MODELING COMPLEX SYSTEM DYNAMICS WITH FLOW MATCHING ACROSS TIME AND CONDITIONS

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ABSTRACT

Modeling the dynamics of complex real-world systems from temporal snapshot data is crucial for understanding phenomena such as gene regulation, climate change, and financial market fluctuations. Researchers have recently proposed a few methods based either on the Schrödinger Bridge or Flow Matching to tackle this problem, but these approaches remain limited in their ability to effectively combine data from multiple time points and different experimental settings. This integration is essential in real-world scenarios where observations from certain combinations of time points and experimental conditions are missing, either because of experimental costs or sensory failure, and ultimately to uncover general principles shared across different temporal processes. To address this challenge, we propose a novel method named *Multi-Marginal Flow Matching* (MMFM). MMFM first constructs a flow using smooth spline-based interpolation across time points and conditions and regresses it with a neural network using the classifier-free guided Flow Matching framework. This framework allows for the sharing of contextual information about the dynamics across multiple trajectories. We demonstrate the effectiveness of our method on both synthetic and real-world datasets, including a recent single-cell genomics data set with around a hundred chemical perturbations across time points. Our results show that MMFM significantly outperforms existing methods at imputing data at missing time points.

1 INTRODUCTION

Understanding the dynamics governing complex systems is essential for modeling their underlying mechanisms as well as for predicting future behavior, such as stock price fluctuations (Gontis et al., 2010), climate change (Franzke et al., 2015), and gene regulation leading to cell differentiation or response to drugs (Yeo et al., 2021; Schiebinger et al., 2019). In many real-world applications, measurements are collected at various time points and under diverse conditions, such as different environmental factors or experimental settings. Additionally, measurements are often unpaired across time and conditions. This may be attributed to the difficulty of matching patients across cohorts (Manton et al., 2008) in a clinical context or to the destructive nature of single-cell genomics (Ding et al., 2022) in modern experimental assays. This results in an extensive yet fragmented view of the system, necessitating models that can effectively integrate these data.

Such data fragmentation is prevalent in the field of drug development. For example, researchers aim to document the response of cells to various genetic and chemical perturbations in order to understand mechanisms of action and predict responses to novel conditions (Rood et al., 2024). Historically, technological and budgetary constraints limited researchers' ability to generate datasets that

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captured cell profiles either across time for a single condition or across multiple conditions but at a single time point. Existing methods reflect these limitations, either modeling conditions without temporal components (Yu & Welch, 2022; Lotfollahi et al., 2023; Piran et al., 2024; Bunne et al., 2022; 2023) or modeling dynamics without interventions (Schulz et al., 2012; Tong et al., 2020; Wang et al., 2023). Recent advances in screening technologies enable cost-effective, large-scale measurement of cell populations over time under multiple conditions. This advancement motivates the development of new modeling strategies that can effectively leverage this combined complexity. Moreover, even with such advances, the sheer scale of biology and chemical space makes it prohibitive to experimentally characterize the entire temporal and perturbation space. When human patient data are concerned, these abilities are further diminished. Thus, better models are essential to generalize to unseen lab experiments and into human biology.

To leverage the rich and complex data now available and deliver better models, we propose framing the problem of learning population dynamics as modeling the transport of the probability distribution of cellular states across time and conditions. This approach allows us to capture changes over time and across conditions, while accommodating unpaired samples. Recent advances in generative modeling, such as diffusion models (Ho et al., 2020) and Flow Matching (FM) (Lipman et al., 2023), constitute effective methods for learning mappings between arbitrary distributions. This makes them particularly suitable for our task. However, despite the popularity of these approaches, they have been hitherto limited to transporting between two marginal distributions. Although multiple time points could be naively modeled by decomposing the problem into a series of two-marginal problems, such an approach would have significant limitations. It would fail to (1) leverage dependencies between the dynamics of multiple (more than two) related conditions (*i.e.,* similar conditions are assumed to follow similar dynamics), and (2) incorporate prior knowledge or constraints on the long-range dynamics of the system.

To address the aforementioned challenges, we introduce Multi-Marginal Flow Matching (MMFM), a general Flow Matching framework that learns system dynamics from populations measured at multiple time points and under various conditions. Notably, our model uniquely leverages dynamic dependencies between conditions and enables both interpolation and extrapolation to unobserved time points and/or conditions. Through extensive experiments, we demonstrate MMFM's superior performance and generality compared to existing methods. We apply our MMFM to a real-world dataset of immune cells subjected to each of a hundred kinase inhibitor perturbations measured over four time points and to a dataset of air pollutants concentrations. Empirically, our method successfully predicts cellular trajectories and air pollutants concentrations for unobserved conditions and time points.

2 BACKGROUND

In this section, we introduce the concepts of vector fields and probability density paths and then provide an overview of the Flow Matching (FM) framework. Unless mentioned otherwise, $\mathcal{X}$ denotes an Euclidean space (i.e., $\mathcal{X} = \mathbb{R}^d$).

