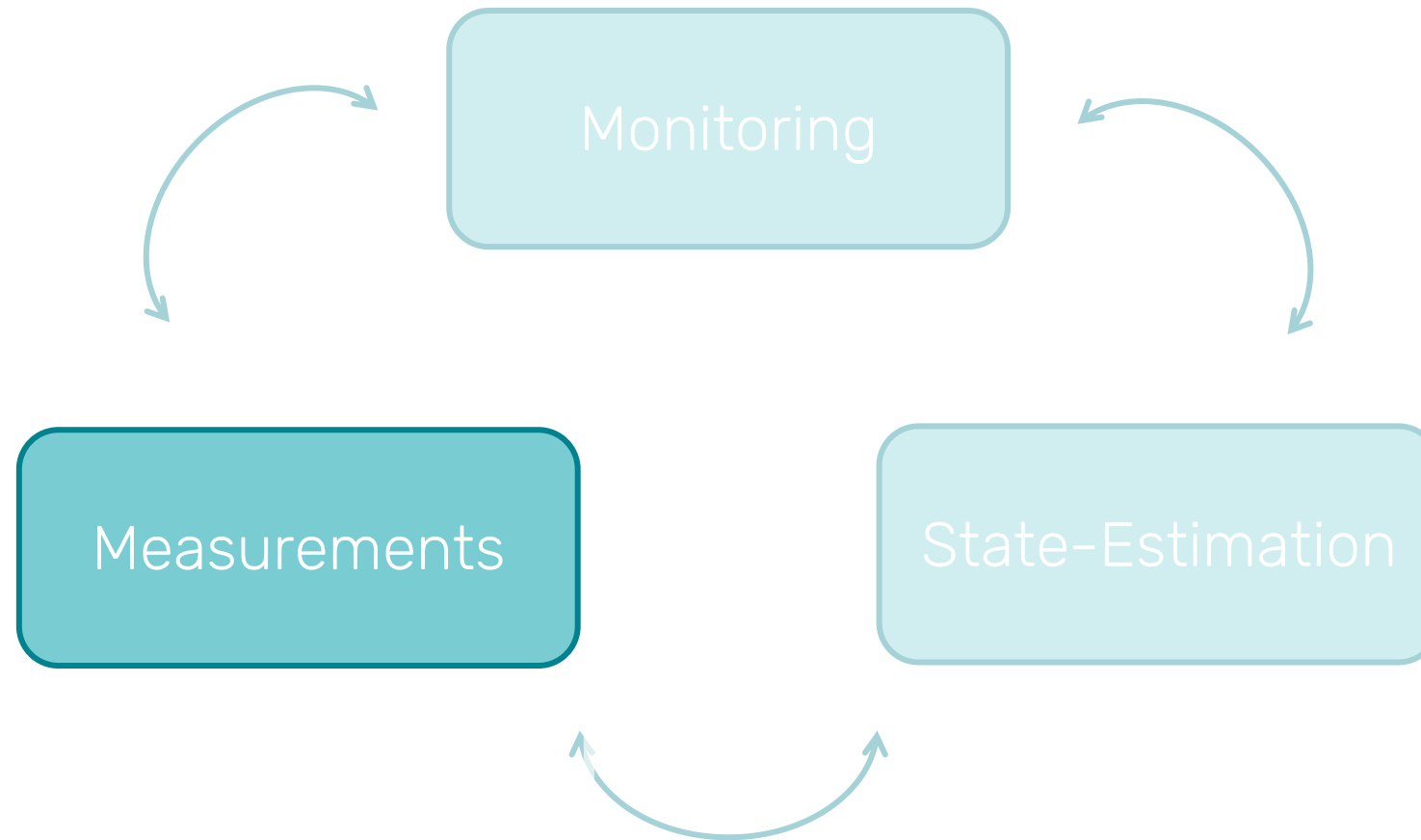
- Fed-batch refolding process with consequent batch period vs. batch process
- Final protein concentration: 1 g/L
- Feed rates (r): 0.17, 0.25, 0.5 mL/min
- Yield depends on solubilized protein concentration in vessel



