
Multi-Marginal Schrödinger Bridge Matching

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Abstract

Understanding the continuous evolution of populations from discrete temporal snapshots is a critical research challenge, particularly in fields like developmental biology and systems medicine where longitudinal tracking of individual entities is often impossible. Such trajectory inference is vital for unraveling the mechanisms of dynamic processes. While Schrödinger Bridge (SB) offer a potent framework, their traditional application to pairwise time points can be insufficient for systems defined by multiple intermediate snapshots. This paper introduces Multi-Marginal Schrödinger Bridge Matching (MSBM), a novel algorithm specifically designed for the multi-marginal SB problem. MSBM extends iterative Markovian fitting (IMF) to effectively handle multiple marginal constraints. This technique ensures robust enforcement of all intermediate marginals while preserving the continuity of the learned global dynamics across the entire trajectory. Empirical validations on synthetic data and real-world single-cell RNA sequencing datasets demonstrate the competitive or superior performance of MSBM in capturing complex trajectories and respecting intermediate distributions, all with notable computational efficiency.

1 Introduction

Understanding the continuous evolution of populations from discrete temporal snapshots represents a significant challenge in various scientific disciplines, particularly in fields like developmental biology [7, 42] and systems medicine [29] where tracking individual entities longitudinally is often unfeasible. The ability to infer trajectories from such snapshot data is crucial for elucidating the underlying mechanisms of dynamic processes. The Schrödinger Bridge (SB) problem, originally rooted in statistical mechanics [43], has garnered substantial interest in machine learning as an entropy-regularized, continuous-time formulation of optimal transport [20, 30]. It seeks to identify the most probable evolutionary path between prescribed initial and terminal distributions, and has been successfully employed in generative modeling [3, 4, 9, 26, 27, 37, 38, 45, 49].

However, many real-world scenarios present observations or constraints at multiple time points, not just at the beginning and end of a process. For instance, in single-cell RNA sequencing (scRNA-seq) experiments, which are pivotal for studying complex biological processes like cell differentiation, cells are typically destroyed upon measurement [6, 17, 28]. This destructive nature makes it impossible to track individual cells over time, thus necessitating the inference of developmental trajectories from population-level snapshots collected at several intermediate stages. Similarly, meteorological systems may have partial observations across various times [11, 32]. Such situations necessitate a multi-marginal generalization of the SB problem (mSBP), where the path measure must align with prescribed marginal distributions at multiple intermediate time points. While the traditional SB framework offers a powerful approach, its standard application to pairwise time points can prove insufficient for systems characterized by multiple intermediate snapshots. Although more specialized methods for mSBP have recently been developed [8, 18, 44], the direct application of some multi-marginal approaches can lead to error accumulation if not carefully managed, particularly

when learned controls are even slightly inaccurate. These challenges highlight the need for robust and scalable solutions for the mSBP that can effectively integrate information across all observed time points.

This paper introduces Multi-Marginal Schrödinger Bridge Matching (MSBM), a novel algorithm specifically developed to address the multi-marginal SB problem by building upon and extending the Iterative Markovian Fitting (IMF) algorithms [36, 45]. MSBM is designed to effectively manage multiple marginal constraints by constructing local SBs on each interval and seamlessly integrating them. This local construction strategy, underpinned by a shared global parametrization of control functions, ensures the robust enforcement of all intermediate marginal distributions while crucially preserving the continuity of the learned global dynamics across the entire trajectory. Empirical validations conducted on synthetic datasets as well as real-world single-cell RNA sequencing data demonstrate that MSBM achieves competitive or superior performance in capturing complex trajectories and accurately respecting intermediate distributions, all while exhibiting notable computational efficiency. Our work aims to provide a robust and scalable computational method for these multi-marginal settings, addressing the critical need for consistent and tractable dynamic inference when data is available as snapshots at multiple time points.

We summarize our contributions as follows:

- We extend the theoretical and algorithmic foundations of SBs, including the IMF iteration and optimal control perspectives, to the challenging multi-marginal setting.
- We introduce an efficient modeling approach for trajectory inference, that constructs and smoothly integrates local SBs across sub-intervals, inherently allows for parallelized training, leading to significant speed-ups.
- Through comprehensive experiments on both synthetic and real-world single-cell RNA sequencing data, we demonstrate that MSBM accurately models complex population dynamics and outperforms state-of-the-art methods in both trajectory fidelity and computational speed.

Notation. Let $\mathcal{P}_{[0,T]}$ denote the space of continuous functions taking values in $\mathbb{R}^d$ on the interval $[0, T]$. We use an uppercase letter $\mathbb{P} \in \mathcal{P}_{[0,T]}$ to represent a path measure. For a path measure $\mathbb{P} \in \mathcal{P}_{[0,T]}$, the marginal distribution at discrete time points $\mathcal{T} = \{t_0, \dots, t_k\}$, where $0 = t_0 < t_1 < \dots < t_k = T$ is denoted by $\mathbb{P}_{\mathcal{T}} \in \mathcal{P}_{\mathcal{T}}$, where we define $\mathcal{P}_{\mathcal{T}}$ as the set of measures $\mathbb{P}$ over $\mathbb{R}^{d \times |\mathcal{T}|}$. Additionally, the conditional distribution of $\mathbb{P}$, given $\mathcal{T}$, is denoted by $\mathbb{P}_{|\mathcal{T}} \in \mathcal{P}_{[0,T]}$. Moreover, a path measure $\mathbb{P}$ can be defined as mixture. For any Borel measurable set $A \in \mathcal{B}(\Omega)$, $\mathbb{P}$ can be defined by $\mathbb{P}(A) = \int_{\mathbb{R}^{d \times |\mathcal{T}|}} \mathbb{P}_{|\mathcal{T}}(A | \mathbf{x}_{\mathcal{T}}) d\mathbb{P}_{\mathcal{T}}(\mathbf{x}_{\mathcal{T}})$, where $\mathbb{P} \in \mathcal{P}_{0,T}$ and $\mathbb{P} \in \mathcal{P}_{\mathcal{T}}$, and we use the shorthand $\mathbf{x}_{\mathcal{T}} := (\mathbf{x}_1, \dots, \mathbf{x}_k)$ and $[0 : k] := \{0, 1, \dots, k\}$. The Kullback-Leibler (KL) divergence between two probability measures μ and ν on space $\mathcal{X}$ is defined as $D_{\text{KL}}(\mu | \nu) = \int_{\mathcal{X}} \log \frac{d\mu}{d\nu}(\mathbf{X}) d\mu(\mathbf{X})$ when μ is absolutely continuous with respect to ν ($\mu \ll \nu$), and $D_{\text{KL}}(\mu | \nu) = +\infty$ otherwise. We will often refer to probability measures on $\mathbb{R}^d$ and their Lebesgue densities interchangeably, under the standard assumption of absolute continuity. Finally, for a function $\mathcal{V} : [0, T] \times \mathbb{R}^d \rightarrow \mathbb{R}$, we define the gradient and laplacian operators with respect to $\mathbf{x} \in \mathbb{R}^d$ as $\nabla \mathcal{V}$ and $\Delta \mathcal{V}$, respectively, and its partial derivative with respect to time $t \in [0, T]$ as $\partial_t \mathcal{V}$.