Vector Fields We model the underlying dynamics of a system using a time-dependent[1] vector field $u : [0, 1] \times \mathcal{X} \to \mathcal{X}$. This vector field induces a time-dependent diffeomorphic map on $\mathcal{X}$, called a flow, $\phi : [0, 1] \times \mathcal{X} \to \mathcal{X}$, defined by the Ordinary Differential Equation (ODE)

$$\frac{d}{dt}\phi_t(x) = u_t(\phi_t(x)), \tag{1}$$

with the initial condition $\phi_0(x) = x$. Given an initial probability distribution $p_0 : \mathcal{X} \to \mathbb{R}^+$, the flow reshapes the distribution p_0 into a *probability density path* $p_t(x)$ defined via the push-forward equation $p_t(x) = [\phi_t]_* p_0(x)$. The resulting density for each time t is then obtained via the change of variable formula.

Flow Matching The original FM framework for generative modeling (Lipman et al., 2023) considers two marginal distributions: the source distribution p_0 (e.g., Gaussian random noise) and the target distribution p_1 (e.g., a set of images), both with support contained in $\mathcal{X}$. The goal is to approximate the target vector field u_t that generates a probability path $p_t(x)$ satisfying the boundary

[1] We use the subscript notation for the time parameter, e.g., $u_t(x)$.

conditions p_0 and p_1 with a trainable vector field $v_t(.\,;\theta)$ parameterized by θ. This leads to the Flow Matching objective:

$$\mathcal{L}_{\text{FM}}(\theta) = \mathbb{E}_{t,x\sim p_t(x)} \left\| v_t(x;\theta) - u_t(x) \right\|_2^2, \tag{2}$$

with t sampled from the uniform distribution $t \sim \mathcal{U}([0,1])$. Given an approximation of the target vector field $u_t(x)$, one can easily sample from the distribution p_1 given samples from p_0 (or the other way around), as well as predict dynamics of individual samples over time. However, the objective function in Equation 2 is generally intractable, as both p_t and u_t are unknown. Lipman et al. therefore introduced Conditional Flow Matching (CFM), a tractable yet equivalent objective that aims to approximate a *conditional* vector field $u_t(x \mid z)$:

$$\mathcal{L}_{\text{CFM}}(\theta) = \mathbb{E}_{t,z\sim q(z),x\sim p_t(x|z)} \left[\left\| v_t(x;\theta) - u_t(x \mid z) \right\|_2^2 \right]. \tag{3}$$

The conditioning variable z and conditional probability paths $p_t(x \mid z)$ are chosen such that the marginals match the boundary distributions p_0 and p_1. In general, one chooses z as a pair of samples from the source and target distributions (x_0, x_1) according to a joint distribution $q(z) = \pi(x_0, x_1)$ with marginals p_0 and p_1. Remarkably, $\mathcal{L}_{\text{FM}}(\theta)$ and $\mathcal{L}_{\text{CFM}}(\theta)$ are equivalent objectives as they have identical gradients with respect to θ (Theorem 2 of Lipman et al. (2023)).

Conditional Probability Paths A common choice for the form of conditional probability paths is

$$p_t(x \mid z) = \mathcal{N}(x \mid \mu_t(z), \sigma_t(z)^2 I). \tag{4}$$

where $\mu : [0,1] \times \mathcal{Z} \to \mathcal{X}$ and $\sigma : [0,1] \times \mathcal{Z} \to \mathbb{R}^+$ represent the time-dependent mean and standard deviation of a Gaussian distribution. Since the number of potential vector fields inducing a desired path is infinite, a reasonable approach is to select a *simple* vector field, *e.g.*, one that results in a flow of the form:

$$\phi_t(x \mid z) = \mu_t(z) + \sigma_t(z) \left(\frac{x - \mu_0(z)}{\sigma_0(z)} \right). \tag{5}$$

The above functional form leads to a unique inducing vector field (Theorem 3 in Lipman et al. (2023)), defined as

$$u_t(x \mid z) = \frac{\sigma_t'(z)}{\sigma_t(z)}(x_t - \mu_t(z)) + \mu_t'(z). \tag{6}$$

Given this parameterization, different $\mu_t(z)$ and $\sigma_t(z)$ are possible, as long as the marginals coincide with the boundary conditions (*i.e.*, $\int p_0(x \mid z) q(z) dz \approx p_0(x)$ and $\int p_1(x \mid z) q(z) dz \approx p_1(x)$). The most natural is to consider a small variance function at the boundaries with an interpolation function for $\mu_t(z)$, such that $\mu_0(z) = x_0$ and $\mu_1(z) = x_1$. For instance, Tong et al. (2024) considered a linear interpolation for the mean $\mu_t(z) = tx_0 + (1-t)x_1$, with a constant (small) variance $\sigma_t(z) = \sigma > 0$, and $q(z) = p_0(x_0)p_1(x_1)$, for their Independent-CFM (I-CFM) method.

Optimal Transport Tong et al. (2024) highlighted that sampling points x_0 and x_1 independently (*i.e.,* $\pi(x_0, x_1) = p_0(x_0)p_1(x_1)$) could lead to training instabilities and poor performance. Their improved method, OT-CFM, instead sampled using the optimal transport coupling between p_0 and p_1, $\pi^*(x_0, x_1)$, and resulted in stabilized training and better performance.

