

# Data-Driven Process Modeling and Optimization Aided by Material and Energy Balances: The Case of a Batch Polymerization Process

Ahmed Bardooli, Yachao Dong, and Christos Georgakis

Chemical and Biological Engineering Department, Tufts University, Medford, MA 02155, USA  
(e-mail: Christos.Georgakis@Tufts.edu).

---

**Abstract:** Our group recently defined two novel data-driven modeling methodologies: The Design of Dynamic Experiments (DoDE) and the Dynamic Response Surface Methodology (DRSM). These two methods enable the quick and efficient data-driven modeling of processes with a partial understanding of their inner workings. They generalize the Design of Experiments (DoE) and the Response Surfaces Methodology (RSM). DoDE allows time-varying inputs, and DRSM models time-varying process outputs.

In this paper, we combine the above data-driven tools and partial knowledge of a batch polymerization process to develop an integrated data and knowledge-driven model. The optimization objective is to minimize the process's batch time while producing the same product quality, increasing productivity. The process knowledge incorporated into the model consists of material and energy balances in which we lack a quantitative description of the rate phenomena, such as reaction or mass/heat transfer rates. The optimization is evolutionary; initially, targeting small improvements through constrained extrapolations around the normal operating conditions. Then, we build the first models and use such models to design the next set of experiments that meet our specifications. This cycle of running experiments and updating the models is repeated until an optimum is reached. After three cycles, we succeeded in reducing the batch time by 26%, while producing acceptable product.

*Keywords:* Industrial Applications of Process Control, Batch and Semi-batch Process Control, Modeling of Manufacturing Operations, Data-driven Modeling and Optimization, Design of Dynamic Experiments, Dynamic Response Surface Model.

---

## 1. INTRODUCTION

One of the most traditional ways to optimize a batch process of any type is to develop a knowledge-driven model in the form of material and energy balances quantifying the process's inner workings. Due to the complexity of batch processes, such knowledge-driven models are time and effort-intensive in their development. Because batch processes are also characterized by small production rates, such knowledge-driven models' development is often difficult to justify financially. Furthermore, such models might not even be possible due to our lack of detailed understanding of the process's inner workings.

This paper uses two recently developed data-driven modeling tools, the Design of Dynamic Experiments (DoDE) (Georgakis 2013) and the Dynamic Response Surface Methodology (DRSM) (Klebanov and Georgakis 2016; Wang and Georgakis 2017). Both are generalizations of the classical Design of Experiments (DoE) and Response Surface Modeling (RSM) methodologies to enable dynamic inputs and model time-resolved output data. Here we combine the DoDE and DRSM tools and our partial knowledge of the inner workings of the batch process of interest to gradually optimize it in each cycle of new experiments. Despite the partial understanding of the process, we postulate mass and energy balances for the reactor and the cooling section. These are used to back-calculate, from the online measurements, an estimate of the heat transfer rate between the reactor and cooling section, the reaction rate, and

eventually the adiabatic temperature,  $T_{ad}$ . Adiabatic temperature is the temperature the reactor could reach if cooling is lost. For all new experiments,  $T_{ad}$  needs to meet a safety constraint limit. From the back-calculated  $T_{ad}$  values from the first set of experiments, a DRSM model is estimated and used as a constraint in optimizing the process. The proposed methodology is dependent on our ability to define the approximate material and energy/mass balances without the detailed knowledge of the corresponding rate phenomena. This hybrid modeling approach is applicable to many other processes.

## 2. POLYMERIZATION PROCESS

To explicitly introduce our novel methodology, it is best to describe the specific process of interest here. The process studied is a semi-batch polymerization process making propylene glycol, an exothermic process. The process simulation, used *in silico* to perform the experiments, uses the detailed knowledge-driven model by Nie and Biegler (Nie et al., 2013) for a semi-batch jacketed stirred tank where the monomer is fed continuously to the reactor.

