DNAEdit: Direct Noise Alignment for Text-Guided Rectified Flow Editing

Chenxi Xie[1,2,⋆], **Minghan Li**[3,⋆], **Shuai Li**[1], **Yuhui Wu**[1,2], **Qiaosi Yi**[1,2], **Lei Zhang**[1,2,†]
[1]The Hong Kong Polytechnic University, [2]OPPO Research Institute,
[3]Harvard University
chenxi.xie@connect.polyu.hk mili4@meei.harvard.edu cslzhang@comp.polyu.edu.hk
⋆Equal contribution †Corresponding author
Project Page: https://xiechenxi99.github.io/DNAEdit/

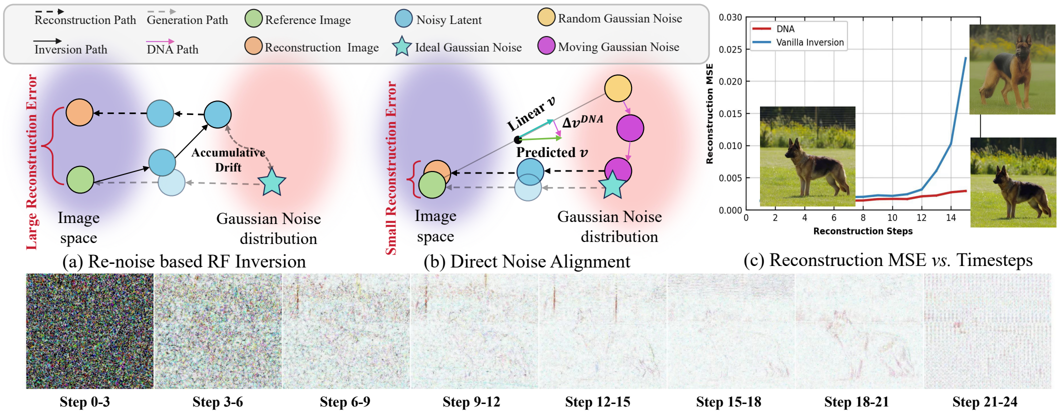
Abstract

Leveraging the powerful generation capability of large-scale pretrained text-to-image models, training-free methods have demonstrated impressive image editing results. Conventional diffusion-based methods, as well as recent rectified flow (RF)-based methods, typically reverse synthesis trajectories by gradually adding noise to clean images, during which the noisy latent at the current timestep is used to approximate that at the next timesteps, introducing accumulated drift and degrading reconstruction accuracy. Considering the fact that in RF the noisy latent is estimated through direct interpolation between Gaussian noises and clean images at each timestep, we propose Direct Noise Alignment (DNA), which directly refines the desired Gaussian noise in the noise domain, significantly reducing the error accumulation in previous methods. Specifically, DNA estimates the velocity field of the interpolated noised latent at each timestep and adjusts the Gaussian noise by computing the difference between the predicted and expected velocity field. We validate the effectiveness of DNA and reveal its relationship with existing RF-based inversion methods. Additionally, we introduce a Mobile Velocity Guidance (MVG) to control the target prompt-guided generation process, balancing image background preservation and target object editability. DNA and MVG collectively constitute our proposed method, namely DNAEdit. Finally, we introduce DNA-Bench, a long-prompt benchmark, to evaluate the performance of advanced image editing models. Experimental results demonstrate that our DNAEdit achieves superior performance to state-of-the-art text-guided editing methods. Our code, model, and benchmark will be made publicly available.

1 Introduction

Recent advances in text-to-image (T2I) generation have been driven by Rectified Flow (RF)-based models [12, 11], which significantly reduce sampling timesteps, enabling faster generation. Leveraging large-scale T2I models such as SD3 [3] and FLUX [8], training-free text-guided image editing methods [17, 22, 7, 30] can achieve high-quality editing results with fewer sampling steps. Existing RF-based editing methods [17, 7, 2, 22, 25, 27, 30] typically follow earlier Diffusion Model (DM)-based editing approaches [15, 6, 14], first reversing the generative trajectory by gradually adding noise to the clean image, obtaining an inverted noise and then re-denosing it under new conditions to generate the edited image, as shown by the black path in Fig. 1 (a). The inverted noise is critical for the preservation of fidelity, as it retains the structural information of the reference image, ensuring consistency between the edited and the reference images. However, this inversion process introduces

This work is supported by the PolyU-OPPO Joint Innovative Research Center.



(a) Re-noise based RF Inversion

(b) Direct Noise Alignment

(c) Reconstruction MSE *vs.* Timesteps

(d) Visualization of Moving Noise Difference in DNA Process

Figure 1: Illustration of (a) existing re-noise based RF inversion methods and (b) our DNA. The ideal Gaussian noise refers to the noise that can exactly reproduce the reference image. (c) The curves of reconstruction MSE *vs.* timesteps for DNA and re-noise based RF inversion. (d) Visualization of the difference in Gaussian noise between steps.

accumulated drifts that significantly degrade reconstruction accuracy and editing fidelity. These drifts arise because the noise latent at the current timestep is unavailable and it has to be approximated using the noise latents from the previous timesteps. The approximated latent is then used to estimate the velocity field for inversion, resulting in shifted velocity fields. As the process continues, the drifts accumulate, leading to significant distortions in the final noise.