2 Preliminaries

2.1 Schrödinger Bridge Matching (SBM)

The Schrödinger Bridge problem (SBP) [16, 43] is a stochastic optimal transport problem [30] that seeks the optimal transport plan for endpoint marginals ρ_0 and ρ_T . In this paper, we focus on the dynamical representation, where a reference distribution $\mathbb{Q} \in \mathcal{P}_{[0,T]}$ is induced by the SDEs:

$$d\mathbf{X}_t = f_t(\mathbf{X}_t) dt + \sigma d\mathbf{W}_t, \quad \mathbf{X}_0 \sim \rho_0, \quad (1)$$

where $f_t : \mathbb{R}^d \rightarrow \mathbb{R}^d$ is a drift, $\sigma \in \mathbb{R}$ is a diffusion, and $\mathbf{W}_t \in \mathbb{R}^d$ is a standard Wiener process. With the base reference path measure $\mathbb{Q}$, the dynamic representation of the SB [20, 35, 39] is:

$$\min_{\mathbb{P} \in \mathcal{P}_{[0,T]}} D_{\text{KL}}(\mathbb{P} | \mathbb{Q}), \quad \text{subject to} \quad \mathbb{P}_0 \sim \rho_0, \quad \mathbb{P}_T \sim \rho_T. \quad (\text{SBP})$$

Recent advancements in dynamical optimal transport [37, 45] have introduced a novel numerical methodology for solving SBP. This approach reframes SBP by decomposing its dynamical constraints into the time-evolving marginal distributions $\mathbb{P}_t$ for all $t \in [0, T]$ and the joint coupling $\mathbb{P}_{0,T}$. This optimization relies on IMF [45], a technique that iteratively refines the path measure $\mathbb{P} \in \mathcal{P}_{[0,T]}$. IMF alternates between two projection called Markovian and Reciprocal projections to preserve the correct endpoint marginals (ρ_0, ρ_T) throughout the optimization.

Reciprocal Projection $\mathcal{R}$. For a given reference measure $\mathbb{Q}$ from (1), and a path measure $\mathbb{P}$ with marginals specified at end points $\mathcal{T} = \{0, T\}$ the reciprocal projection is defined as:

$$\mathcal{R}(\mathbb{P}, \mathcal{T}) := \mathbb{P}_{\mathcal{T}} \mathbb{Q}_{|\mathcal{T}} = \mathbb{P}_{0,T} \mathbb{Q}_{|0,T}. \quad (2)$$

This projection constructs a new path measure by taking the endpoint coupling $\mathbb{P}_{0,T}$ from $\mathbb{P}$ and forming a mixture of bridge process using $\mathbb{Q}$ conditioned on these end points. Sampling from $\Pi := \mathcal{R}(\mathbb{P}, \mathcal{T})$ involves drawing end points samples $(\mathbf{X}_0, \mathbf{X}_T) \sim \mathbb{P}_{0,T}$ and then generating a path $\mathbf{X}_t^{\mathcal{T}}$ between them using conditional reference measure $\mathbb{Q}_{|0,T}$ which induced by following SDEs, for any $(\mathbf{x}_0, \mathbf{x}_T)$:

$$d\mathbf{X}_t^{\mathcal{T}} = [f_t(\mathbf{X}_t^{\mathcal{T}}) + \sigma^2 \nabla \log \mathbb{Q}_{T|t}(\mathbf{x}_T | \mathbf{X}_t^{\mathcal{T}})] dt + \sigma d\mathbf{W}_t, \quad \mathbf{X}_0^{\mathcal{T}} = \mathbf{x}_0, \quad (3)$$

If $\mathbb{Q}_{|0,T}$ has tractable bridge formulation, for example, when $\mathbb{Q}$ is chosen as a Brownian motion i.e., $d\mathbf{X}_t = \sigma d\mathbf{W}_t$, sampling the path at time t given the endpoints can be performed as:

$$\mathbf{X}_t^{\mathcal{T}} \sim \mathcal{N}\left(\left(1 - \frac{t}{T}\right)\mathbf{X}_0 + \frac{t}{T}\mathbf{X}_T, t\left(1 - \frac{t}{T}\right)\sigma^2\right), \quad \text{where } (\mathbf{X}_0, \mathbf{X}_T) \sim \mathbb{P}_{0,T}. \quad (4)$$

Markov Projection $\mathcal{M}$. Although the reciprocal projection $\mathcal{R}$ in (2) preserves end point marginals (ρ_0, ρ_T) , its sampling process in (4) requires both $(\mathbf{X}_0, \mathbf{X}_T)$, making it non-Markovian and thus ill-suited for generative modeling aimed at sampling from ρ_T without knowing $\mathbf{X}_T$. The Markov projection $\mathcal{M}$ resolves this by projecting $\Pi := \mathcal{R}(\mathbb{P}, \mathcal{T})$ into a family of Markov process while ensuring $\mathbb{P}^* = \Pi_t$ for all $t \in [0, T]$. Again, when $\mathbb{Q}$ is chosen as a Brownian motion i.e., $d\mathbf{X}_t = \sigma d\mathbf{W}_t$, the Markov projection of Π , $\mathbb{P}^* = \mathcal{M}(\Pi, \mathcal{T})$, is induced by following SDEs:

$$d\mathbf{X}_t^* = \sigma v^*(t, \mathbf{X}_t^*) dt + \sigma d\mathbf{W}_t, \quad \mathbf{X}_0^* \sim \Pi_0, \quad (5)$$

$$\text{where } v^*(t, \mathbf{x}) = \frac{1}{T-t} \left(\mathbb{E}_{\mathbb{Q}_{T|t}} [\mathbf{X}_T | \mathbf{X}_t = \mathbf{x}] - \mathbf{x} \right). \quad (6)$$

Intuitively, the term $\mathbb{E}_{\mathbb{Q}_{T|t}} [\mathbf{X}_T | \mathbf{X}_t = \mathbf{x}]$ can be understood as a prediction of the target state $\mathbf{X}_t^*$. Flow matching [23] of Bridge matching [37] tackles the approximation $\mathbf{X}_T^* \approx \mathbb{E}_{\mathbb{Q}_{T|t}} [\mathbf{X}_T | \mathbf{X}_t = \mathbf{x}]$ by learning a drift function. This learned drift guides the evolution of $\mathbf{X}_t^*$ such that its terminal state aligns with the target, often by regressing the drift against a target drift derived from samples of $(\mathbf{X}_0, \mathbf{X}_T)$ under the reference conditional bridge measure $\mathbb{Q}_{|0,T}$.