3 Condition-aware Multi-Marginal Flow Matching

We first extend the Flow Matching framework to multiple temporal snapshots, and then present a condition-aware variant that leverages information across various marginals and contexts.

Problem Statement Generalizing the Flow Matching framework that considers two distributions p_0 and p_1 only, we assume the data is sampled from a collection of distributions $\{p_{t_k}(x \mid c) : c \in [C], k \in [K+1]\}$ over C different conditions and $K+1$ different sampling times. Given these observations, our goal is to learn an approximation of a target vector field $u_t(x \mid c)$ that generates a probability path $p_t(x \mid c)$ that satisfies the boundary conditions at $t_0, t_1, \ldots, t_K$ for all conditions.

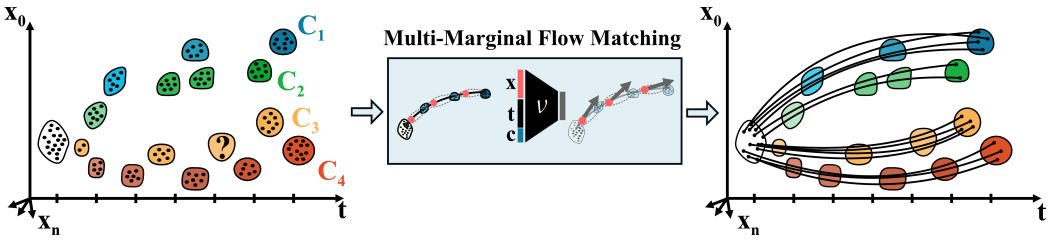

Figure 1: Schematic overview of the data and our modeling approach. **Left**: Data are observed across multiple time points and varying conditions, originating from a common source distribution (white), with "?" marking an unmeasured point of interest. **Middle**: Learning process. We train a neural network to regress the derivative (arrow) at points x (red) sampled around the interpolation path (equipped with time-dependent variance, dashed gray lines). **Right**: Estimated trajectories after learning the underlying vector field – allowing the generation of paths for novel samples, imputing missing time points, and generalizing to unseen domains.

3.1 Multi-Marginal Flow Matching

We consider a collection of $K+1$ discrete time stamps $\{t_0, \ldots, t_K\}$. Without loss of generality, we consider that the time stamps are distinct, ordered, and scaled so that $0 = t_0 < t_1 < \cdots < t_K = 1$. We don't impose any constraints on the spacing between consecutive time points. This flexibility accommodates scenarios where data collection occurs at irregular intervals, which is often the case in real-world applications. At each discrete time point t_k, we observe samples from a data density p_{t_k} valued in $\mathcal{X}$.

Flow Matching Objective We define $z \coloneqq (x_0, \ldots, x_K) \in \mathcal{Z} = \mathcal{X}^{K+1}$ and for now, define q as the data distribution with independent samples from each marginal. q admits as density $q(z) = \Pi_{k=0}^{K} p_{t_k}(x_k)$. Applying Equation 3 with the augmented vector z leads to the Multi-Marginal Flow Matching (MMFM) objective:

$$\mathcal{L}_{\text{MMFM}}(\theta) = \mathbb{E}_{t, z\sim q(z), x\sim p_t(x|z)}\Big[\|v_t(x;\theta) - u_t(x \mid z)\|_2^2\Big], \tag{7}$$

for any probability density path $p_t(x \mid z)$ and conditional vector field $u_t(x \mid z)$. This objective has the same form as Equation 3, but the density $q(z)$ and the probability density path is defined differently (over multiple time steps), resulting in a different target conditional vector field u_t. As demonstrated below, this remains a valid surrogate objective function for Flow Matching across multiple time points (the proof appears in Appendix A).

Proposition 1. *Assuming that $p_t(x) > 0$ for all $x \in \mathcal{X}$ and $t \in [0,1]$, then, up to a constant independent of θ, $\mathcal{L}_{FM}$ and $\mathcal{L}_{MMFM}$ are equal. Hence, for all values of the parameters θ:*

$$\nabla_\theta \mathcal{L}_{FM}(\theta) = \nabla_\theta \mathcal{L}_{MMFM}(\theta). \tag{8}$$

Conditional Probability Paths A key feature of MMFM is the specification of a Gaussian probability density path $p_t(x \mid z)$ that goes through all the time points $(x_0, \ldots, x_K)$. In contrast to classical FM, the MMFM framework can naturally incorporate prior knowledge about the system's dynamics over multiple time steps. For physical systems, a meaningful prior for μ_t is defined as an interpolating path of minimum energy or minimal curvature:

$$\mu_t(z) = \arg\min_{\gamma \in \mathcal{H}^2([t_0,t_K])} \int_{t_0}^{t_K} \|\gamma''(t)\|_2^2 \, dt \quad \text{s.t. } x_k = \gamma(t_k) \quad \text{for all } k \in \{0, \ldots, K\}, \tag{9}$$

where $\mathcal{H}^2([t_0, t_K])$ denotes the set of functions whose first derivative is absolutely continuous on $[t_0, t_K]$ and admit a weak second derivative. The celebrated Holladay's theorem (Holladay, 1957) demonstrates that μ is the natural cubic spline interpolation between the points $\{(x_k, t_k)\}_{k=0}^K$, whose coefficients can be computed efficiently since they only require solving a tri-diagonal system of linear equations.