Existing RF-based methods [17, 2, 13, 22, 25] aim to reduce the drift to improve editing fidelity. For example, RF-inversion [17] employs two conditional velocity fields: one for inversion (conditioned on Gaussian noise) and one for editing (conditioned on the source image). However, its global application of guidance ignores region specificity, often degrading edit quality. Subsequent methods [2, 22, 13], such as RF-solver [22], refine the discretization process using higher-order ordinary differential equation (ODE) solvers, often combined with attention injection during editing to enhance fidelity. More recently, FTEdit [25] reduces errors by performing iterative average at each inversion timestep, increasing the number of sampling steps. While these approaches reduce errors through finer discretization of the reverse ODE process, they incur additional Neural Function Evaluations (NFEs), decreasing the efficiency. Despite offering slight improvements over RF inversion, these methods remain inefficient and struggle to mitigate the accumulation and amplification of drift.

Actually, existing editing methods overlook the unique properties of RF. Unlike DM, RF models the generation process as a straight trajectory between noise and image, allowing noise latent to be derived via linear interpolation at each timestep. Keeping this in mind, let us revisit the editing process. Note that inversion aims to estimate a noise sample that corresponds to the reference image, enabling an accurate reconstruction of it during sampling. In RF, a better noise sample means a more direct path between the noise and the reference image. Based on this, an intuitive question is: *can we directly refine the desired noise sample in the Gaussian noise domain, rather than gradually transforming the image into noise?* To answer this question, we propose a novel method in this work, called **D**irect **N**oise **A**lignment **Edit**ing (**DNAEdit**). Unlike gradually transforming an image back to Gaussian noise, *DNAEdit directly refines the randomly initialized noise in the Gaussian noise domain, gradually aligning it with a better target noise sample*, as shown in Fig. 1 (b).

To achieve Direct Noise Alignment (DNA), we start from a Gaussian noise sample and iteratively interpolate between it and the clean reference image at each timestep. As shown in Fig. 1 (b), the predicted velocity field often deviates from the expected one derived from linear interpolation. DNA, thus, corrects it by feeding the deviation back into the noise, refining the trajectory. We visualize the changes during the DNA process in Fig. 1 (d). These changes contain the structure of the original image, indicating that the original content is gradually infused into the initial random noise, resulting structured noise. This process produces straighter paths and reduces the accumulated error by avoiding dependence on previous random noise and latents. Finally, the noise converges to a sample that is well aligned with the reference image, as verified by the reconstruction MSE in

Fig. 1(c). We also provide a theoretical analysis showing that DNA shares the same principle with RF-based methods in the **Appendix**.

To better balance editability and fidelity, we introduce a Mobile Velocity Guidance (MVG) to guide denoising by computing the difference between source- and target-conditioned velocity fields in the image domain, which yields a smooth transition from source to target images. In addition, existing benchmarks [6, 10, 28, 16] focus on short prompts, limiting semantic richness. To address this, we introduce **DNA-Bench**, a long-prompt benchmark to evaluate RF editing under detailed textual guidance. Experiments on PIE-Bench and DNA-Bench show that our DNAEdit method strikes a better balance between fidelity and editability, demonstrating the best performance.

2 Related Work

Inversion for Image Editing. Inversion seeks to transform an image into a corresponding Gaussian noise. A successful inversion generates an initial noise vector that can accurately recreate the reference image, which is essential for further editing. According to DDIM [18], the initial noise can be gradually obtained by iteratively adding predicted noise, but the approximation error can accumulate over timesteps. Various strategies have been developed to address this issue. Null-text inversion [15] optimizes null text embeddings at each inversion step, but it is inefficient. Negative-prompt-inversion improves efficiency by replacing null texts with negative prompts. Unlike DMs, RF has a notably straighter generation path. However, current RF inversion methods still adhere to DM principles, reversing the ODE to gradually add noise. RF inversion [17] aims to tackle this issue by optimizing the reverse ODE process using dynamic optimal control through a linear quadratic regulator to balance editability and fidelity. RF-solver [22] and FireFlow [2] use higher-order solvers to better approximate the reverse ODE and reduce errors at each step. FEEdit [7] employs a fixed-point iteration strategy, refining the added noise and averaging it to suppress approximation errors. Although these approaches can reduce reconstruction error to some extent, they all follow the iterative re-noising paradigm, making error accumulation inevitable. In contrast, our proposed DNA framework directly aligns the noisy latent with the ideal noise derived from model priors within the noise space, significantly reducing the error accumulation.