Fed-batch or continuous is the process mode of choice for efficient IB refolding

Monitoring of Refolding Processes

Monitoring of Refolding Processes



Measurement of Protein States

Tools & Methods

Method	Type	Information	Limit of Detection
DOT and Redox signal	Inline	Soft-Sensor approach S-S bond formation	Independent of protein concentration
Raman Spectroscopy	Inline Atline	Secondary structure and dynamics S-S bond formation	1 mg/ml
ATR-FTIR	Inline	Secondary structure and dynamics	0.01 mg/ml
Size Exclusion Chromatography	Offline Atline	Differentiation between states	0.01 mg/ml
Reversed-Phase Chromatography	Offline Atline	Differentiation between states	0.01 mg/ml
Enzymatic Assay	Offline Atline	Activity, native structure	Depending on enzyme and assay

[1]

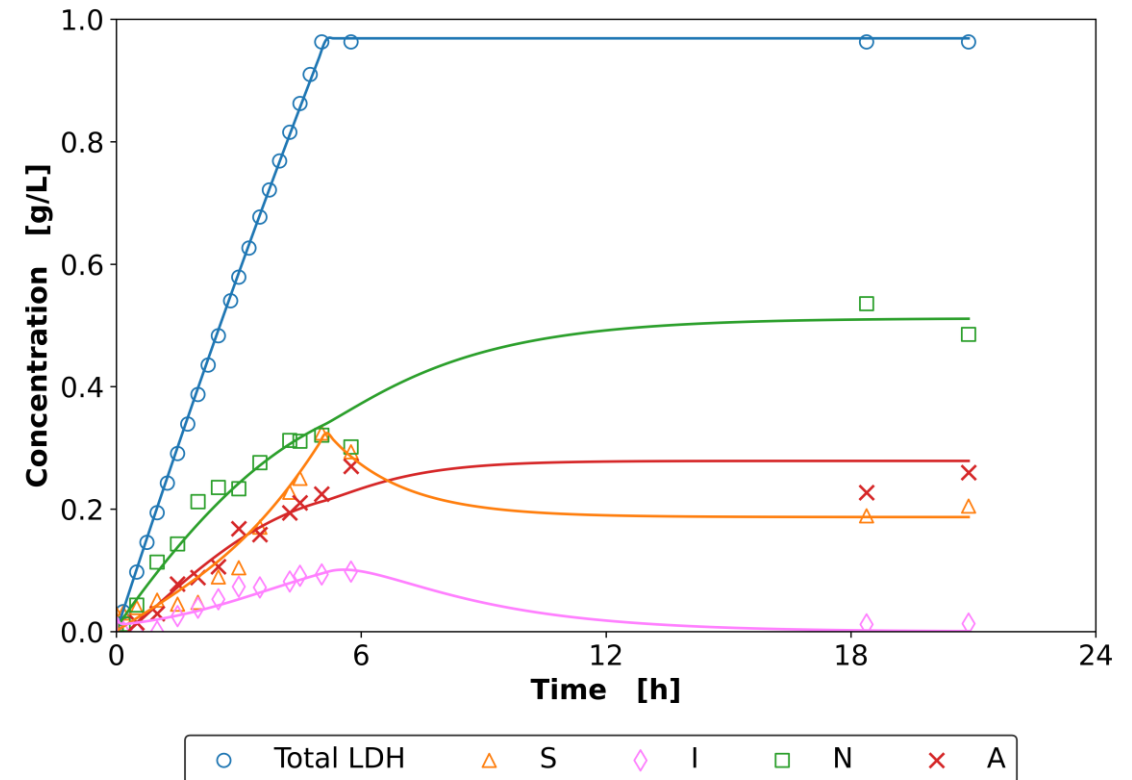
Experimental Setup



Measurement of Protein States

Application – Lactate Dehydrogenase (LDH)

- Simple model protein
- Fed-batch with subsequent batch phase
- Constant feed rate
- Result:
 - Rapid refolding to active form
 - Accumulation of solubilized protein lowers yield