Unlike the typical constant variance σ_t employed in CFM, we also use a time-dependent variance function defined piece-wise on each time interval as

$$\sigma_t(z) = \frac{4(t_{k+1} - t)(t - t_k)}{(t_{k+1} - t_k)^2}, \tag{10}$$

for $t \in [t_k, t_{k+1}]$. Intuitively, this variance function adds noise to the vector field estimation in-between observed time points and is a crucial component for sharing information across conditions. Derivations for the temporal derivatives of $\mu_t(z)$ and $\sigma_t(z)$ are provided in Appendix D.

Optimal Transport Following the enhancements proposed by Tong et al. (2024) in the case with two marginals, we propose to sample data points across marginals using a joint distribution, computed as the solution of a multi-marginal optimal transport (MMOT) problem (Pass, 2015): $q(z) = \pi^*(x_0, \ldots, x_K)$. Notably, when the cost structure is pairwise additive for each pair of marginals, the MMOT problem reduces to a set of K independent OT problems, such that $\pi^*(x_0, \ldots, x_K) = \frac{\prod_{k=1}^{K-1} \pi_k^*(x_k, x_{k+1})}{\prod_{k=2}^{K-1} p_{t_k}(x_k)}$, where $\pi_k^*(x_k, x_{k+1})$ is the solution of the OT problem between p_{t_k} and $p_{t_{k+1}}$ (the proof is provided in Appendix B). Throughout this work, we assume such a pairwise additive cost structure. We pre-compute the solutions of the OT problems on the training data using the squared Euclidean distance as a cost function and use the multi-marginal optimal transport coupling for q in Equation 7. When the dataset is too large, OT can be approximated using mini-batches, (Tong et al., 2024), although this was not necessary in our experiments.

Relationship with CFM MMFM is a generalization of CFM in the following sense. When the conditional vector field is defined with a piece-wise linear interpolation function for the mean and a constant variance, and in addition, the neural network v_t is defined piece-wise on $[t_0, t_K]$, the MMFM problem is equivalent to solving K distinct CFM problems between consecutive time points.

Proposition 2. *Let us assume that for all $z = (x_0, \ldots, x_K) \in \mathcal{Z}$, $\mu_t(z)$ is defined as the piecewise linear function going through all the points of z, and $\sigma_t(z) = \sigma$ is constant for all z. Additionally, let us assume that the vector field is learned separately on each time interval: $v_t(z; \theta) = \sum_{k=1}^{K} v_t(z; \theta_k) \mathbf{1}_{[t_k, t_{k+1})}(t)$. Then, the MMFM problem is equivalent to solving K separate CFM problems between each pair of consecutive marginals.*

The proof appears in Appendix A. This result highlights a key advantage of MMFM over multiple pairwise CFMs when the system's behavior exhibits similarities across time periods (or conditions, below). In such scenarios, MMFM can utilize a single set of parameters to model the dynamics across all time points (or, different conditions, below). This approach allows MMFM to leverage common patterns in the data that would be treated independently in separate pairwise CFM problems, leading to more efficient and robust modeling, and a deeper understanding of the underlying phenomena (e.g., biological commonalities).

3.2 Conditional MMOT-based Multi-Marginal Flow Matching

We now extend our framework to consider cases where each observation x_k^c from time point t_k is associated with a condition $c \in \{1, \ldots, C\}$. We assume the condition information is provided for each observation. We use the notation $x_k^c \sim p_{t_k}(x_k^c \mid c)$ to indicate the data density for condition c at time point t_k. Additionally, we define $z^c = (x_0^c, \ldots, x_K^c)$. Importantly, our model can handle incomplete data scenarios, where not all conditions are observed at all time points. This extension enables us to capture and analyze condition-specific dynamics, such as the response of cells to different drugs in a chemical screen.

We leverage the conditional information in our architecture by (1) modifying the coupling $q(z)$ to be condition specific, and (2) extending to architecture of the vector field neural network v_t to use the condition as input.

For the coupling, we use a condition-wise multi-marginal optimal transport coupling:

$$q^c(z^c) = \pi_c^*(x_0^c, \ldots, x_K^c) = \frac{\prod_{k=1}^{K-1} \pi_{c,k}^*(x_k^c, x_{k+1}^c)}{\prod_{k=2}^{K-1} p_{t_k}(x_k^c \mid c)}, \tag{11}$$

where $\pi_{c,k}^*$ is the optimal transport coupling between $p_{t_k}(x_k^c \mid c)$ and $p_{t_{k+1}}(x_{k+1}^c \mid c)$, and the second equality follows from the assumption of pairwise additive structure of the cost function (Section 3.1 and proof in Appendix B).

For the vector field neural network, we integrate the condition as an additional input to the neural model, modifying it to $v_t(x, c; \theta)$. This neural network takes as input a condition index c that is used to internally retrieve a learnable condition embedding (details about the architecture are provided in

Appendix D). Importantly, we learn a set of shared weights θ across all conditions, which enables the model to generalize across different conditions and potentially improve performance on conditions with limited data.