Rectified Flow-based Editing. Compared to DM-based editing methods [1, 21, 4, 5], RF-based editing methods are not fully explored. Unlike most DM models that use the U-Net architecture, RF models [8, 3] primarily use the MM-DiT architecture, which makes strategies relying on U-Net's cross-attention map unsuitable for RF-based editing methods. Some approaches [2, 22] adapt the attention injection scheme to maintain fidelity during editing. Other methods [25] focus on the exchange of text-image information in MM-DiT, manipulating features through AdaLN to control the editing process. While these methods have achieved certain success, they often require additional adaptations for different RF models, limiting their applicability. Some model-agnostic methods have also been developed. FlowEdit [7] uses an inversion-free approach by calculating the difference between the source and the target velocity fields, enabling direct image editing in the image space. However, this method relies on editing the velocity difference of the reference image and restricts the range of editable space, making it difficult to perform global editing tasks (*e.g.*, changing style). Our DNAEdit employs two model-agnostic processes: DNA and MVG. DNA minimizes cumulative error and obtain a better initial Gaussian noise aligned with the source text. MVG guides the editing process to preserve background fidelity while minimizing compromise on editability.

3 Direct Noise Alignment Editing (DNAEdit)

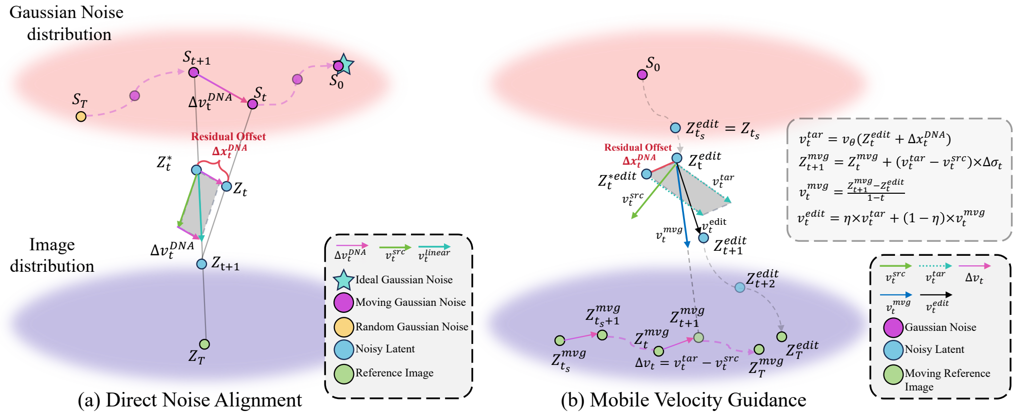
3.1 Approximation Errors in RF Inversion

Preliminary. Rectified Flow (RF) [12, 11] models the transition between two observed distributions π_0 and π_1 using an ordinary differential model (ODE):

$$\mathrm{d}Z_t = v_\theta(Z_t)\mathrm{d}t, \quad Z_0 \sim \pi_0,\ Z_1 \sim \pi_1,\ t \in [0, 1], \tag{1}$$

where $v_\theta(\cdot)$ is the learnable velocity field parameterized by θ. To encourage a near-linear trajectory of the transition, RF employs the following objective to train v_θ:

$$\min_\theta \int_0^1 \mathbb{E}[\|(Z_1 - Z_0) - v_\theta(Z_t)\|^2]\mathrm{d}t, \quad Z_t = tZ_1 + (1-t)Z_0, \tag{2}$$



(a) Direct Noise Alignment

(b) Mobile Velocity Guidance

Figure 2: Illustration of (a) DNA and (b) MVG, which collectively build our DNAEdit algorithm.

where Z_t denotes the linear interpolation between $Z_0 \sim \pi_0$ and $Z_1 \sim \pi_1$.

Approximation Errors in Inversion. The denoising process maps the standard Gaussian distribution ($\pi_0 = \mathcal{N}(0, 1)$) to the image distribution π_1, while its reverse maps π_1 back to π_0. To solve the ODE in Eq. (1), the time interval $[0, 1]$ is discretized into T steps, denoted as $\{\sigma_0, \dots, \sigma_T\}$. The Euler solver is used to approximate the solution, with the forward and reverse steps given by:

$$\mathbf{Fwd}: \; Z_{t+1} = Z_t + v_\theta(Z_t)(\sigma_{t+1} - \sigma_t), \quad \mathbf{Inv}: \; Z_t = Z_{t+1} - v_\theta(Z_t)(\sigma_{t+1} - \sigma_t), \tag{3}$$

where the timestep index increases from 0 to T in the forward process and decreases from T to 0 in the reverse process. It is evident that in the reverse process, at each step only the noisy latent Z_{t+1} is available, while Z_t, the desired output, is unknown. Consequently, the velocity field $v_\theta(Z_t)$ in Eq. (3) cannot be directly evaluated, making the exact inversion intractable.

Considering that the differences between the noisy latents of adjacent timesteps are relatively small, existing RF inversion methods [2, 22, 17, 25] approximate the velocity field at timestep t by evaluating it at timestep $t + 1$, leading to the following inversion formula:

$$\mathbf{Inv\ approx}: v_\theta(Z_t) \approx v_\theta(Z_{t+1}), \quad Z_t \approx Z_{t+1} - v_\theta(Z_{t+1})(\sigma_{t+1} - \sigma_t). \tag{4}$$

However, due to the sequential nature of the inversion process, approximation errors at each step will accumulate over time, resulting in a final latent that can deviate significantly from the expected Gaussian noise (see Fig. 1 (a)). Furthermore, the noise sample obtained through this approximated inversion is not guaranteed to follow the standard Gaussian distribution, mismatching with the model assumption. As a result, the reconstructed or edited image (see Fig. 1 (c)) may be distorted or invalid.