The coolant's inlet temperature,  $T_{cf}(t)$ , and the incoming flow rate,  $q_c(\tau)$ , could be used to control the reactor temperature. Either or both and the outgoing coolant's temperature,  $T_c(\tau)$ , are measured with great frequency. These time-resolved values will be the additional data utilized in the postulated heat and mass balances. These balances are used to calculate the

polymerization rate, amount of unreacted monomer and the  $T_{ad}$  value.

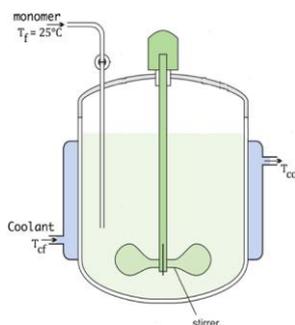


Fig. 1. Sketch of simulated reactor

The optimization objective is to reduce the batch time as much as possible, subject to meeting the product specifications and avoiding the violation of the adiabatic temperature rise constraint. The product quality constraints include the number average molecular weight, the number of unsaturated chains, and the unreacted monomer's concentration. The desired values are given in Table 1. Additionally, a safety constraint on the adiabatic temperature rise is set at a known maximum value  $T_{ad} < T_{safety}$

Output Constraints	$y_1 = MW$ (g/mol)	$y_2 = \text{Unsaturated Chains}$ (mmol/g)	$y_3 = \text{Unreacted Monomer}$ (ppm)
Literature Base Case (Nie et al. 2013)	950	0.033	120
Literature Base Case (Nie et al. 2013) using our simulation	947	0.031	118
Literature Optimum (Nie et al. 2013) using our simulation	835	0.028	134

Using the detailed knowledge-driven model, the maximum reduction in batch time obtained by Nie et al. (Nie et al., 2013) was 47%. Here we will demonstrate that our data-driven approach will also significantly reduce the batch duration, namely 26%, without any knowledge of the detailed model. Our method's advantage is that it is simple, quick, and can be used in many processes. The simulation model, developed by us in MatLab to simulate the literature's base case, yields the following values for the above three quality variables:  $y_1 = 947$ ,  $y_2 = 0.033$  and  $y_3 = 118$ . They are shown in the middle row of Table 1, along with the Nie values. The slight differences in values are negligible.

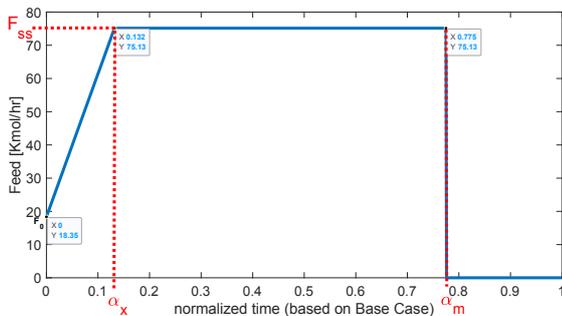


Fig. 2. Base Case Operation of the Process

The process operation can be defined by four inputs: batch time, monomer feeding duration, reactor temperature, and monomer feed rate. The base case temperature is constant at  $T(\tau) = 397K$ . The monomer feed rate initially rises linearly and then remains constant with time, as shown in Fig. 2.

### 3. OPTIMIZATION METHODOLOGY

We start from the process's present operating conditions, denoted as the Base Case (BC). The assumption is that these experiments are done at the production plant. Thus, we will aim for the smallest number of experiments. The DoDE methodology will define this set of experiments allowing them to only deviate from the BC operation by a controlled percentage. While we aim to learn how changes in the operating conditions affect the product specifications, we also wish to minimize the chance of producing an off-spec product.

After the experiments are concluded, three RSM models are estimated to quantify the impact on the product's three specifications. This has been detailed elsewhere (Georgakis et al. 2016) and (Georgakis et al., 2020). In the present paper, we utilize the available time-resolved measurements from the process not used in the previous study, such as the coolant's flow rate and exit temperature, to estimate the polymerization rate taking place and the amount of unreacted monomer in each experiment at each instant. This is achieved by using the following balances:

- An overall energy balance for the cooling section to calculate the energy removed from the reactor.
- An overall energy balance on the reactor side to estimate the energy released from the polymerization reaction.
- An overall monomer balance to estimate the amount of unreacted monomer.