To train the conditional model, we employ classifier-free guidance as proposed by Zheng et al. (2023). The objective for the condition-informed version of MMFM, termed ***C-MMFM***, is defined as:

$$\mathcal{L}_{\text{C-MMFM}}(\theta) = \mathbb{E}_{t,b\sim\text{Ber}(p_\text{u}),c\sim\text{Cat}(C),z^c\sim\pi_c^*,x\sim p_t} \left\| v_t\Big(x, (1-b)c + bc_\varnothing; \theta\Big) - u_t(x \mid z^c) \right\|_2^2, \tag{12}$$

where p_u represents the probability of switching to the unconditional model, and $c_\varnothing$ represents the null conditioning. The null conditioning $c_\varnothing$ is an additional condition index that retrieves a learnable embedding corresponding to a condition-independent model. When the Bernoulli variable b is 1, the model uses a conditional-independent model. Otherwise, the conditional model is used. This approach allows information sharing across conditions via joint training of conditional $v_t(x, c; \theta)$ and unconditional $v_t(x, c_\varnothing; \theta)$ models.

At inference time, we use a weighted combination of the two vector fields (details about the sampling appear in Appendix C):

$$\tilde{v}_t(x, c; w, \theta) = (1-w)v_t(x, c_\varnothing; \theta) + wv_t(x, c; \theta) \tag{13}$$

and therefore can model the trajectory of a sample x_0 in condition c as:

$$\hat{x}_T = x_0 + \int_0^T \tilde{v}_t(x, c; w, \theta)dt. \tag{14}$$

The parameters p_u and w are selected based on the value of the objective function on held-out validation data.

4 Related Work

Flow Matching Flow-based generative models have gained significant attention in recent years due to their ability to efficiently model generative processes for complex data distributions. Flow Matching, introduced by Lipman et al. (2023), proposed a simulation-free approach to train neural ODEs for generative modeling – a computationally attractive alternative to maximum likelihood training of continuous normalizing flows (Chen et al., 2018). Building upon this, Tong et al. (2024) extended FM by (1) allowing flows between arbitrary distributions (I-CFM), (2) proposing OT-CFM coupling samples using optimal transport theory (linking FM to dynamic optimal transport), and (3) introducing Schrödinger Bridge Conditional FM (SB-CFM), linking FM to Schrödinger Bridges. Kapusniak et al. (2024) improved FM by estimating the data manifold to adjust the linear interpolation path and ensuring it remains within high-density regions of the data. However, none of these methods takes into account multiple (more than two) time points.

Label-Guided Flow Matching Zheng et al. (2023); Dao et al. (2023); Isobe et al. (2024) first integrated conditional information into FM. Guided Flows (Zheng et al., 2023) extended the FM framework to incorporate conditional information, allowing for more precise control over the generation process. At the same time, Dao et al. (2023) modeled the flows in a jointly learned latent space, offering improved computational efficiency. Meta Flow Matching (Atanackovic et al., 2024) extends traditional FM by modeling the flow over populations, *e.g.*, a set of cells from a patient, by embedding it using Graph Neural Networks. As with other Flow Matching studies, none of these methods consider multiple time points.

Fast and Smooth Interpolation The approach in Chewi et al. (2021) shares similarities with MMFM in its use of OT principles to guide the interpolation process but differs in its specific implementation by directly using splines rather than neural network-based Flow Matching and cannot handle multiple conditions. Therefore, it also has the disadvantage of not being able to make inferences at test time using learned dynamics from other conditions.

Multi Marginal Schrödinger Bridges In contrast to Flow Matching, Schrödinger Bridge (SB) models, which are based on Stochastic Differential Equations (SDEs) and therefore predominantly estimated using Diffusion Models, have already been extended to make use of multiple marginals. The Deep Multi-Marginal Momentum Schrödinger Bridge (DMSB), introduced by Chen et al. (2023), extends the classical SB problem to scenarios with multiple marginal distributions by adjusting the Bregman iteration approach.

Modeling of biological single-cell time series data Understanding cellular mechanisms from biological time series data or *pseudo* time series data is a popular research area, as it helps understand fundamental dynamic processes in cells, from differentiation during development to pathogenesis (Schiebinger et al., 2019; Weinreb et al., 2020; Setty et al., 2019; Yeo et al., 2021; Qiu et al., 2022; Farrell et al., 2023; Bergen et al., 2020; Tong et al., 2020; Zhang et al., 2024). Advancements in single-cell profiling have enabled researchers to capture temporal snapshots of individual cell states across cell populations, from which computational methods can infer temporal trajectories and the underlying gene regulatory networks that control them. Despite the fact that temporal processes both span across multiple time points and are often shared across conditions, models to date have focused on either a single condition monitored along multiple time points (through modeling consecutive pairs) or on a series of conditions measured in a single time point.