3.2 Direct Noise Alignment (DNA)

Our DNAEdit method consists of two key components: DNA and MVG (see Section 3.3). DNA is used to obtain a structured noise sample, enhancing the fidelity of the editing process. The resulting noise is then re-denoised under the guidance of MVG to generate the final image. From the analysis in Section 3.1, we see that the primary source of error comes from the use of the noisy latent Z_{t+1} to replace Z_t to compute the velocity field: $v_\theta(Z_t) \approx v_\theta(Z_{t+1})$. Since the noise levels of Z_t and Z_{t+1} are different, this approximation introduces inconsistencies with the model prior.

Using RF, fortunately, the latent variables Z_t can be constructed via linear interpolation between the clean image and Gaussian noise. One can sample a noise $S \sim \mathcal{N}(0, 1)$ and interpolate it with the image. However, since S is randomly sampled, the resulting path may lead to reconstruction errors under text guidance. According to Eq. (2), there exists an optimal noise such that the RF-driven trajectory forms a nearly linear path to the reference image. Motivated by this, we propose *directly shifting the random noise toward the target noise in the Gaussian space over timesteps:* $S_T \sim \mathcal{N}(0, 1) \to S_{T-1} \to \cdots \to S_0$.

To achieve this goal, we need to devise an effective algorithm to optimize random Gaussian noise S_T. This can be done by aligning the velocity v_t^{src} predicted by the RF model with the expected

Algorithm 1 Direct Noise Alignment (DNA)

```
**Input**: Number of optimization steps $T$, Source image $Z_T$, Source text $\psi^{src}$, Timesteps $\{\sigma_t\}_{t=T}^{0}$, RF model $v_\theta$ with parameters $\theta$, Randomly sampled start noise $S_T \sim \mathcal{N}(0,1)$.
**Output**: Noisy latents $\{Z_t\}_{t=T-1}^{0}$ and residual offset $\{\Delta x_t^{\text{DNA}}\}_{t=T-1}^{0}$, Terminal noise sample $S_0$
for $t = T-1, ..., 1, 0$ do
    $Z_t^* \leftarrow Z_{t+1} \times \frac{\sigma_t}{\sigma_{t+1}} + S_{t+1} \times (1 - \frac{\sigma_t}{\sigma_{t+1}})$    ▷ Interpolate to get noisy latent $Z_t^*$
    $v_t^{\text{linear}} = (S_{t+1} - Z_{t+1})/\sigma_{t+1}$    ▷ Calculate the expected velocity on the linear path
    $v_t^{src} = v_\theta(Z_t^*, \psi^{src})$    ▷ Calculate the predicted velocity by SD3 or FLUX
    $\Delta v_t^{\text{DNA}} = v_t^{\text{linear}} - v_t^{src}$
    $S_t \leftarrow S_{t+1} + \Delta v_t^{\text{DNA}} \times \sigma_{t+1}$    ▷ Move Gaussian noise from $S_{t+1}$ to $S_t$
    $Z_t \leftarrow Z_t^* + \Delta v_t^{\text{DNA}} \times (\sigma_{t+1} - \sigma_t)$    ▷ Move interpolated latent from $Z_t^*$ to $Z_t$
    $\Delta x_t^{\text{DNA}} = Z_t^* - Z_t$    ▷ Compute the residual offset
end for
return $S_0$, $\{Z_t\}_{t=T-1}^{0}$ and $\{\Delta x_t^{\text{DNA}}\}_{t=T-1}^{0}$
```

velocity v_t^{linear} along the linear path from Gaussian noise to image latent. Specifically, at timestep t, we construct the linear path from noise S_{t+1} to latent Z_{t+1} and obtain latent Z_t^* by interpolation:

$$Z_t^* = \frac{\sigma_t}{\sigma_{t+1}} \times Z_{t+1} + (1 - \frac{\sigma_t}{\sigma_{t+1}}) \times S_{t+1}. \tag{5}$$

The estimated noisy latent Z_t^* is obtained via direct interpolation, eliminating the need to approximate it using Eq. (4). We then compute the velocity field Z_t^* using the RF model as $v_t^{\text{src}} = v_\theta(Z_t^*, \psi^{\text{src}})$, and define the expected velocity along the linear path as $v_t^{\text{linear}} = (S_{t+1} - Z_{t+1})/\sigma_{t+1}$. However, as shown in Fig. 2(a), a discrepancy arises between v_t^{linear} and v_t^{src} due to the offset between the actual noise S_{t+1} and the noise S_t derived by the predicted velocity. We denote this mismatch as the velocity gap Δv_t^{DNA}, and correct it by shifting the noise from S_{t+1} to S_t:

$$\Delta v_t^{\text{DNA}} = v_t^{\text{linear}} - v_t^{src}, \quad S_t = S_{t+1} + \Delta v^{\text{DNA}} \times \sigma_{t+1}. \tag{6}$$