Building upon the projections $\mathcal{R}$ and $\mathcal{M}$, Schrödinger Bridge Matching (SBM) methods [37, 45] refines the path measure through an alternating iterative procedure:

$$\mathbb{P}^{(2n+1)} := \mathcal{M}(\mathbb{P}^{(2n)}, \mathcal{T}), \quad \mathbb{P}^{(2n+2)} := \mathcal{R}(\mathbb{P}^{(2n+1)}, \mathcal{T}). \quad (7)$$

Initialized with $\mathbb{P}^{(0)} = \mathbb{P}_{\mathcal{T}}^{(0)} \mathbb{Q}_{|0,T}$, utilizing $\mathbb{P}_{\mathcal{T}}^{(0)}$ is independent coupling of ρ_0 and ρ_T along with the reference conditional bridge measure $\mathbb{Q}_{|\mathcal{T}}$. Please refer to [37, 45] for more details.

3 Multi-Marginal Iterative Markovian Fitting

Dynamic SB methods, as discussed in Section 2, have traditionally focused on problems defined by two endpoint marginal distributions, (ρ_0, ρ_T) . However, in real-world applications, particularly in fields like developmental biology (e.g., scRNA-seq studies of cellular differentiation), systems are often observed through snapshots at multiple intermediate time points, not just at the beginning and end of a process. This prevalence of multi-stage data highlights a critical limitation of standard SB approaches. While the theoretical extension of SB methods to handle multiple marginals has been explored [1, 31], the development of robust and scalable computational methods for these multi-marginal settings has lagged. Recently, methods with IPF-type objectives have been derived for multi-marginal cases [8, 44]. However, challenges persist in ensuring global dynamic consistency across all intervals, maintaining computational tractability as the number of marginals increases.

In this section, we extend the SBM framework—conventionally applied to problems with two endpoint marginals (ρ_0, ρ_T) and foundational to IMF methods—to handle cases involving $k + 1$ multiple snapshots $(\rho_0, \rho_{t_1}, \dots, \rho_T)$ on discrete time stamps $\mathcal{T} = \{t_0, t_1, \dots, t_k\}$ where $0 = t_0 < t_1 < \dots < t_k = T$ ¹. Similar to **SBP**, the dynamic multi-marginal Schrödinger Bridge problem can be formally defined as [10] the entropy minimization problem:

$$\min_{\mathbb{P} \in \mathcal{P}_{[0, T]}} D_{\text{KL}}(\mathbb{P} | \mathbb{Q}), \quad \text{subject to} \quad \mathbb{P}_t \sim \rho_t, \quad \forall t \in \mathcal{T}. \quad (\text{mSBP})$$

To find a most probable path $\mathbb{P}^{\text{mSBP}}$, the solution of **mSBP** under multiple constraints, we will generalize the principles of SBM in Section 2.1 to the multi-marginal cases in Section 3.1. The extension of dynamic SB optimality [20, 35] and the associated stochastic optimal control problem [39] to multi-marginal settings is presented in Appendix A.

3.1 Multi-Marginal Projection operators

To develop multi-marginal extension of SBM, we investigate how the IMF framework can be adapted to scenarios with multiple snapshots (*i.e.*, where the set of time points $\mathcal{T}$ has cardinality $|\mathcal{T}| > 2$). This adaptation necessitates extending the fundamental building blocks of SBM—specifically, the reciprocal projection $\mathcal{R}$ and the Markov projection $\mathcal{M}$ —to handle multiple marginal constraints.

Multi-Marginal Reciprocal Projection $\mathcal{R}^{\text{mm}}$. First, we state and prove a proposition that characterizes the reciprocal structure of conditional path measures. In particular, we focus on a mixture of bridges $\Pi = \Pi_{\mathcal{T}} \mathbb{Q}_{|\mathcal{T}} \in \mathbb{P}_{[0, T]}$ constrained by the marginals at multiple timestamps in $\mathcal{T}$.

Proposition 1 (Reciprocal Property). *For any $\mathbf{x}_{\mathcal{T}} := (\mathbf{x}_0, \mathbf{x}_{t_1}, \dots, \mathbf{x}_T) \in \mathbb{R}^{d \times (k+1)}$ and $t \in [t_{i-1}, t_i]$, the marginal distribution of $\mathbb{Q}_{|\mathcal{T}}(\cdot | \mathbf{x}_{\mathcal{T}})$ at t satisfies:*

$$\mathbb{Q}_{|\mathcal{T}}(\mathbf{x}_t | \mathbf{x}_{\mathcal{T}}) = \mathbb{Q}_{|t_{i-1}, t_i}(\mathbf{x}_t | \mathbf{x}_{t_i}, \mathbf{x}_{t_{i-1}}). \quad (8)$$

Therefore, for any $\mathbb{P} \in \mathcal{P}_{[0, T]}$ the reciprocal projection $\mathcal{R}^{\text{mm}}(\mathbb{P}, \mathcal{T})$ admits the following factorization:

$$\mathcal{R}^{\text{mm}}(\mathbb{P}, \mathcal{T}) = \mathbb{P}_{\mathcal{T}} \mathbb{Q}_{|\mathcal{T}} = \mathbb{P}_{t_0, \dots, t_k} \mathbb{Q}_{|t_0, \dots, t_k} = \mathbb{P}_{t_0, \dots, t_k} \prod_{i=1}^k \mathbb{Q}_{|t_{i-1}, t_i}, \quad \mathbb{P}\text{-a.e.} \quad (9)$$

A key implication of the reciprocal property, detailed in Proposition 1, is that a mixture of diffusion bridges constrained on $\mathcal{T}$ factorizes into independent segments over successive time intervals. This factorization simplifies the analysis and simulation of the overall path measure. Since each segment can then be treated as a standard conditional bridge process as in (3), closed-form sampling, such as in (4), can be applied independently in parallel to each subinterval $\{t_{i-1}, t_i\}_{i \in [1:k]}$. This tractability is essential for developing an efficient multi-marginal SBM algorithm.

Multi-Marginal Markov Projection $\mathcal{M}^{\text{mm}}$. With the reciprocal property and factorization in (9), we show that the Markov projection on multi-marginal case can be constructed by similar fashion.