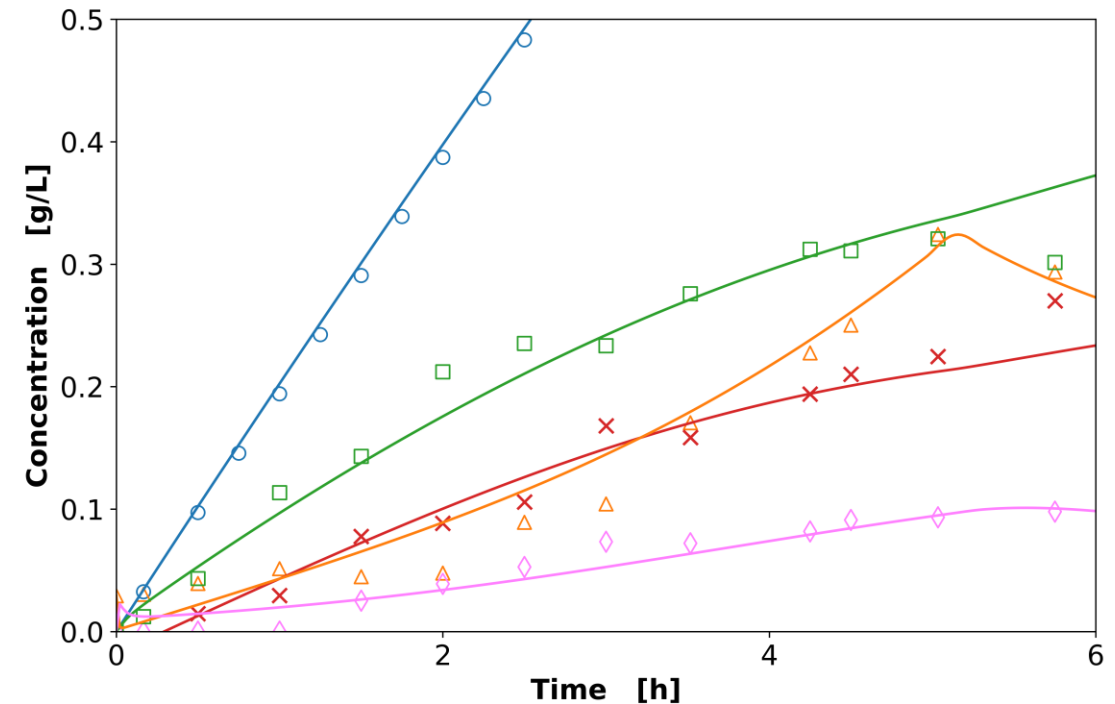


Final protein concentration: 0.96 g/L, feed-rate: 0.33 mL/min, final denaturant concentration: 0.33 M, refolding in phosphate buffer (pH 6, 1 mM EDTA, 20 μM NADH), pH control (NaOH, HCl), solubilization with 4 M Guanidin Hydrochloride

Measurement of Protein States

Application – Lactate Dehydrogenase (LDH)

- Simple model protein
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- Constant feed rate
- Result:
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 - Accumulation of solubilized protein lowers yield