As the noise moves to S_t, the interpolated noisy latent Z_t^* in Eq. (5) can be refined to a better estimate $Z_t = \frac{\sigma_t}{\sigma_{t+1}} \times Z_{t+1} + (1 - \frac{\sigma_t}{\sigma_{t+1}}) \times S_t$. It can be easily derived that the updated linear velocity $v_t^{\text{linear}} = (S_t - Z_{t+1})/\sigma_{t+1}$ matches the predicted velocity $v_\theta(Z_t^*, \psi^{src})$. The difference between the updated latent Z_t and the initial estimate Z_t^* can be expressed as:

$$Z_t - Z_t^* = \frac{\sigma_{t+1} - \sigma_t}{\sigma_{t+1}} \times (S_t - S_{t+1}). \tag{7}$$

By substituting Eq. (6) into Eq. (7), we can derive that $Z_t = Z_t^* + \Delta v^{\text{DNA}} \times (\sigma_{t+1} - \sigma_t)$. Eq. (7) implies that although the random Gaussian noise S_T may initially deviate from the ideal Gaussian noise, the difference will become much smaller for interpolated latent Z_t due to the small scaling coefficient $(\sigma_{t+1} - \sigma_t)/\sigma_{t+1}$, where $\sigma_{t+1} : 1 \to 0$. Therefore, it can be deduced that $v_\theta(Z_t, \psi^{src}) \approx v_\theta(Z_t^*, \psi^{src})$. Starting from Z_t, the predicted velocity field can lead to Z_{t+1} with a small error. Eq. (7) suggests aligning from large to small timesteps to avoid early errors, so we iteratively adjust noise from σ_T to σ_0. We also show that the residual offset $\Delta x_t^{\text{DNA}} = Z_t^* - Z_t$ allows exact reconstruction. Adding it back to Z_t, we recover Z_t^* and compute $v_\theta(Z_t^*, \psi^{\text{src}})$ for precise updates from Z_t to Z_{t+1}. The algorithm is presented in Algorithm 1, and a theoretical analysis between DNA and existing RF-based methods is provided in the **Appendix**.

3.3 Mobile Velocity Guidance (MVG)

Although DNA can estimate a noise sample with small reconstruction error, directly using target texts to guide image generation may destroy the original structure of the reference image. Inspired by [17], we can control the fidelity of the edited image by integrating the velocity field pointed to the reference image. However, if the velocity field is introduced improperly, it can interfere with the denoising process, resulting in *an undesired overlay of the reference and target images* and degrading editability. To address this, we introduce *Mobile Velocity Guidance* (MVG), as illustrated in Fig. 2(b), which adaptively guides the editing process to balance fidelity and editability.

The denoising process starts from a noise sample and gradually moves it to the target image, forming a trajectory from Gaussian noise to the target, called Z_t^{edit}. Specifically, at timestep t, we first

Algorithm 2 Mobile Velocity Guidance (MVG)

```
Input: Source image $Z_T$, Timesteps $\{\sigma_t\}_{t=0}^{T}$, RF $v_\theta(\cdot)$, Noisy latents $\{Z_t\}_{t=T-1}^{0}$, Residual gaps $\{\Delta x_t^{\mathrm{DNA}}\}_{t=T-1}^{0}$, Start Step $t_s$, Target text $\psi^{tgt}$
Output: Edited Image $Z_T^{\mathrm{edit}}$
Init: $Z_{t_s}^{edit} = Z_{t_s}, \quad Z_{t_s}^{\mathrm{mvg}} = Z_T$
for $t = t_s, t_s + 1, \cdots, T - 1$ do
    $v_t^{tgt} = v_\theta(Z_t^{*\mathrm{edit}}, \psi^{tgt}), \quad Z_t^{*\mathrm{edit}} \leftarrow Z_t^{\mathrm{edit}} + \Delta x_t^{\mathrm{DNA}}$    ▷ Involve residual gap to get target velocity
    $v_t^{src} = v_\theta(Z_t^*, \psi^{src}) = \frac{Z_{t+1} - Z_t}{\sigma_{t+1} - \sigma_t}, \quad \Delta v_t = v_t^{tgt} - v_t^{src}$    ▷ Reuse source velocity from DNA latents
    $Z_{t+1}^{\mathrm{mvg}} \leftarrow Z_t^{\mathrm{mvg}} + \Delta v_t \times (\sigma_{t+1} - \sigma_t)$    ▷ Move the mobile latent toward the target image
    $v_t^{\mathrm{mvg}} = (Z_t^{\mathrm{edit}} - Z_{t+1}^{\mathrm{mvg}})/(1 - \sigma_t)$    ▷ Calculate the mobile velocity guidance
    $v_t^{\mathrm{edit}} = \eta \times v_t^{tgt} + (1 - \eta) \times v_t^{\mathrm{mvg}}$    ▷ Calculate the synthesized denosing velocity
    $Z_{t+1}^{\mathrm{edit}} \leftarrow Z_t^{\mathrm{edit}} + v_t^{\mathrm{edit}} \times (\sigma_{t+1} - \sigma_t)$    ▷ Perform denoising step
end for
return $Z_T^{\mathrm{edit}}$
```

incorporate $\Delta x_t^{\mathrm{DNA}}$ to shift Z_t^{edit} to $Z_t^{*\mathrm{edit}}$, enabling the exact computation of target velocity v_t^{tgt}:

$$Z_t^{*\mathrm{edit}} = Z_t^{\mathrm{edit}} + \Delta x_t^{\mathrm{DNA}}, \quad v_t^{tgt} = v_\theta(Z_t^{*\mathrm{edit}}, \psi^{tgt}). \tag{8}$$