Proposition 2 (Multi-Marginal Markovian Projection). *Let $\Pi \in \mathcal{P}_{[0, T]}$ admit factorization in (9). The multi-marginal Markov projection of Π , $\mathbb{P}^* := \mathcal{M}^{\text{mm}}(\Pi, \mathcal{T}) \in \mathcal{P}_{[0, T]}$, is associated with the SDE:*

$$d\mathbf{X}_t^* = [f_t(\mathbf{X}_t^*) + \sigma v^*(t, \mathbf{X}_t^*)] dt + \sigma d\mathbf{W}_t, \quad \mathbf{X}_0^* \sim \Pi_0, \quad (10)$$

$$\text{where } v^*(t, \mathbf{x}) = \sum_{i=1}^k \mathbf{1}_{[t_{i-1}, t_i)} \mathbb{E}_{\Pi_{t_i} | t} [\nabla \log \mathbb{Q}_{t_i | t}(\mathbf{X}_{t_i} | \mathbf{X}_t) | \mathbf{X}_t = \mathbf{x}]. \quad (11)$$

Moreover, v^* satisfies the Fokker-Planck equation (FPE) [40]:

$$\partial_t \rho_t = -\nabla \cdot (v_t^*(\mathbf{x}) \rho_t(\mathbf{x})) + \frac{\sigma^2}{2} \Delta \rho_t(\mathbf{x}) = 0, \quad \rho_t = \Pi_t, \quad \forall t \in \mathcal{T}, \quad (12)$$

where ρ_t is marginal density of Π_t . In other words, $\mathbb{P}_t^* = \Pi_t$ for all $t \in [0, T]$. d

As established in Proposition 2, constructing a global diffusion process via (10) with the optimal control v^* (11) yields a multi-marginal Markov projection $\mathbf{X}_{[0, T]}^*$ that is continuous over the entire time interval $[0, T]$. The continuity arises because the local Markov projections, $\mathbf{X}_{[t_{i-1}, t_i]}^*$, on each sub-interval are derived from factorized conditional bridge $\mathbb{Q}_{|t_{i-1}, t_i}$ in (9). These bridges are

¹Our framework accommodates arbitrary time intervals between successive time stamps.

anchored by identical marginal distributions at there shared boundaries; for instance, both $\mathbf{X}_{[t_{i-1}, t_i]}^*$ and $\mathbf{X}_{[t_i, t_{i+1}]}^*$ is guaranteed to match the marginal distribution ρ_{t_i} at time t_i . Consequently, these local diffusion processes connect seamlessly at adjacent timestamps, resulting in a smooth and well-defined path for $\mathbf{X}_{[0, T]}^*$. The well-defined nature of the global path, in conjunction with the projections $\mathcal{R}^{\text{mm}}$ and $\mathcal{M}^{\text{mm}}$, is fundamental to successfully applying the SBM framework to the *mSBP*. Finally, the uniqueness condition for standard SB [45, Proposition 5] can also be extended to multi-marginal case.

Proposition 3 (Uniqueness). *Let $\mathbb{P}^*$ be a Markov measure which is reciprocal class of $\mathbb{Q}$ satisfying $\mathbb{P}_t^* = \rho_t$ for all $t \in \mathcal{T}$. Then, $\mathbb{P}^*$ is unique solution $\mathbb{P}^{\text{mSBP}}$ of the *mSBP*.*

Building on the projection operators $\mathcal{R}^{\text{mm}}$, $\mathcal{M}^{\text{mm}}$ with the uniqueness result of Proposition 3, we can apply the iterative algorithm used in SBM algorithm [45, Algorithm 1] to the multi-marginal setting:

$$\mathbb{P}^{(2n+1)} := \mathcal{M}^{\text{mm}}(\mathbb{P}^{(2n)}, \mathcal{T}), \quad \mathbb{P}^{(2n+2)} := \mathcal{R}^{\text{mm}}(\mathbb{P}^{(2n+1)}, \mathcal{T}), \quad |\mathcal{T}| > 2. \quad (13)$$

The convergence guarantees proved for the iteration apply equally well to the multi-marginal case.

Proposition 4 (Convergence). $\mathbb{P}^{(n)} = \mathbb{P}^{\text{mSBP}}$ of *mSBP* as $n \uparrow \infty$ with iterative procedure in (13).

3.2 Practical Implementation.

In practice, at each iteration n of (13) we approximate the optimal control v^* from (11) by a neural network v_θ . By Girsanov theorem, θ are chosen to minimize the following training objective function:

$$\mathcal{L}(\theta, \mathcal{T}, \Pi_{\mathcal{T}}) = \int_0^T \mathbb{E}_{\Pi_{t, \mathcal{T}}} [|\sigma \nabla \log \mathbb{Q}_{\beta_{\mathcal{T}}(t)|t}(\mathbf{X}_{\beta_{\mathcal{T}}(t)} | \mathbf{X}_t) - v_\theta(t, \mathbf{X}_t)|^2 dt], \quad (14)$$

where $\beta_{\mathcal{T}}(t) = \min_u \{u > t | t \in \mathcal{T}\} \in [0, T]$ is the most recent time point in $\mathcal{T}$ after time t . With this notation, the SBM can be generalized to the case of multi-marginal constraints. For example, when $\mathcal{T} = \{0, T\}$ then (14) reduces to the objective function described in [45].

The learned Markov control $v_{\theta^*}(t, \mathbf{x}_t)$ then ensures $\mathbb{P}_t^{\theta^*} = \Pi_t$ for all $t \in [0, T]$. Moreover, prior SBM algorithms interleave forward and backward-time Markov projections to re-anchor the terminal distribution and prevent bias between $\mathbb{P}_T^{(n)}$ and Π_T accumulate for each $n \in \mathbb{N}$. In the multi-marginal setting, we again build the backward-time Markov projection as in Proposition 2 by *gluing* the local bridge reversals, so that $\mathbb{P}^*$ is governed by both SDEs (10) and the corresponding backward dynamics:

$$d\mathbf{Y}_t^* = [-f_{T-t}(\mathbf{Y}_t^*) + \sigma u^*(t, \mathbf{Y}_t^*)] dt + \sigma d\mathbf{W}_t, \quad \mathbf{Y}_0^* \sim \Pi_T, \quad (15)$$

$$\text{where } u^*(t, \mathbf{y}) = \sum_{i=1}^k \mathbf{1}_{(t_{i-1}, t_i]}(t) \mathbb{E}_{\Pi_{t|t_{i-1}}} [\nabla \log \mathbb{Q}_{t|t_{i-1}}(\mathbf{Y}_t | \mathbf{Y}_{t_{i-1}}) | \mathbf{Y}_t = \mathbf{y}], \quad (16)$$

where the backward optimal control u^* in (16) can be approximated with neural network u_ϕ where ϕ is chosen to minimize the following training objective function with $\gamma_{\mathcal{T}}(t) = \max_u \{u < t | t \in \mathcal{T}\}$:

$$\mathcal{L}(\phi, \mathcal{T}, \Pi_{\mathcal{T}}) = \int_0^T \mathbb{E}_{\Pi_{t, \mathcal{T}}} [|\sigma \nabla \log \mathbb{Q}_{t|\gamma_{\mathcal{T}}(t)}(\mathbf{Y}_t | \mathbf{Y}_{\gamma_{\mathcal{T}}(t)}) - u_\phi(t, \mathbf{Y}_t)|^2 dt]. \quad (17)$$