Optimization of recovery yield requires real-time adaption of feed rate

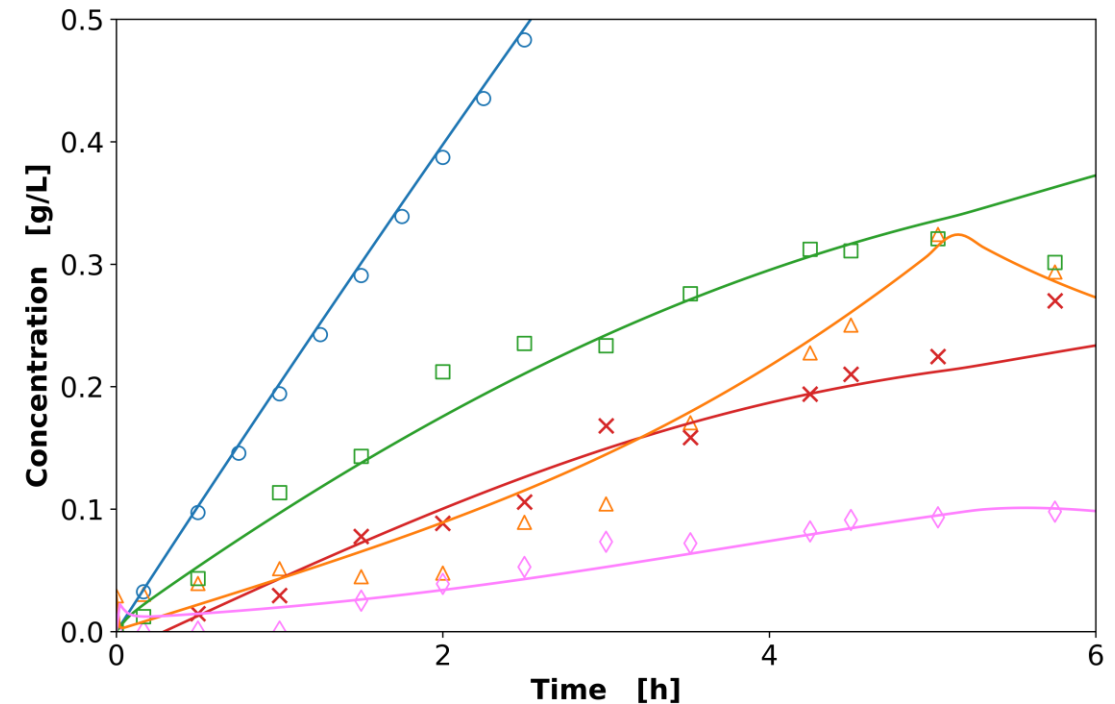
Measurement of Protein States

Limitations

Delay between sampling and response

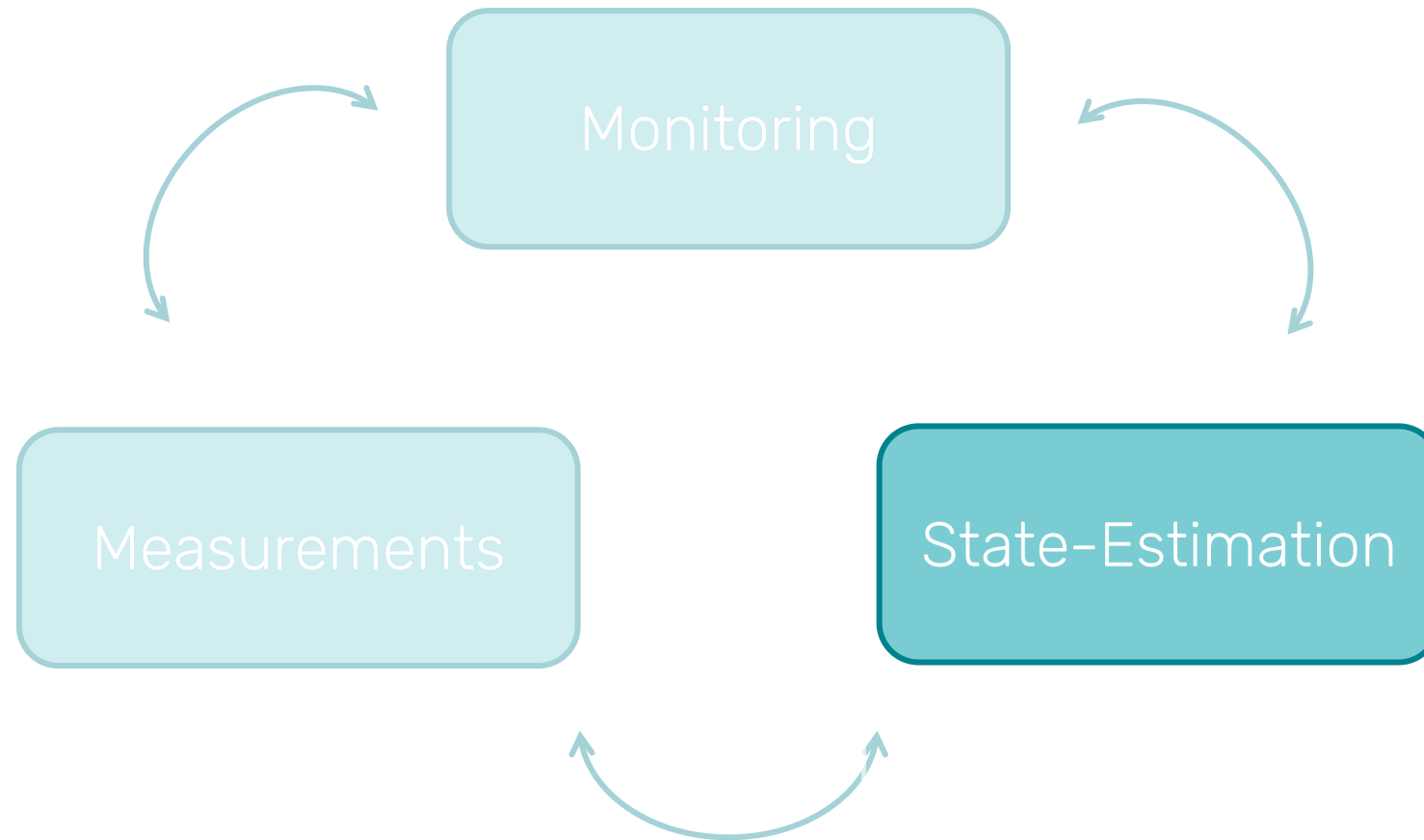
Time shift between different measurements