From the above estimations of the unreacted monomer amount and the measured reactor temperature at each time instant, one can estimate the adiabatic temperature rise,  $T_{ad}$ . This will tell us if the current experiment meets the safety constraint throughout the batch duration. The data from all experiments and at frequent time instants during each experiment can be used to estimate a DRSM model for  $T_{ad}(t, X)$ , where  $X$  represents the factor values. This DRSM model can be used to forecast if a planned new experiment meets the safety constraint. The development and use of these DRSM models from inferred and not measured data is the main novelty we introduce. One should emphasize that we achieve this without detailed knowledge of the polymerization kinetics or the heat transfer rates between the reactor and the cooling section.

The above hybrid modeling methodology, combining data-driven tools with partial process knowledge, is applied to the above semi-batch polymerization reactor. The optimization is done by running experiments around the normal plant operation to maintain the same product spec as much as possible. This, we hope, will motivate industrial applications in the future.

#### 4. PARTIAL PROCESS KNOWLEDGE DERIVATION: OVERALL HEAT AND MASS BALANCES

Here we describe the mass and energy balances utilized to obtain approximate information about the process's inner workings. We start with the energy balance of the cooling section, assumed to be well-mixed.

$$V_c C_{pc} \rho_c \frac{dT_c}{dt} = UA(t)(T - T_c) + q_c C_{pc} \rho_c (T_{cf} - T_c) \quad (7)$$

From the measurements of  $q_c(t)$ ,  $T_c(t)$ ,  $T_{cf}(t)$  and the known values of all the constants, we can back-calculate the amount of heat transferred from the reactor  $Q_{HT}(t) \equiv UA(t)(T - T_c)$ .

We now examine the reactor side. A similar energy balance for the reactor can be written as

$$C_p \frac{d(m_T T)}{dt} = q_m(t) \rho_m C_{pm} (T_{mf} - T_{ref}) + Q_{HT}(t) + Q_R \quad (8)$$

Here  $Q_R$  is the heat generated by the polymerization reaction, proportional to the polymerization rate  $P_R$ ;  $Q_R = (-\Delta H_r) P_R$ .

Since we know the incoming volumetric flow rate of the monomer,  $q_m(t)$ , we can calculate the total mass in the reactor  $m_T(t)$  (monomer, and polymer) through the following equation  $m_T(t) = \rho_m \int_0^t q_m(t) dt$

Then, along with the measured reactor temperature  $T(t)$  and its smoothed time derivative, we can back-calculate the overall polymerization rate in the reactor  $P_R(t)$  from (8). Since we lack detailed information on the polymerization kinetics, we assume the very approximate reaction of  $M \rightarrow P$ . The total amount of unreacted monomer,  $M$ , can be calculated by the monomer mass balance:

$$\frac{dM}{dt} = q_m(t) \rho_m - P_R(t) \quad (9)$$

Which can be integrated to give

$$M(t) = M(0) + \int_0^t (q_m(s) \rho_m - P_R(s)) ds \quad (10)$$

Finally, we can calculate the adiabatic temperature  $T_{ad}(t)$ .

$$T_{ad}(t) = T(t) + (-\Delta H_r) M(t) / C_p m \quad (11)$$

After the first set of experiments is performed, the back-calculated time-resolved values of  $T_{ad}(t)$  for each experiment are used to estimate the DRSM model for  $T_{ad}(t, X)$  under different operating conditions. Then, through this DRSM model, the  $T_{ad}(t)$  profiles can be used as constraints on the design of the subsequent cycle of experiments.