5 EXPERIMENTS

We assessed the performance of MMFM using synthetic data as well as a single-cell RNA-seq dataset where each of multiple conditions (perturbations) was measured along multiple time points. We compared the performance of MMFM to that of several other methods, first considering methods explicitly designed to incorporate multiple time points. We considered FSI (Chewi et al., 2021), a method interpolating data densities using OT and natural cubic splines, and as an ablation study, we assessed the performance of a variant of MMFM with a piece-wise linear interpolation function (L-MMFM). We also sought to report the performance of DMSB (Chen et al., 2023) but did not see meaningful outputs after a long training time and, therefore, were not able to draw conclusions. We therefore considered more direct applications of the FM framework, applying OT-CFM (Tong et al., 2024) across consecutive pairs of marginals, and applied separately per condition (PCFM). Finally, we also compared to an OT-CFM model that would ignore all intermediate time points (CFM). We used three metrics for evaluation: Mean-Squared-Error (MSE), Maximum-Mean Discrepancy (MMD), and Wasserstein-2 (W_2) distance. The MSE provides a straightforward comparison of cluster centers, while MMD and W_2 offer more sophisticated assessments of distributional differences by considering higher-order moments and geometric properties. To ensure a fair comparison, we provided the condition-specific OT couplings as input to all models. Additional details about these experiments, including hyperparameter search grids and hold-out-based validation strategies, are provided in Appendix D. Considerations about computational complexity are given in Appendix J.

5.1 SYNTHETIC EXPERIMENTS

To evaluate MMFM's ability to estimate condition-specific vector fields from time course data, we created two-dimensional synthetic datasets with a known ground truth vector field. Data were generated for 12 conditions, defined as $c_m = m$ for $m \in \{1, \dots, 12\}$ using the vector field

$$\begin{cases} u_t(x_t, c_m) = \left[\dfrac{3}{(\frac{c_m}{2} + 1)^{7/4}} \cos(5\pi t) \right] \\ \\ x_0(m) = \left[0, \dfrac{c_m - 2}{4} \right]. \end{cases} \tag{15}$$

We sampled from the time points and conditions described in Table 1. An overview of the data and the actual underlying trajectories appear in Figure 2A. We generated 50 data points per condition and time point according to the initial value problem above and included an additive Gaussian noise with variance σ_c^2. This scenario is similar to that in single-cell genomics, where the experimental assay is destructive, so each cell (sample) can be measured at most once. We held-out time point $t = 0.15$ during training for hyperparameter tuning of all FM-based models (but left it as input for the FSI model).

Table 1: Sampling times and conditions for the synthetic experiments.

c \ t	0	0.1	0.15	0.3	0.5	0.7	0.9	1.0
c_3	✓	✓	✓	_	✓	_	✓	✓
c_5	✓	_	✓	✓	✓	✓	_	✓
Rest	✓	✓	✓	✓	✓	✓	✓	✓

Note: ✓ indicates that samples from that combination are available in the training set.

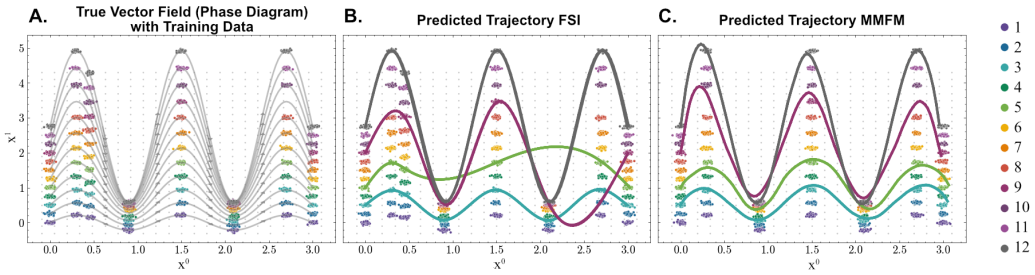

Figure 2: Assessment on synthetic data. (A) Ground truth vector field, which incorporates training samples for ten distinct conditions, each represented by a different color. (B,C) Interpolated paths generated by FSI (B) and MMFM (C) – illustrated for conditions $c \in [3, 5, 9, 12]$.

For evaluation, we compared deviations from the ground truth at the mean-level, estimated with the Mean-Square Error (MSE), and at the distribution-level, estimated by the Maximum Mean Discrepancy (MMD) between predicted samples and samples from the ground-truth vector field at 21 equidistant-spaced time points (from $t = 0$ to $t = 1$, by increments of $\Delta t = 0.05$).

The experimental results (Table 2) demonstrate the superior performance of MMFM on this time course data, as it most effectively predicts trajectories for conditions c_3 and c_5, where measurements are sparse and irregularly spaced. While FSI struggles to capture the right dynamics for the inferred trajectories (Figure 2) and systematically underestimated the number of inflection points, MMFM accurately adjusted the trajectories and aligned them with the curvature profile of other conditions (visualization of interpolation quality for other conditions and methods appear in Appendix E).

FSI and PCFM both cannot leverage information from other conditions, leading to incorrect trajectories and much higher errors. By contrast, CFM and MMFM have access to multiple conditions. However, CFM only considers the first and last time points, resulting in a higher loss than MMFM. Finally, L-MMFM performs substantially worse than MMFM, suggesting that the cubic splines are effective models for the dynamics of this dataset. Further results are provided in Appendix F, where we also discuss the extrapolation properties of MMFM.