Not all states measurable and at every measurement cycle



Estimation of remaining protein states needed for effective monitoring

Monitoring of Refolding Processes



State-Estimation

Application - Particle Filter

Filter initialization

Prediction

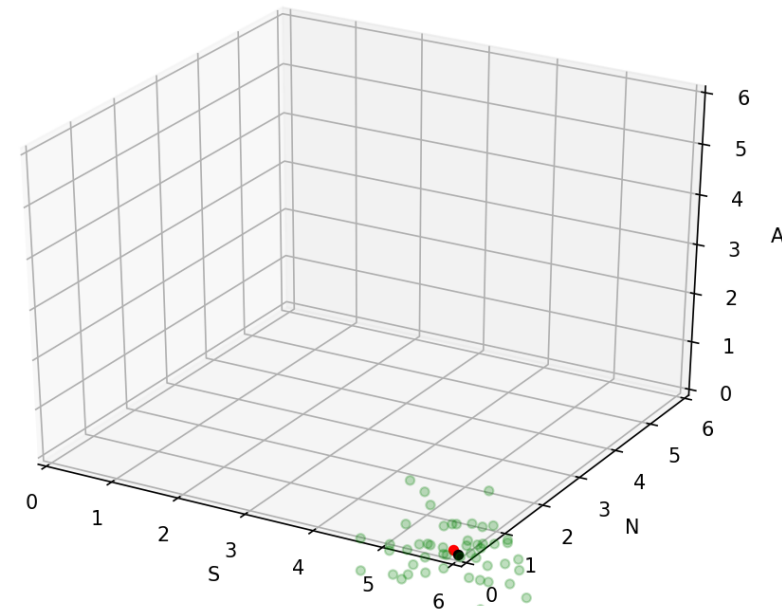
Update

Resample

Compute estimate



Initial particle distribution



- Measured data
- Predicted particles
- Mean of prediction

State-Estimation

Application - Particle Filter

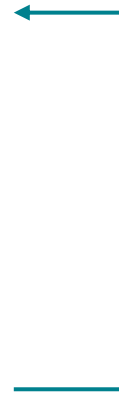
Filter initialization

Prediction

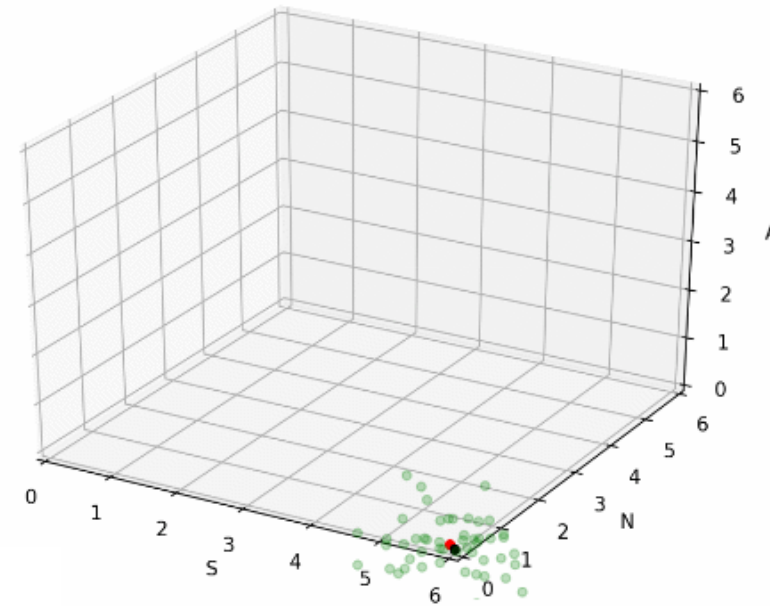
Update