#### 5. EVOLUTIONARY DESIGN OF DYNAMIC EXPERIMENTS (DODE)

In this paper, multiple cycles of experiments are designed, conducted, and modeled in an evolutionary optimization of the batch reactor. For example, the 2<sup>nd</sup> cycle of experiments is appended to the 1<sup>st</sup> cycle. The model based on the data from the first two cycles of experiments would be more accurate than that based on the 1<sup>st</sup> or 2<sup>nd</sup> cycle alone. The initial DoDE experiments' operating conditions are allowed to deviate from the BC

operation by only 10%, as not to disturb the product quality too much. The collected data will model the cause-and-effect relationship between the four process inputs mentioned above and the process outputs. In the 1<sup>st</sup> cycle of DoDE, we only use the domain around the BC defined by the constraints. In the 2<sup>nd</sup> cycle of DoDE experiments, the range over which each factor can be selected is increased to explore larger departures from the BC operation. We now also impose the product quality constraints through the three estimated RSMs. This was also done in (Georgakis et al. 2020) and (Georgakis et al. 2016). In a significant departure, here we impose the  $T_{ad}(t, X)$  constraint on the design of the 2<sup>nd</sup> and subsequent cycles of experiments. In the 2<sup>nd</sup> cycle of experiments, we are interested in shorter batch times than those in the 1<sup>st</sup> cycle, which were only reduced by 10%. This is critical in enabling us to reduce that batch time further. We explore cases in which the batch time is reduced between 10% and 30%. The temperature and monomer feed profiles are allowed to vary by 20% from the base case value, instead of the 10% allowed in the 1<sup>st</sup> cycle.

All the constraints imposed in the 2<sup>nd</sup> cycle of experiments are linear, except four, which are nonlinear. The four nonlinear constraints are applied in the 2<sup>nd</sup> and subsequent cycles of experiments as they are not available during the 1<sup>st</sup> cycle. Three of the four nonlinear constraints model, through three RSMs, the impact of the operating conditions on the product specifications. One additional and special constraint of particular interest for this publication is the  $T_{ad}(t, X)$  safety constraint applied through the estimated DRSM model. The applicable constraints are not listed here due to space limitations.

Ideally, one should define the new runs through the D-Optimality criterion so that the uncertainty of the subsequent model's estimated parameters is the smallest. What further complicates this task is the desire to account for the uncertainty of the parameters of the DRSM and RSM models used in the constraints. These requirements make the optimization algorithm impossible to converge and forced us to abandon a rigorous pursuit of the D-Optimal design. Instead, we did the following.

First, we generated a space-filling design using only the linear constraints on the factors. Among the 5000 possible experiments satisfying the linear constraints, we select those that also meet the nonlinear safety and quality constraints defined by the DRSM and three RSM models, respectively. If we allow a 7% violation of the product quality constraints, 32 experiments satisfy these constraints. This deviation from the strict quality constraints is reasonable as the initial RSM models are approximate. If the 7% allowed deviation is reduced to 5%, only nine experiments survive this filter. This shows how restrictive such constraints are.

Out of the 32 points obtained with the 7% deviation, 20 have been selected for the second cycle of DoDE experiments because they have the largest value of the D-optimality criterion.

#### 6. DATA COLLECTION

The initial set of 23 experiments consists of 20 distinct experiments and three replicated ones at the BC conditions. The latter might already exist in the historical records of the process. The replicated experiments are needed to estimate the normal variability of the process. Because these experiments are performed

*in silico* here, random noise of 5% is added to the BC experiments' simulated output values.

The batch time,  $t_b$  is initially allowed to decrease up to 10% from the BC value  $t_{b_{BC}}$ . Similarly, the monomer feeding time,  $t_m$ , initially equal to 77.5% of  $t_{b_{BC}}$ , is also reduced by a maximum of 10% of its initial value. The monomer feeding time is shorter than the batch time; their difference is called digestion time. This digestion period allows the polymerization of the remaining monomer in the reactor (Fig. 2). We write

$$t_b = t_{b_{BC}}(1 + 0.1A) \text{ with } -1 \leq A \leq 0 \text{ and}$$

$$t_m = a_m t_b = 0.775 t_{b_{BC}}(1 + 0.1A)$$

To avoid excessive departures from the present operating conditions, a moderate deviation of  $\pm 10\%$  is allowed in the reactor setpoint temperature (Fig. 3). This setpoint is permitted to have a quadratic dependence on time.