Together, these results validate that MMFM is beneficial in scenarios where one has access to measurements taken at different time points and across different conditions.

Table 2: Results on synthetic data. We report the mean square error (MSE) and maximum mean discrepancy (MMD), with lower values indicating better performance. Means and standard deviations are computed over 21 time points. Best-performing models are highlighted in bold.

	$c_m = 3$		$c_m = 5$	
	MSE ↓	MMD ↓	MSE ↓	MMD ↓
FSI	0.72 ± 0.60	0.42 ± 0.37	0.72 ± 0.93	0.33 ± 0.45
CFM	0.46 ± 0.25	0.25 ± 0.15	0.93 ± 0.52	0.60 ± 0.33
PCFM	0.75 ± 0.49	0.45 ± 0.35	0.78 ± 0.73	0.43 ± 0.44
L-MMFM (ours)	0.39 ± 0.25	0.20 ± 0.17	0.36 ± 0.27	0.17 ± 0.19
MMFM (ours)	**0.13 ± 0.08**	**0.04 ± 0.02**	**0.22 ± 0.15**	**0.12 ± 0.08**

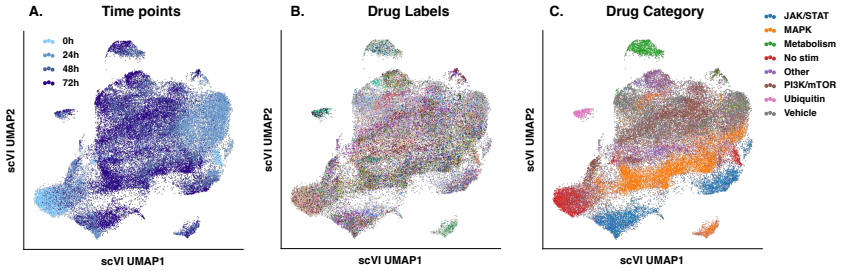

Figure 3: UMAP embeddings of single-cell RNA sequencing data visualizing drug responses over time. (A) Cells colored by time point (0h, 24h, 48h, 72h), highlighting the temporal progression of cellular states. (B) The same embedding colored by individual drugs (93 distinct labels), showcasing response heterogeneity. (C) Cells colored by drug categories, highlighting shared response patterns within drug classes. UMAP coordinates were derived using scVI (single-cell Variational Inference) (Lopez et al., 2018).

5.2 Application to Single-Cell Perturbation Screening Data

We assessed the performance of MMFM on a real-world single-cell perturbation screen dataset. The dataset records single-cell gene expression ($18,250$ genes) profiles of T cells treated with kinase inhibitors and undergoing activation, measured at four time points (0h, 24h, 48h, and 72h). The dataset includes 93 distinct inhibitors, each used at varying concentrations (100 nM, 1 μM, and 10 μM), as well as negative control conditions (vehicle and non-activation). In each condition (combination of inhibitor, concentration and time point), hundreds of cells have been profiled. We treated the non-activation data as the $t = 0h$ time point for all conditions. To focus on the most significant effects, we filtered the data and retained $M = 123$ distinct treatments, each representing a unique combination of compound and concentration (Figure 3). We then randomly selected 60 of those treatments for analysis. For evaluation purposes, we withheld ten non-overlapping random treatments for each of the three time points. Standard single-cell data processing pipelines were used to normalize and scale the features, with the first 25 principal components used as input features (details regarding data preparation appear in Appendix H).

Because the ground-truth vector field is unknown in this setting, we evaluated the capacity of the methods to generalize to held-out time points. We thus assessed model performance at the mean-level, estimated with the Mean-Square Error (MSE), and at the distribution-level, estimated by the Wasserstein distance W_2 between predicted and hold-out samples. The training was conducted with five random seeds, using one held-out treatment to select the best model for testing. For this benchmark, the PCFM baseline was applied once using data from all conditions, as it otherwise required training 150 individual models, which was prohibitively time-consuming.

Table 3: Results for the drug response imputation task. We report the mean-square error (MSE) between the predicted and actual distributions' means and Wasserstein distance (W_2), where in both cases lower is better. Means and standard deviations are computed over five folds. Best-performing models are highlighted in bold.

	$t = 24h$		$t = 48h$		$t = 72h$	
	MSE ↓	W_2 ↓	MSE ↓	W_2 ↓	MSE ↓	W_2 ↓
FSI	07.77 ± 01.49	56.13 ± 13.44	04.52 ± 01.14	38.93 ± 08.56	06.62 ± 01.65	78.46 ± 23.48
CFM	09.10 ± 01.59	60.86 ± 14.67	04.92 ± 01.88	33.28 ± 13.53	_	_
PCFM	08.88 ± 01.58	56.68 ± 12.12	04.13 ± 01.21	34.85 ± 08.01	06.07 ± 01.32	61.83 ± 16.74
L-MMFM (ours)	08.05 ± 01.29	**50.82** ± 10.79	03.56 ± 01.50	26.07 ± 08.62	06.30 ± 01.92	47.97 ± 19.69
MMFM (ours)	**07.54** ± 00.99	51.86 ± 07.84	**03.38** ± 01.34	**26.01** ± 07.72	**04.92** ± 01.61	**37.71** ± 12.24

Our experimental results (Table 3) demonstrate the superior performance of MMFM at imputing missing data across multiple time points. Interestingly, MMFM and L-MMFM have similar performance for the $t = 24h$ and $t = 48h$, but MMFM significantly outperforms L-MMFM at the $t = 72h$ time point. This suggests that the cubic spline is a more desirable prior for this modeling problem. In contrast, the reliance of PCFM on linear paths may introduce a bias towards straight-line trajectories, limiting its flexibility in capturing complex dynamics. Overall, MMFM demonstrates robust performance in handling complex datasets with missing temporal information, emphasizing its potential for diverse applications in generative modeling.