Resample

Compute estimate



Initial particle distribution

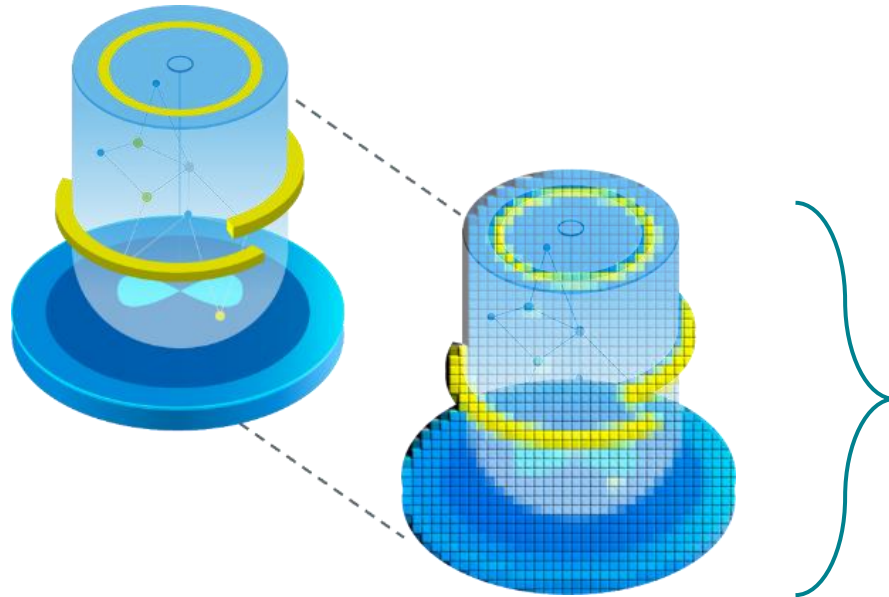


- Measured data
- Predicted particles
- Mean of prediction

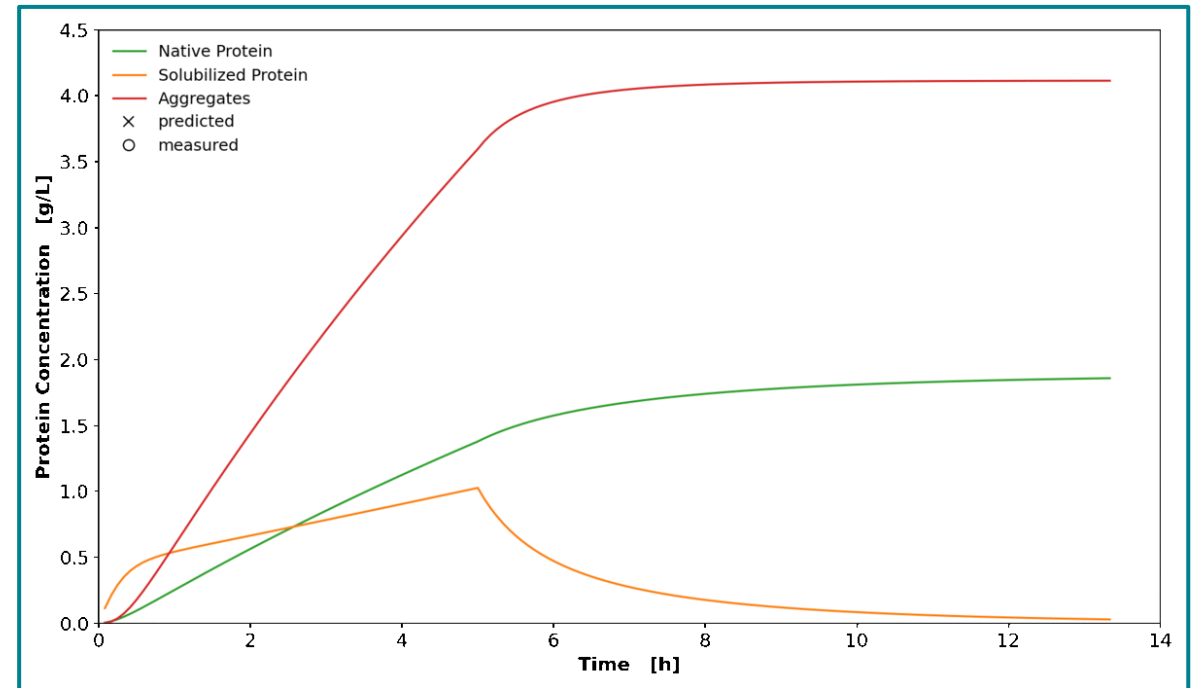
State-estimation is the basis for model-based-control

State-Estimation

Application



Basis for model-based-control



Digital Twin: control of the system by a process model

Novelty & Benefits

Platform technology for monitoring and control of protein refolding using fed-batch dilution

Online monitoring of refolding kinetics

Optimal control of KPIs

Adaptability to new products