4 Multi-Marginal Schrödinger Bridge Matching

A naïve extension of the standard SBM using, multi-marginal projections $\mathcal{R}^{\text{mm}}$ and $\mathcal{M}^{\text{mm}}$ in Sec 3, encounters significant limitations not present in the traditional two-endpoint setting. In such an extension, each iteration typically enforces marginal constraints only at the global endpoints (ρ_0, ρ_T) . The multi-marginal coupling $\Pi_{\mathcal{T}}^{(n)}$ at each iteration n of (13) is then derived by propagating the projected dynamics in (10) or (15) solely from these end points ρ_0 or ρ_T , respectively.

This approach leads to critical issues specific to the multi-marginal context. Firstly, if the learned controls, such as v^* (forward) or u^* (backward), are even slightly inaccurate, significant biases can arise between the inferred intermediate marginals $(\Pi_{t_1}^{(n)}, \dots, \Pi_{t_{k-1}}^{(n)})$ and the target marginals $(\rho_{t_1}, \dots, \rho_{t_{k-1}})$. Secondly, these discrepancies tend to accumulate iteratively. This accumulation is exacerbated because, beyond an initialization $\Pi^{(0)} = \mathbb{P}_{\mathcal{T}}^{(0)} \mathbb{Q}_{|\mathcal{T}}$ with $\mathbb{P}_{\mathcal{T}}^{(0)}$, independent joint coupling of $\{\rho_t\}_{t \in \mathcal{T}}$, where the joint distribution might be informed by all prescribed data distributions, the subsequent self-refinement process for the dynamics often does not directly incorporate the

Algorithm 1 Training of MSBM

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1: Input: Snapshots  $\{\rho_t\}_{t \in \mathcal{T}}$ , bridge  $\mathbb{Q}_{|\mathcal{T}}, N \in \mathbb{N}$ 
2: Let  $\{\mathbb{P}_{\mathcal{T}_i}^{(0)}\}_{i \in [1:k]}$  joint coupling of  $\{\rho_{t \in \mathcal{T}_i}\}_{i \in [1:k]}$ .
3: for  $n \in \{0, \dots, N-1\}$  do
4:   for  $i \in \{1, \dots, k-1\}$  do in parallel
5:     Let  $\Pi_{\mathcal{T}_i}^{(2n)} = \mathbb{P}_{\mathcal{T}_i}^{(2n)}$ 
6:     Estimate  $\mathcal{L}(\phi, \mathcal{T}_i, \Pi_{\mathcal{T}_i}^{(2n)}, \mathbb{Q}_{|\mathcal{T}_i})$ 
7:     Estimate  $\tilde{\mathcal{L}}(\phi) = \sum_{i=1}^k \mathcal{L}(\phi, \mathcal{T}_i, \Pi_{\mathcal{T}_i}^{(2n)}, \mathbb{Q}_{|\mathcal{T}_i})$ 
8:      $u_{\phi^*} = \arg \min_{\phi} \sum_{i=1}^k \tilde{\mathcal{L}}(\phi)$ 
9:     Simulate local backward SBs  $\{\mathbb{P}^{i, (2n+1)}\}_{i \in [1:k]}$ 
10:    for  $i \in \{1, \dots, k-1\}$  do in parallel
11:      Let  $\Pi_{\mathcal{T}_i}^{(2n+1)} = \mathbb{P}_{\mathcal{T}_i}^{(2n+1)}$ 
12:      Estimate  $\mathcal{L}(\theta, \mathcal{T}_i, \Pi_{\mathcal{T}_i}^{(2n+1)}, \mathbb{Q}_{|\mathcal{T}_i})$ 
13:      Estimate  $\tilde{\mathcal{L}}(\theta) = \sum_{i=1}^k \mathcal{L}(\theta, \mathcal{T}_i, \Pi_{\mathcal{T}_i}^{(2n+1)}, \mathbb{Q}_{|\mathcal{T}_i})$ 
14:       $v_{\theta^*} = \arg \min_{\theta} \sum_{i=1}^k \tilde{\mathcal{L}}(\theta, \mathcal{T}_i, \Pi_{\mathcal{T}_i}^{(2n+1)})$ 
15:      Simulate local forward SBs  $\{\mathbb{P}^{i, (2n+2)}_{[t_{i-1}, t_i]}\}$ 
16:    end for
17: Output:  $v_{\theta^*}, u_{\phi^*}$ 

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Algorithm 2 Simulation of MSBM (forward)

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Input: Initial  $\rho_0$ , learned control  $v_{\theta^*}$ 
Sample  $\mathbf{X}_0 \sim \rho_0$ 
Simulate forward SDE over  $[0, T]$ 
 $d\mathbf{X}_t^* = [f_t + \sigma v_{\theta^*}(t, \mathbf{X}_t^*)] dt + \sigma d\mathbf{W}_t$ ,
Output: Trajectory  $\mathbf{X}_{[0, T]}^*$ 

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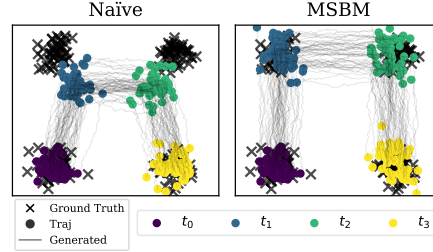


Figure 1: **(Left)** The naïve extension fails to model intermediate states due to the accumulation of errors. **(Right)** In contrast, MSBM successfully models the ground truth data.

intermediate data distributions $(\rho_{t_1}, \dots, \rho_{t_{k-1}})$ into its training objective except ρ_0 and ρ_T . Without explicit targets for the intermediate marginals guiding each iteration, the inferred paths between ρ_0 and ρ_T can “collapse” or drift away from the desired states. Consequently, precisely satisfying all intermediate constraints becomes increasingly challenging as iterations proceed.