This step is crucial. According to Eq. (7), the residual $\Delta x_t^{\mathrm{DNA}} = Z_t^* - Z_t$ is equivalent to the weighted difference between two Gaussian noise samples and therefore free from image content. Essentially, this operation ensures that the regions intended to be preserved in $Z_t^{*\mathrm{edit}}$ are perfectly aligned with the noisy latent in the reverse process, *i.e.*, Z_t^* in Eq. (5). As a result, the computed target and source velocities (v_t^{tgt} and v_t^{src}) become near-identical in those preserved regions, which not only improves reconstruction accuracy but also significantly enhances editing fidelity. Our ablation study in **Appendix** further supports this finding.

In addition, there exists another trajectory that transitions from the source image to the target image purely within the image space, denoted as Z_t^{mvg}. Before using v_t^{tgt} to update the noisy latent Z_t^{edit} conditioned on the target text, we first apply the velocity difference between the source and target to shift Z_t^{mvg} from the reference image toward the target image. This velocity difference and the corresponding mobile latent modification are defined as:

$$\Delta v_t = v_t^{tgt} - v_t^{src}, \quad Z_{t+1}^{\mathrm{mvg}} = Z_t^{\mathrm{mvg}} + \Delta v_t \times (\sigma_{t+1} - \sigma_t). \tag{9}$$

Here, we use the saved latents in DNA to calculate the velocity v_t^{src}, which not only reduces the number of function evaluations (NFEs) but also accurately captures the velocity field associated with the reconstruction of the reference image. The velocity difference Δv_t is then applied to the mobile reference image Z_t^{mvg}, modifying specific regions to reflect the differences induced at timestep t under the source and target text conditions. Using the updated latent Z_{t+1}^{mvg}, we obtain the final denoising velocity by blending the velocity fully conditioned on the target text v_t^{tgt} with the MVG v_t^{mvg} using a weighting coefficient η as :

$$v_t^{\mathrm{mvg}} = (Z_t^{\mathrm{edit}} - Z_{t+1}^{\mathrm{mvg}})/(1 - \sigma_t), \quad v_t^{\mathrm{edit}} = \eta \times v_t^{tgt} + (1 - \eta) \times v_t^{\mathrm{mvg}}, \tag{10}$$

where $\eta \in [0, 1]$ controls the trade-off between fidelity and editability.

Finally, we apply the synthesized velocity to perform the denoising by $Z_{t+1}^{\mathrm{edit}} = Z_t^{\mathrm{edit}} + v_t^{\mathrm{edit}}(\sigma_{t+1} - \sigma_t)$. This process is applied across all timesteps, as shown in Fig. 2(b). To avoid excessive changes during editing, we skip the initial step and select Z_{t_s} as the starting point for editing. The complete algorithm of MVG is summarized in Algorithm 2. Using a fixed reference image for guidance, as in [17], we maintain the denoising direction close to the reconstruction of the source image during the early editing stages, thereby enhancing the fidelity. However, in later stages, as the image content undergoes substantial changes, relying on the original reference image can severely hinder editability. In contrast, our proposed MVG v_t^{mvg} mitigates this issue by employing a moving reference for guidance, effectively balancing fidelity and editability throughout the editing process.

Table 2: Quantitative comparison on PIE-Bench. Red , blue , yellow represents top 3 performers.

Method	Model	Structure	Background Preservation				CLIP Similarity		Rank
		Distance ↓	PSNR ↑	LPIPS ↓	MSE ↓	SSIM ↑	Whole ↑	Edited ↑	Avg. ↓
PnP[21]	SD1.5	27.35	22.31	112.76	82.95	79.25	25.41	22.52	9.17
MasaCtrl[1]	SD1.4	27.12	22.19	105.44	86.37	79.91	24.03	21.15	10.42
DI+PnP[6]	SD1.5	23.35	22.46	105.51	79.94	79.88	25.49	22.64	6.83
DI+MasaCtrl[6]	SD1.4	23.58	22.68	87.41	80.63	81.51	24.39	21.41	8.75
InfEdit[26]	LCM	19.31	27.31	56.32	47.80	85.30	24.90	22.14	5.67
InsP2P[4]	InsP2P	58.13	20.80	159.23	221.3	76.47	23.61	21.68	13.42
RF-Inv[17]	FLUX	42.29	20.20	179.54	139.2	69.91	24.57	22.20	12.42
RFEdit[22]	FLUX	21.79	24.83	113.15	52.46	83.38	25.57	22.26	6.42
FireFlow[2]	FLUX	29.03	23.33	133.40	70.83	81.22	26.19	22.99	7.42
FlowEdit[7]	FLUX	27.82	21.96	112.19	94.99	83.08	25.25	22.58	9.50
FlowEdit[7]	SD3	27.12	22.22	104.12	85.96	93.22	26.53	23.57	5.58
FTEdit[25]*	SD3.5	18.17	26.62	80.55	40.24	91.50	25.74	22.27	3.50
DNAEdit (Ours)	FLUX	18.87	24.99	95.06	50.45	85.71	25.79	22.87	3.42
DNAEdit (Ours)	SD3.5	14.19	26.66	74.57	32.76	88.63	25.63	22.71	2.50