CHASE

Chika Linda Igwe

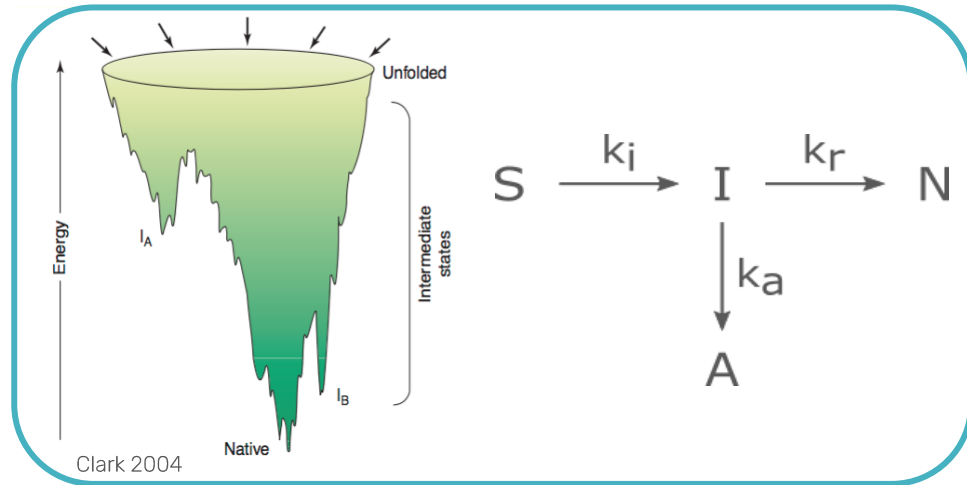
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BILFINGER



Protein Refolding Models



$$k_r = a_r (1 + c_{DL})^{b_r}$$

$$k_a = a_a (1 + c_{DL})^{b_a}$$

$$\frac{dc_{SL}}{dt} = -(k_r \cdot c_{SL} + k_a \cdot c_{SL}^2) + \frac{F_R \cdot c_{SR}}{V_L} - \frac{F_R \cdot c_{SL}}{V_L}$$

$$\frac{dc_{NL}}{dt} = k_r \cdot c_{SL} - \frac{F_R \cdot c_{NL}}{V_L}$$

$$\frac{dc_{AL}}{dt} = k_a \cdot c_{SL}^2 - \frac{F_R \cdot c_{AL}}{V_L}$$

$$\frac{dc_{PL}}{dt} = \frac{F_R \cdot c_{SR}}{V_L} - \frac{F_R \cdot c_{PL}}{V_L}$$