To address this issue of error accumulation and ensure all marginal constraints $\{\rho_t\}_{t \in \mathcal{T}}$ are satisfied, we propose a method that involves constructing local SBs on each interval $[t_{i-1}, t_i]$ and then seamlessly *gluing* them together. Instead of propagating dynamics from the global endpoints ρ_0 and ρ_T alone, our approach first establishes local SBs for each segment. The resulting local couplings are then systematically integrated to satisfy all specified marginal distributions $\{\rho_t\}_{t \in \mathcal{T}}$ across the entire time interval $[0, T]$. This local construction strategy helps prevent the compounding of errors at intermediate time points while still aiming to achieve the overall multi-marginal SB solution, $\mathbb{P}^{\text{mSBP}}$. The theoretical basis is provided by the following result.

Corollary 5 (Multi-Marginal Schrödinger Bridge). *Assume a sequence of controls $\{v^i, u^i\}_{i \in [1:k]}$, where each v^i, u^i induced local SBs $\mathbb{P}^i$ of **SBP** over local interval $[t_{i-1}, t_i]$ with distributions $(\rho_{t_{i-1}}, \rho_{t_i})$ in a forward and backward direction, respectively. If $\lim_{t \uparrow t_i} v^i(t, \mathbf{x}) = v^{i+1}(t, \mathbf{x})$ and $\lim_{t \downarrow t_{i-1}} u^i(t, \mathbf{x}) = u^{i-1}(t, \mathbf{x})$ for all $i \in [1:k]$, then $\mathbb{P}^{\text{mSBP}}$ of **mSBP** induced by following SDEs:*

$$d\mathbf{X}_t^* = [f_t(\mathbf{X}_t^*) + \sigma v^*(t, \mathbf{X}_t^*)] dt + \sigma d\mathbf{W}_t, \quad \mathbf{X}_0^* \sim \rho_0. \quad (18a)$$

$$d\mathbf{Y}_t^* = [-f_{T-t}(\mathbf{Y}_t^*) + \sigma u^*(t, \mathbf{Y}_t^*)] dt + \sigma d\mathbf{W}_t, \quad \mathbf{Y}_0^* \sim \rho_T, \quad (18b)$$

$$\text{where } v^*(t, \mathbf{x}) = \sum_{i=1}^k \mathbf{1}_{[t_{i-1}, t_i]}(t) v^i(t, \mathbf{x}), \quad u^*(t, \mathbf{x}) = \sum_{i=1}^k \mathbf{1}_{(t_{i-1}, t_i]}(t) u^i(t, \mathbf{x}). \quad (18c)$$

Building upon Corollary 5, we introduce our Multi-Marginal Schrödinger Bridge Matching (MSBM) method to solve the **mSBP**. A cornerstone of MSBM is divide the global **mSBP** into local **SBPs** while maintaining the continuity of the composite drift functions v^* and u^* in (18c) across adjacent intervals, which guarantees a globally continuous diffusion process inducing $\mathbb{P}^{\text{mSBP}}$. Furthermore, by explicitly constraining each local SBs, $\mathbb{P}^i$, on its corresponding marginals $(\rho_{t_{i-1}}, \rho_{t_i})$, MSBM is designed to mitigate the accumulation of bias at intermediate marginals, as shown in Figure 1.

A key challenge of the MSBM is rigorously satisfying the continuity conditions at the boundaries of local controls: $\lim_{t \uparrow t_i} v^i(t, \mathbf{x}) = v^{i+1}(t, \mathbf{x})$ and $\lim_{t \downarrow t_{i-1}} u^i(t, \mathbf{x}) = u^{i-1}(t, \mathbf{x})$ for all $i \in [1:k]$. If these conditions are not met, discontinuities or “kinks” can arise at the intermediate time steps. Such kinks would imply that the overall path measure $\mathbb{P}^* \neq \mathcal{M}^{\text{mm}}(\mathbb{P}^*, \mathcal{T})$. This would, in turn, hinder the optimality for **mSBP**, because, following Proposition 3, the desired continuous Markov process is a fixed point of both $\mathcal{R}^{\text{mm}}$ and Markov projections $\mathcal{M}^{\text{mm}}$ under multiple time points $\mathcal{T}$:

$$\mathbb{P}^* = \mathcal{R}^{\text{mm}}(\mathbb{P}^*, \mathcal{T}) = \mathcal{M}^{\text{mm}}(\mathbb{P}^*, \mathcal{T}). \quad (19)$$

228 To construct local SBs such that the continuity requirements for forming a valid global solution are
 229 met, thereby preventing the aforementioned kinks and ensuring (19), our MSBM introduces a shared
 230 global parametrization v_θ, u_ϕ for its respective local controls $\{v^i, u^i\}_{i \in [1:k]}$ for each sub-interval,
 231 where each local controls are parallel updated with following aggregate objective function:

$$\tilde{\mathcal{L}}(\theta) = \sum_{i=1}^k \mathcal{L}(\theta, \mathcal{T}_i, \Pi_{\mathcal{T}_i}), \quad \tilde{\mathcal{L}}(\phi) = \sum_{i=1}^k \mathcal{L}(\phi, \mathcal{T}_i, \Pi_{\mathcal{T}_i}), \quad (20a)$$

232 where $\mathcal{T}_i = \{t_{i-1}, t_i\}$ define sub-intervals with local coupling $\Pi_{\mathcal{T}_i}$ for end-points marginals in
 233 interval $[t_{i-1}, t_i]$ and $\mathcal{L}$ is defined in (14) and (17) for forward and backward direction, respectively.

234 The MSBM training procedure, summarized in Algorithm 1, adapts the standard IMF algorithm
 235 presented in [45, Algorithm 1]. A key distinction in our MSBM approach is the parallel application
 236 of the IMF procedure to each local time interval, utilizing globally shared forward v_θ and backward
 237 u_ϕ across all local intervals. This parallel processing across sub-intervals contributes to a significant
 238 reduction in overall training time.

239 5 Related Work

240 The solution of SBP often utilize Iterative Proportional Fitting (IPF) [19], with modern adaptations
 241 learning SDE drifts for two-marginal settings [4, 9, 13, 49]. A distinct iterative approach, IMF, as
 242 featured in [37, 45], offers improved stability by alternating projections onto different classes of
 243 path measures. Moreover, emerging research also explores non-iterative algorithm [12, 38]. These
 244 methodologies primarily concentrate on the SB problem itself, iteratively refining path measures or
 245 directly computing the bridge measure. Moreover, the SB algorithm is studied under the assumption
 246 that the optimal coupling is given [27, 46]. While recent studies have extended foundational SB ideas
 247 to the multi-marginal setting of mSBP, research in this area remains relatively limited.