4 Experiments

4.1 Experimental Settings

DNA-Bench. Text-guided editing has been extensively studied, and evaluation benchmarks [6, 10, 16] have been proposed to evaluate and compare the different editing methods. However, most of these benchmarks are developed in conjunction with diffusion-based models. Due to the limitations of text encoders and pre-trained models, diffusion models struggle to accurately understand long text inputs. As a result, existing benchmarks typically feature short descriptions. For example, PIE-Bench [6] has an average prompt length of **9.46** words. In contrast, RF-based models have shown significant improvements in understanding long text input, but the short descriptions in existing benchmarks cannot fully evaluate the editing capabilities of RF-based models.

To bridge this gap, we propose an extended version of PIE-Bench, called DNA-bench, which is tailored for long-text prompts. To construct DNA-Bench, we design target-aware prompts and leverage the powerful multimodal large language model GPT-4o [20] to generate detailed descriptions of the source images as source prompts. In addition, we modify and extend the original target prompts to align with the editing tasks. The average prompt length in DNA-bench is **33.17** words. More details of the construction process and example prompts of DNA-Bench can be found in the **Appendix**.

Implementation and Compared Methods. Two versions of DNAEdit are provided, which are based on FLUX-dev [9] and SD3.5-medium [19], respectively. In both versions, the MVG coefficient η is fixed at 0.8. Detailed hyper-parameter settings can be found in the **Appendix**. We compare DNAEdit with representative DM-based methods [1, 21, 26] and latest RF-based editing methods [17, 22, 2, 7, 25] using their official implementations and default settings in a shared environment, except FTEdit, where we use provided results.

Evaluation and Metrics. We first conduct **reconstruction** and **text-guided editing** experiments on the PIE-bench [6]. The PIE-bench consists of 700 natural and artificial images to evaluate editing methods across 9 distinct dimensions. It provides the source and target prompts for each image, along with the editing area masks to assess background preservation and local editing ability. We then conduct experiments on our proposed DNA-bench. To evaluate the reconstruction and preservation performance of non-edited areas, we adopt the commonly used image quality metrics, including

Table 1: Quantitative results on reconstruction.

Method	NFE↓	MSE↓	LPIPS↓	SSIM↑
Vallina Inversion	60	0.028	0.342	0.601
RF-Inversion [17]	56	0.023	0.279	0.526
RFEdit [22]	60	0.022	0.244	0.677
FireFlow [2]	57	0.015	0.200	0.726
DNA	56	**0.010**	**0.110**	**0.830**

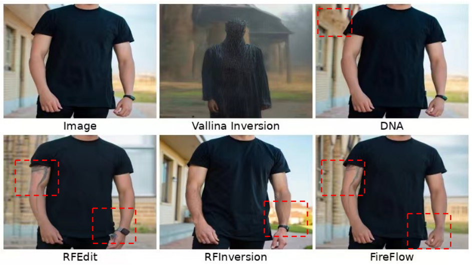


Figure 3: Qualitative comparison on reconstruction.