$$T(t) = T_{BC}(1 + 0.1w_1(\tau_1)) \text{ with } -1 \leq w_1(\tau_1) \leq 1 \quad (12)$$

Here  $\tau_1$  is the dimensionless time of the batch duration,  $\tau_1 = t/t_b$ , and  $w_1(\tau_1)$  is parametrized as in (2)

$$w_1(\tau_1) = BP_0(\tau_1) + CP_1(\tau_1) + DP_2(\tau_1) \quad (13)$$

with the following constraints  $-1 \leq B \pm C \pm D \leq 1$ .

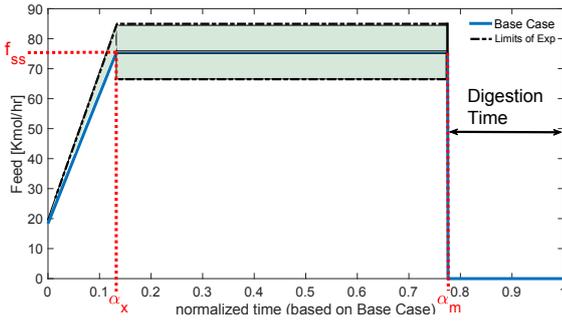


Fig. 2. Monomer Feed Domain: BC operating conditions (blue line) and allowed range of experiments (green)

The BC monomer feeding profile (blue line in Fig 2) is a piecewise function. Between 0 and  $t_x = a_x t_b$ , it is linearly increasing, and then it is kept at a constant value. The entire feed profile is allowed to vary within 10% of the base case value for the designed experiments. The monomer flow rate in the second segment is varied  $\pm 10\%$  using the  $w_2(\tau_2)$  dynamic factor, where  $\tau_2$  is the dimensionless time during this segment, defined by  $\tau_2 = t/t_m$ . We now parametrize  $w_2(\tau_2)$  with three polynomials

$$w_2(\tau_2) = EP_0(\tau_2) + FP_1(\tau_2) + GP_2(\tau_2) \quad (14)$$

To ensure more monomer is fed at the start of the batch, we require that  $E - F + G \geq 0$ . Since we are interested in minimizing the amount of unreacted monomer at the end of the batch, we will impose the following constraint  $dw_2/d\tau_2 \leq 0$  at the end of monomer feeding,  $\tau_2 = 1$ . For the same reason, we impose a  $dw_1/d\tau_1 \geq 0$  constraint at the end of the batch,  $\tau_1 = 1$ , forcing the reactor temperature to be non-decreasing with time at the end of the batch.

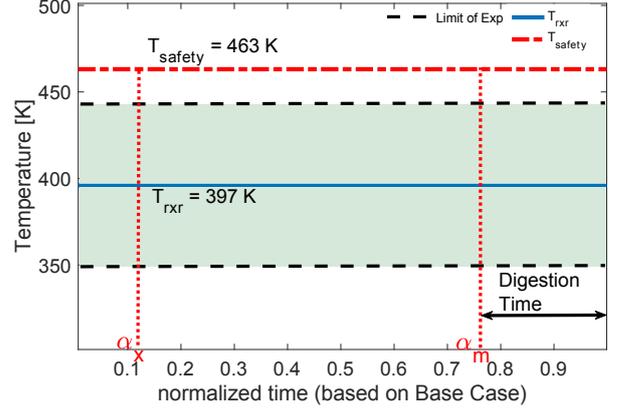


Fig. 3. Temperature Domain: BC operating condition (blue line) and allowed range of experiments (green)