248 In multi-marginal setting, [8] extends the problem to phase space to encourage smoother trajectories
 249 and introduces a novel training methodology inspired by the Bregman iteration [5] to handle multiple
 250 marginal constraints. Relatedly, [44] presented an approach that, similar to our work, segments the
 251 problem across intervals; they learn piecewise SBs and use likelihood-based training to iteratively
 252 refine a global reference dynamic. While these methods are often IPF-based or focus on specific
 253 reference refinement strategies, our MSBM extends the previous IMF-type algorithm into multi-
 254 marginal setting and effectively handles multiple constraints. We demonstrate that our MSBM
 255 framework offers substantial gains in training efficiency. This enhanced efficiency is primarily
 256 attributed to its direct multi-marginal formulation that adeptly manages multiple constraints, thereby
 257 circumventing the computationally intensive iterative refinements common in IPF-based methods

258 Paralleling these SB-centric developments, other significant lines of work model dynamic trajectories
 259 by directly learning potential functions or velocity fields, often drawing from optimal transport
 260 or continuous normalizing flows. For instance, [18, 24–26] extend SBs to incorporate potentials
 261 or mean-field interactions, connecting to stochastic optimal control and earlier mean-field game
 262 frameworks [22, 41]. The broader field of trajectory inference from snapshot data, crucial for
 263 applications like scRNA-seq, has seen methods like [48] using CNFs with dynamic OT, and [15]
 264 employing Neural ODEs on learned data manifolds. More recently, [33, 34] offer variational
 265 objectives to learn dynamics from marginal samples.

266 6 Experiments

267 In this section, we empirically demonstrate the effectiveness of our MSBM. Specifically, our goal
 268 is to infer a dynamic model from datasets composed of samples from marginal distributions ρ_t
 269 observed at discrete time points. We evaluate MSBM on both synthetic datasets and real-world single-
 270 cell RNA sequencing datasets, including human embryonic stem cells (hESC) [11] and embryoid
 271 body (EB) [32]. To ensure consistency and fair comparison, our experiments follow the respective
 272 experimental setups established by baseline methods. In particular, for the petal dataset, we adopt
 273 the experimental setup from DMSB [8], and for the hESC dataset, we follow SBIRR [44]. For
 274 the EB dataset, we perform evaluations on both 5-dim and 100-dim PCA-reduced data; here, we
 275 follow the 100-dim experimental setup of DMSB and the 5-dim setup from NLSB [18]. Accordingly,

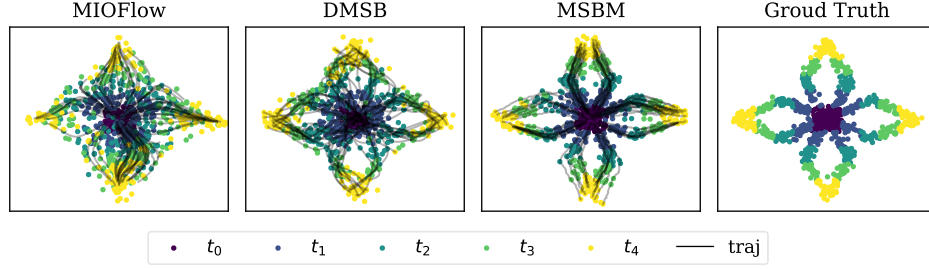


Figure 3: Comparison of generated population dynamics using MIOFlow, DMSB and MSBM on a 2-dim petal dataset. All trajectories are generated by simulating the dynamics from ρ_{t_0} .

we utilize evaluation metrics consistent with previous studies, including the Sliced-Wasserstein Distance (SWD)[2], Maximum Mean Discrepancy (MMD)[14], as well as the 1-Wasserstein ($\mathcal{W}_1$) and 2-Wasserstein ($\mathcal{W}_2$) distances. All experimental results reported are averaged mean value over three independent runs with different random seeds. We highlight the best-performing results in **bold** and the second-best results in **blue**. Further experimental details are provided in Appendix C.

6.1 Synthetic Data

Petal The petal dataset [15] serves as a simple yet complex challenge because it mimics the natural dynamics seen in processes such as cellular differentiation, which include phenomena like bifurcations and merges. We compare our MSBM with MIOFlow [15] and DMSB [8] in Figure 2. As shown in Figure 3, we observe that MSBM exhibits the most accurate and clearly defined trajectory, closely resembling the ground truth. Furthermore, Figure 2 demonstrates the evaluation results for the trajectories through $\mathcal{W}_2$ and MMD distances, highlighting that MSBM consistently outperforms MIOFlow and DMSB.

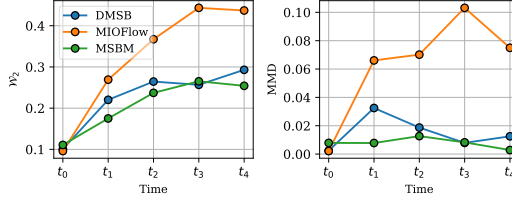


Figure 2: Evaluation results of $\mathcal{W}_2$ and MMD.

6.2 Single-cell Sequencing Data

We evaluated our MSBM on real-world single-cell RNA sequencing data from two sources: **1)** human embryonic stem cells (hESCs) [11] undergoing differentiation into definitive endoderm over a 4-day period, measured at 6 distinct time points (t_0 :0 hours, t_1 :12 hours, t_2 :24 hours, t_3 :36 hours, t_4 :72 hours, and t_5 :96 hours); **2)** embryoid body (EB) cells [32] differentiating into mesoderm, endoderm, neuroectoderm, and neural crest over 27 days, with samples collected at 5 time windows (t_0 :0-3 days, t_1 :6-9 days, t_2 :12-15 days, t_3 :18-21 days, and t_4 :24-27 days). Following the experimental setup of baselines, we preprocessed these datasets using the pipeline outlined in [48], and the collected cells were projected into a lower-dimensional space using principal component analysis (PCA).

hESC To follow the experimental setup from SBIRR [44], we reduced the data to the first five principal components and excluded the final time point t_6 from our dataset, resulting in three training time points $\mathcal{T} = \{t_0, t_2, t_4\}$ and two intermediate test points $\mathcal{T}_{\text{test}} = \{t_1, t_3\}$. Our objective was to train the dynamics based on the available marginals at the training points in $\mathcal{T}$ and interpolate the intermediate test marginals at $\mathcal{T}_{\text{test}}$, which were not observed during training. Table 1 demonstrates that our proposed MSBM method performs competitively, achieving lower $\mathcal{W}_2$ distances.