5.3 APPLICATION TO BEIJING AIR QUALITY DATA

To further study how well MMFM generalizes, especially under irregular sampling over time, we applied it to the Beijing multi-site air quality data set (Chen, 2017). This dataset comprises hourly air pollutant data from 12 air-quality monitoring sites across Beijing. We focused on PM2.5 data, which measures the density of particulate matter smaller than 2.5 micrometers, an important air pollution indicator, between January 2015 and February 2017. The 12 monitoring sites were modeled as the condition ($c \in \{1, \dots, 12\}$). For each site, we grouped together the measurements collected over the same month, resulting in 26 temporal snapshots ($t \in \{1, \dots, 26\}$). We selected different months as training data to simulate irregular sampling, with the interval between successive snapshots varying between 1 and 7 months. For 9 out of 12 stations, we selected 50% of the measurements, i.e. 13 months. For the other three stations, we selected only 7, 6 and 7 months as training data to simulate missing sensor data. These three stations are represented by the conditions $c = 4$, $c = 7$ and $c = 10$. We evaluated our method on all months that were not part of the training data set. This experiment represents a common challenge in sensor networks, where some measurements are lost or corrupted and must be imputed using data from other sensors. The results (Table 4) indicate that both MMFM versions (cubic spline and linear paths) show strong performance compared to FSI, CFM, and PCFM when it comes to interpolating the measurements. L-MMFM models show the best performance across all evaluated methods, as measured by MSE, MMFM is in second place in three out of four scenarios. Further details and evaluation metrics can be found in Appendix G.

Table 4: Results on the Beijing data. We report the maximum mean discrepancy (MMD), with lower values indicating better performance. Best-performing models are highlighted in bold.

	$c = 4$	$c = 7$	$c = 10$	Rest
FSI	1.70 ± 0.40	1.89 ± 0.16	1.92 ± 0.10	1.47 ± 0.54
CFM	1.86 ± 0.19	1.78 ± 0.35	1.85 ± 0.21	1.83 ± 0.30
PCFM	1.61 ± 0.45	1.42 ± 0.36	1.86 ± 0.15	1.50 ± 0.50
L-MMFM (ours)	**1.33** ± 0.61	**1.34** ± 0.55	**1.24** ± 0.68	**1.33** ± 0.59
MMFM (ours)	1.52 ± 0.45	1.50 ± 0.49	1.32 ± 0.50	1.52 ± 0.51

6 DISCUSSION

We introduced Multi-Marginal Flow Matching (MMFM), a novel method for modeling complex system dynamics from temporal snapshot data across multiple conditions. We demonstrated that MMFM effectively combines data from various time points and experimental settings, outperforming existing methods in imputing missing time points. Our approach showed particular strength in scenarios with sparse or irregularly spaced measurements, leveraging information across conditions.

An important parameter in the design of MMFM is the time-varying variance function σ_t, as well as the sharing of parameters across conditions. An interesting direction for future work would be to add a set of parameters to the probability density path used in Flow Matching and provide a principled way to learn those parameters while simultaneously solving the FM problem. For example, one could use latent attentive neural processes (Kim et al., 2019) to construct meta-models across conditions. This approach could alleviate the need to find the right set of hyperparameters, ensuring that the conditioning network has sufficient, but not excessive, influence on the model parameters. Another promising avenue for constructing flows on real-world data is to explore more complex cost functions for multi-marginal optimal transport, (*e.g.*, the energy landscape-based loss functions for biological applications, Appendix I).

MMFM opens up new modeling opportunities for single-cell RNA-seq datasets. For example, so-called cellular velocities can be estimated from data either using nascent (unspliced) RNA, or metabolic labeling (La Manno et al., 2018; Bergen et al., 2020). Despite being inherently noisy, this additional information could be a valuable addition to enhance and steer the synthetic gradient flows based on interpolation paths, as previously demonstrated by Tong et al. (2020). Furthermore, constraining the model to satisfy specific stochastic differential equations, such as Ornstein-Uhlenbeck processes (Wang et al., 2023), could help bring interpretability, as well as mechanistic insights. Indeed, such models have analytical steady-state solutions and also accommodate for interventions (Rohbeck et al., 2024) (*e.g.,* modeling gene knock-outs). Lastly, biomedical data often includes various modalities providing multiple measurements on the same target (*e.g.,* a cell's gene expression and chromatin accessibility). Access to these multi-view datasets can allow for modeling coupled trajectories across different spaces (Somnath et al., 2023).

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