$$\frac{dc_{DL}}{dt} = \frac{F_R \cdot c_{DR}}{V_L} - \frac{F_R \cdot c_{DL}}{V_L}$$

$$\frac{dV_L}{dt} = F_R$$

Reaction rates depend on denaturant concentration

Measurement of Protein States

Method	Type of analysis	Information	Necessary protein amount
CD	Offline	Far UV-CD: secondary structure	Far UV-CD: 0.25 mg/ml
	Online	Near UV-CD: tertiary structure	Near UV-CD: 2.5 mg/ml
DLS	Offline	Tertiary and quaternary structure Quantification	0.05 mg/ml
	At line		
	Online		
DOT and Redox Sensor	Online	Soft-Sensor approach Monitor refolding of proteins with S-S bonds	Independent of protein concentration
Fluorescence Spectroscopy	Offline	Tertiary and quaternary structure	0.015 mg/ml depending on protein size
	Online		
ATR-FTIR	Offline	Secondary structure and dynamics	0.01 mg/ml
	At line		
Raman Spectroscopy	Online	Secondary structure and dynamics	1 mg/ml
QCL-IR	Offline	Secondary structure	0.25 mg/ml
RP-HPLC	Offline	Differences in hydrophobicity	0.01 mg/ml
	Online	Oxidized, reduced protein species	
SEC	Offline	Aggregates and native protein	0.01 mg/ml
	Online		

Control of Refolding Processes

Requirements

Adaptable to process changes

Non-linear process control

Fast action against process disturbance

Benefits of model-based control

Adaptable to process changes

Utilization of state predictions

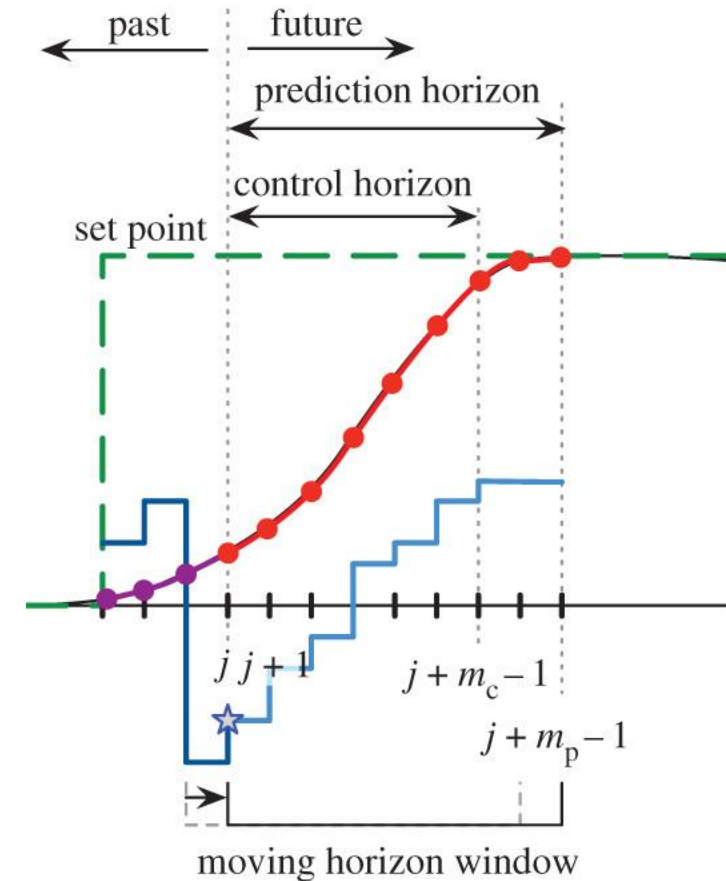
Addition of constraints

Process Control using Model Predictive Control

Online Optimization process

Application of first control step

Repetition of these steps



Platform Refolding Process

Benefits of Model-Based Control

- Adaptable to process variations
- Utilization of state predictions
- Addition of constraints
- Fast action against process disturbance