Embryoid Body We validate our MSBM on both 5-dim and 100-dim PCA spaces. First, for the 5-dim experiment, we adopt the experimental setup from NLSB. Given 5 observation time points $\mathcal{T} = \{t_0, t_1, t_2, t_3, t_4\}$, we divide the data using train/test splits $\rho_{\mathcal{T}}^{\text{tr}}/\rho_{\mathcal{T}}^{\text{te}}$, with the goal of predicting population-level dynamics from $\rho_{t_0}^{\text{tr}}$. Similar to NLSB, we train the dynamics based on $\rho_{t_0}^{\text{tr}}$ and

Table 1: Performance on the 5-dim PCA of hESC dataset. $\mathcal{W}_2$ is compute between test ρ_{t_i} and generated $\hat{\rho}_{t_i}$ by simulating the dynamics from test ρ_{t_0} .

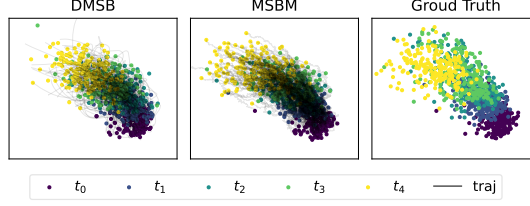
Methods	$\mathcal{W}_2 \downarrow$		Runtime
	t_1	t_3	hours
TrajectoryNet [†]	1.30	1.93	10.19
DMSB [†]	1.10	1.51	15.54
SBIRR [†]	1.08	1.33	0.36 (0.38)*
MSBM (Ours)	1.09	1.30	0.09

[†] result from [44].

Table 3: Performance on the 100-dim PCA of Figure 4: Comparison of generated population dy-EB dataset. MMD and SWD are computed between test $\rho_{t_i}^{\text{te}}$ and generated $\hat{\rho}_{t_i}$ by simulating of EB dataset. The plot displays the first two principal components as the x and y axes, respectively.

Methods	MMD ↓				SWD ↓			
	Full	t_1	t_2	t_3	Full	t_1	t_2	t_3
NLSB [†] [18]	0.66	0.38	0.37	0.37	0.54	0.55	0.54	0.55
MIOFlow [†] [15]	0.23	0.23	0.90	0.23	0.35	0.49	0.72	0.50
DMSB [†] [8]	0.03	0.04	0.04	0.04	0.16	0.20	0.19	0.18
MSBM	0.02	0.04	0.04	0.05	0.11	0.18	0.17	0.19

† result from [8].



316 evaluate the $\mathcal{W}_1$ distance between $\rho_{t_i}^{\text{te}}$ and the generated $\hat{\rho}_{t_i}$ from previous test snapshot $\rho_{t_{i-1}}^{\text{te}}$.
 317 In Table 2, we find that MSBM outperforms several SB methods.

318 For the 100-dim experiment, we borrow the experimental
 319 setup from DMSB, where the goal is predict population
 320 dynamics given that observations are available for all time
 321 points $\mathcal{T}$ (denoted as Full in Table 3), or when one of
 322 the snapshot is left out (denoted as t_i in Table 3, where
 323 snapshot $\rho_{t_i}^{\text{tr}}$ at t_i is excluded during training). The high
 324 performance in this task represent the robustness of the
 325 model to accurately predict population dynamics. In Table
 326 3, MSBM consistently yields performance improvements.
 327 Moreover, as shown in Figure 4, the trajectories
 328 and generated marginal distributions $\hat{\rho}_{\mathcal{T}}$ in PCA space further
 329 justifies the numerical result and highlights the variety
 330 and quality of the samples produced by MSBM.

331 **Computational Efficiency** For an fair comparison of
 332 training efficiency against recent multi-marginal SB al-
 333 gorithms, we benchmarked DMSB and SBIRR on the identical hardware configuration employed
 334 for MSBM (denoted by * in Table 1). On the hESC dataset, MSBM achieved a runtime over 4×
 335 faster than SBIRR. Furthermore, on the petal and 100-dim PCA of EB dataset, MSBM significantly
 336 outperformed DSMB in training speed, with detailed results presented in Figure 5.

337 This enhanced computational efficiency primarily originates from
 338 core algorithmic differences. SBIRR, for example, utilizes maxi-
 339 mum likelihood training, which requires extensive gradient compu-
 340 tations and the storage of all intermediate paths. DMSB employs an
 341 IPF-type objective with Bregman Iteration [5]. In contrast, MSBM
 342 directly optimizes controls using an IMF-type objective, which not
 343 only eliminates the need to store intermediate states but also fa-
 344 cilitates parallel computation across sub-intervals. This approach
 345 substantially promotes faster convergence of the algorithm.

Table 2: Performance on the 5-dim PCA of EB dataset. $\mathcal{W}_1$ is computed between test $\rho_{t_i}^{\text{te}}$ and generated $\hat{\rho}_{t_i}$ by simulating the dynamics from previous test $\rho_{t_{i-1}}^{\text{te}}$.

Methods	$\mathcal{W}_1$ ↓				
	t_1	t_2	t_3	t_4	Mean
Neural SDE [†] [21]	0.69	0.91	0.85	0.81	0.82
TrajectoryNet [†] [48]	0.73	1.06	0.90	1.01	0.93
IPF (GP) [†] [49]	0.70	1.04	0.94	0.98	0.92
IPF (NN) [†] [4]	0.73	0.89	0.84	0.83	0.82
SB-FBSDE [†] [9]	0.56	0.80	1.00	1.00	0.84
NLSB [†] [18]	0.68	0.84	0.81	0.79	0.78
OT-CFM [†] [47]	0.78	0.76	0.77	0.75	0.77
WLF-SB [‡] [34]	0.63	0.79	0.77	0.75	0.73
MSBM (Ours)	0.64	0.73	0.72	0.73	0.71

† result from [18], ‡ result from [34].

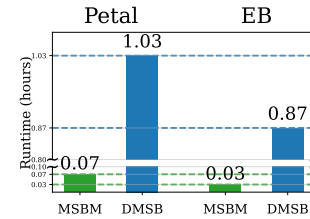


Figure 5: Training time

346 7 Conclusion and Limitation

347 This paper revisits previously established frameworks for the **SBP**, extending them to the **mSBP**.
 348 Specifically, we introduce a computationally efficient framework for **mSBP**, termed **MSBM**, which
 349 builds upon existing **SBM** methods [37, 45]. **MSBM** is tailored for various trajectory inference
 350 problems where snapshots of data are available at multi-marginal time steps. Through the successful
 351 adaptation of the IMF algorithm to this multi-marginal setting, our approach significantly accelerates
 352 training processes while ensuring accurate dynamic modeling when compared to existing methods.

353 Despite these advantages, the performance degradation of **MSBM** is more pronounced than that
 354 of **DMSB** when a time point is omitted in Table 3. This may occur because the including velocity
 355 term could better accommodate unknown trajectory. Furthermore, the current **MSBM** framework
 356 is restricted to the case involving snapshot data samples, highlighting a need for enhancements to
 357 address problems with continuous potentials, such mean-field games [18, 24–26].

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