Table 2. Factor Values for 1<sup>st</sup> Cycle of Experiments

#	A	B	C	D	E	F	G
1	0.00	1.00	0.00	0.00	0.75	0.35	-0.35
2	0.00	0.25	0.95	-0.30	0.40	-0.45	0.15
3	-1.00	-0.05	-0.75	0.25	0.90	0.15	-0.15
4	-1.00	0.85	0.20	-0.05	0.30	-0.45	0.15
5	-1.00	-0.45	0.95	0.50	-0.15	-0.30	-0.15
6	0.00	-0.40	0.95	0.45	0.50	-0.75	-0.75
7	-0.50	-0.05	0.05	1.00	0.35	-0.90	-0.25
8	-0.50	0.40	0.85	-0.25	-0.60	-0.45	0.15
9	-0.50	-0.30	-0.95	0.35	-0.05	-0.35	-0.30
10	0.00	-0.90	-0.15	0.05	-0.15	-0.70	-0.15
11	0.00	-0.10	-0.10	1.00	-0.50	-0.40	0.10
12	-1.00	0.05	0.20	0.35	-0.45	-0.80	0.25
13	-0.53	-0.80	0.25	0.05	0.95	-0.05	0.00
14	-1.00	-0.50	-0.15	1.00	0.50	-0.40	-0.90
15	-0.45	0.15	-0.05	0.15	0.30	-0.50	-0.80
16	-0.53	-0.55	0.60	0.70	0.20	0.15	-0.05
17	-1.00	0.00	0.75	-0.25	0.45	-0.95	-0.50
18	0.00	0.50	0.00	0.50	0.85	-0.25	-0.15
19	0.00	-0.50	-0.85	0.60	-0.25	-0.95	0.30
20	0.00	-0.15	0.20	-0.05	0.30	0.20	-0.09
21	0.00	0.00	0.00	0.00	0.00	0.00	0.00

The adiabatic temperature rise constraint can only be imposed after the 1<sup>st</sup> cycle of experiments. Then, time-resolved data from the 1<sup>st</sup> cycle of experiments would have been collected, and the corresponding values of the adiabatic temperature,  $T_{ad}(t)$ , would have been calculated, using the material and energy balances described in the previous section. The DRSM model for  $T_{ad}(t)$  regresses such values against the remaining degrees of freedom,  $x_1 = A, x_2 = B, x_3 = C, x_4 = D, x_5 = E, x_6 = F$  and  $x_7 = G$ .

The initial set of 23 experiments is designed using the D-optimal design with the MatLab coordinate exchange algorithm. The nonlinear constraints for the product quality and the maximum adiabatic temperature, will be imposed in the 2<sup>nd</sup> cycle of experiments. In the initial design, no such model is available to estimate how the operating conditions will affect the product quality and the adiabatic temperature. In Table 2, the values of

the seven independent factors for these 20 distinct experiments and three replicate experiments at the center point are given.

A schematic representation of the two time-varying factors in these experiments is given in Fig. 4. After these experiments are completed, the collected data estimate three RSM models  $y_1, y_2, y_3$  that represent the product specifications and the DRSM model for  $T_{ad}(t)$ , mentioned above. We omit their detailed description to focus on the evolutionary character of the modeling and optimization tasks.

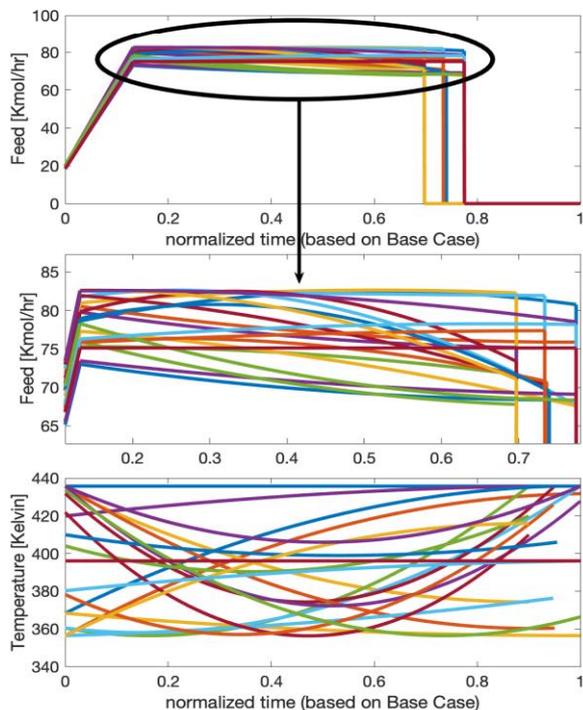


Fig. 4. Monomer Feed (top two subgraphs) and Temperature Profiles (bottom subgraph) for 1st cycle of experiments

## 7. SUBSEQUENT CYCLES OF EXPERIMENTS

Using the models obtained in the 1<sup>st</sup> cycle of experiments, we can now optimize the process both inside the initial and in an enlarged domain, allowing for a small extrapolation. This extrapolation is necessary as we aim for more considerable reductions in the batch time in our 2<sup>nd</sup> cycle of experiments. The present paper's novelty uses the DRSM model to estimate the adiabatic temperature, which is used as an additional constraint in the design of the experiments during the 2<sup>nd</sup> and subsequent cycles.

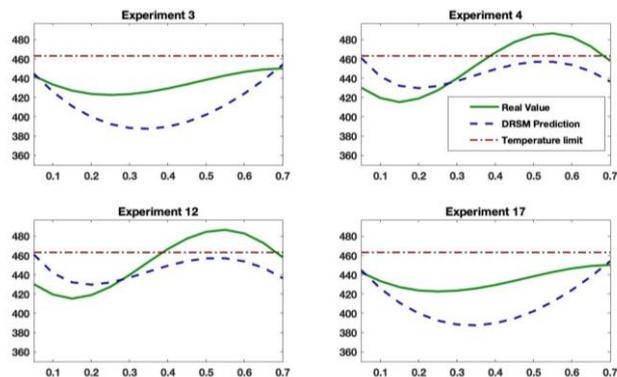


Fig. 5. Predicted (---) versus actual (—) adiabatic temperature profiles against the constraint (-.-)

In the 2<sup>nd</sup> cycle, the initial 23 DoDE experiments are appended with 20 more runs in a new expanded domain. Besides allowing the batch time to be reduced by 25%, the domain for the monomer flow rate and the reactor temperature are allowed to vary by 25% from the BC values instead of the initial 10%. In Fig. 5, we compare the predicted and the actual time profiles via the estimated DRSM model and the detailed simulation, respectively. Although the data are not matched perfectly, the DRSM model's performance is improving after every cycle. The lack of precision is because we approximated the complex polymerization rate in a very simplistic manner. In retrospect, one could have observed that experiments that violated the  $T_{ad}$  limit had a low reactor temperature profile, resulting in monomer accumulation. Therefore, one could have constrained the reactor temperature above 380K to avoid monomer accumulation. Engineers' observations and critical analysis of the data after each cycle can improve the model's performance, but in our study, we did not want to bias and improve our results with the use of heuristic constraints that are bound to help as they are insightful.

Furthermore, as we shift the experimentation domain towards shorter batch durations, the previously estimated DRSM and the RSM models are used in an extrapolative manner. Their predictions are less accurate the further away we extrapolate. To limit such uncertainties, one could have changed the domain more gradually. This necessitates an increased number of cycles. A more accurate DRSM model for  $T_{ad}(t)$  could also have been estimated if a larger number of runs had been designed to determine all of the two-factor interaction terms. Since many runs might not be possible in the actual plant, using a pilot-plant might be a more reasonable avenue for process optimization.

The DoDE-based optimization is stopped after the 3<sup>rd</sup> cycle because the new domain in the third cycle does not provide additional feasible regions compared to the 2<sup>nd</sup> cycle domain. Since no reduction in batch time can be found in the model, the product specification constraints are relaxed by 5%, 10%, and 15% to explore optimum runs at the design space boundary. The predicted optimum experiment in each case is used for the 3<sup>rd</sup> and final cycle of experiments. The batch time is reduced by 26%, but the product specifications deviates by 15%.

## 8. RESULTS

The final data-driven optimal operating recipe after the above three cycles of experiments is shown in Fig. 6. Comparing this result with the optimization results reported in (Nie et al., 2013), the temperature and feed rate profiles are different in the two cases. The one presented here has a 26% reduction in batch time while the knowledge-driven model in the reference above provides a 47% reduction.

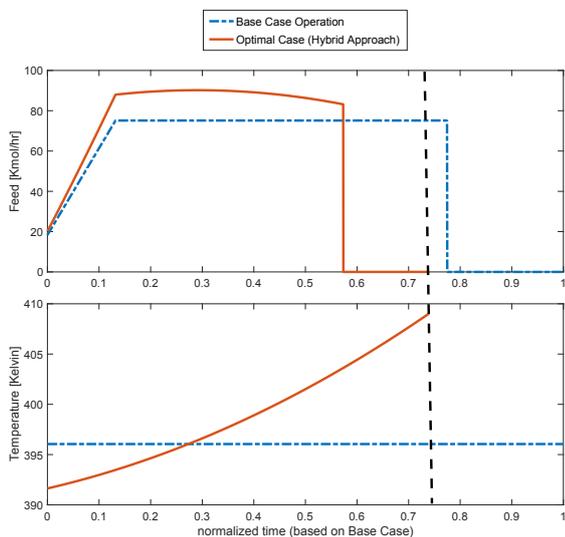


Fig. 6. Optimal profile by us using a data-driven model

## 9. CONCLUSIONS

In this study, a new hybrid data-driven modeling methodology has been presented. It incorporates partial process knowledge through some mass and energy balances. The experiments' design in the three evolutionary cycles was generated using the DoDE methodology. The data collected were used to estimate three RSM models for the product properties and a DRSM model for adiabatic temperature. All DoDE designs, besides those in the first cycle, used these RSM and DRSM models as constraints to design experiments that meet the desired qualities of the product and ensure the reactor's safe operation. The result of this approach is decreasing the batch time by 26%. This is less than what was achieved in the literature using a detailed knowledge-driven model of the process, which consumes significant time and effort.

## 10. REFERENCES

- Georgakis, C, S.-T. Chin, Z Wang, P. Hayot, L.H. Chiang, J. Wassick, and I Castillo. 2020. 'Data-Driven Optimization of an Industrial Batch Polymerization Process Using the Design of Dynamic Experiments Methodology', *Ind. & Eng. Chem. Res.*, 59: 14868-80.
- Georgakis, C. 2013. 'Design of Dynamic Experiments: A Data-Driven Methodology for the Optimization of Time-Varying Processes', *Ind. & Eng. Chem. Res.*, 52: 12369-82.
- Georgakis, C., S.-T. Chin, P. Hayot, J. Wassick, and L.H. Chiang. 2016. "Optimizing an Industrial Batch Process using the Design of Dynamic Experiments Methodology." In *Spring AIChE Meeting*. Houston: AIChE.
- Klebanov, N., and C. Georgakis. 2016. 'Dynamic Response Surface Models: A Data-Driven Approach for the Analysis of Time-Varying Process Outputs', *Industrial & Engineering Chemistry Research*, 55: 4022-34.
- Nie, Y. S., L. T. Biegler, C. M. Villa, and J. M. Wassick. 2013. 'Reactor modeling and recipe optimization of polyether polyol processes: Polypropylene glycol', *Aiche Journal*, 59: 2515-29.
- Valiant, Leslie. 2013. *Probably approximately correct : nature's algorithms for learning and prospering in a complex world* (Basic Books: New York).
- Wang, Z. Y., and C. Georgakis. 2017. 'New Dynamic Response Surface Methodology for Modeling Nonlinear Processes over Semi-infinite Time Horizons', *Industrial & Engineering Chemistry Research*, 56: 10770-82.