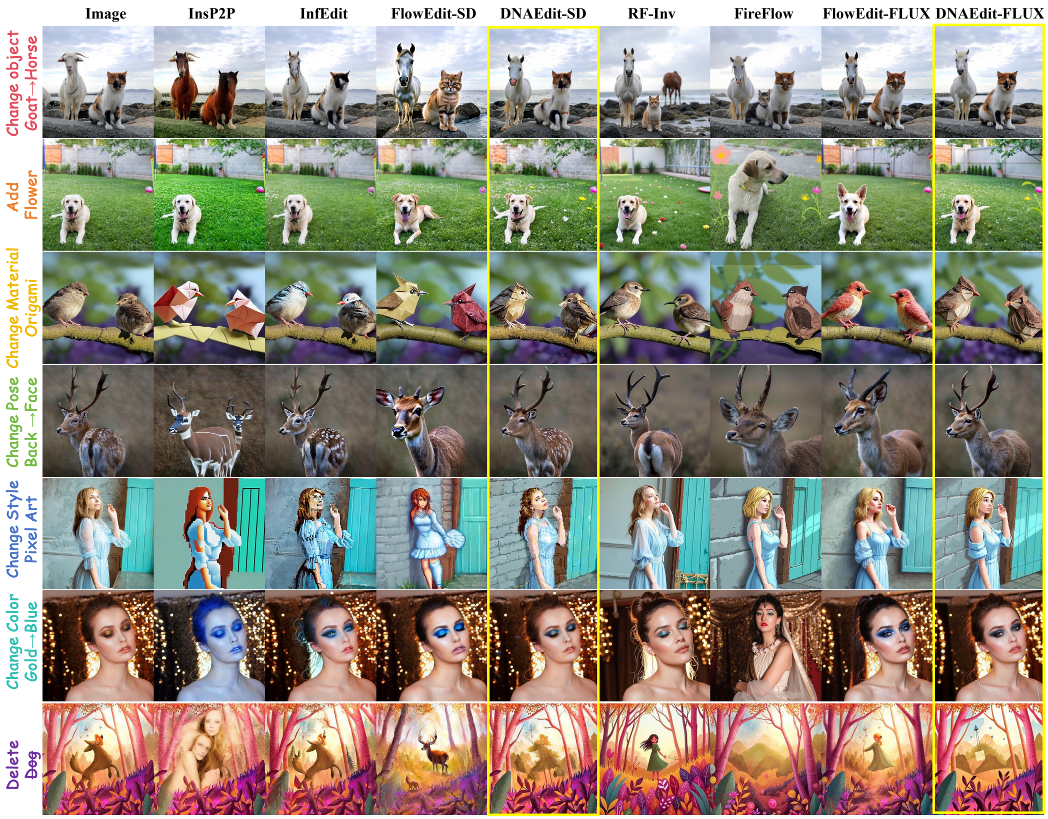


Figure 4: Qualitative comparison of different text-guided image editing methods.

LPIPS [29], SSIM [23], MSE, PSNR and structure distance [6]. Meanwhile, CLIP similarity [24] is employed to assess the consistency between target prompts and edited results.

4.2 Main Results

Results on Reconstruction. In Fig. 3, we present a qualitative comparison among different RF-based reconstruction methods. We see that our DNA method surpasses other approaches in reconstruction accuracy, with only minor differences from the original image in the area highlighted by red-box. FireFlow and RFEdit both use higher-order ODEs to reduce inversion drift, achieving good overall accuracy. However, noticeable differences appear in areas such as the background and arms. RF-Inversion uses the original image as a reference during reconstruction, leading to over-generation, such as the house in the background, which is not faithful to the original image. Moreover, using the original image as a reference can compromise the editability during editing. The quantitative results are reported in Section 4. Compared to existing inversion-based methods [2, 17, 22], our DNA achieves the lowest reconstruction error under similar NFEs.

Quantitative Comparison on Text-guided Editing. In Table 2, we evaluate editing methods in three dimensions: structure preservation, background preservation, and clip similarity. We present the overall ranking for each method by averaging the rankings in these dimensions in the last column of Table 2. Our approach demonstrates superior overall performance, particularly in terms of structure and background preservation. Specifically, while InfEdit shows better PSNR and LPIPS metrics, its CLIP similarity is significantly lower than other methods. This suggests that its strong background preservation hinders its editing capabilities. FlowEdit-SD3 achieves a higher CLIP score but shows weaker background and structure preservation compared to our method (PSNR 22.22dB *vs.* 26.66dB), indicating potential over-editing. This is attributed to its use of a large CFG in the generation, which also leads to poorer visual quality, as illustrated in Fig. 4. Lastly, the recently developed FTEdit shows relatively balanced performance. However, our method excels in background and structure preservation, with similar whole CLIP scores (25.63 *vs.* 25.74). In edited regions, our DNAEdit achieves a notably higher CLIP score, 22.71 *vs.* 22.27, indicating that our approach better preserves

Table 3: Quantitative Results on DNA-Bench. Red , blue , yellow represents top 3 performers.

Method	Model	Structure	Background Preservation				CLIP Similarity		Rank
		Distance ↓	PSNR ↑	LPIPS ↓	MSE ↓	SSIM ↑	Whole ↑	Edited ↑	Avg. ↓
RFEdit	FLUX	20.18	25.13	104.92	49.46	84.01	28.34	22.99	2.92
RF-Inversion	FLUX	41.92	20.18	176.40	139.69	69.96	27.98	22.89	6.83
FlowEdit	SD3	30.93	21.35	118.48	103.52	81.45	28.89	23.58	4.58
FlowEdit	FLUX	29.06	21.57	116.97	102.50	82.54	28.15	22.86	5.33
FireFLow	FLUX	26.97	23.57	124.78	68.51	81.82	28.69	23.32	3.83
DNAEdit	FLUX	18.61	24.89	93.76	50.80	85.80	28.36	22.99	2.41
DNAEdit	SD3.5	25.67	23.24	112.60	67.32	83.69	28.90	23.66	2.08

non-edited areas while accurately editing targeted regions. Furthermore, our method is model-agnostic and does not require alterations to the MM-DiT architecture, enhancing its applicability.

Qualitative Comparison on Text-guided Editing. We present visual comparisons of state-of-the-art editing methods in Fig. 4, including object, attribute, color, material, style, and pose editing. It can be found that InfEdit often results in edits without visible changes (see the 2nd, 4th and 7th rows). In contrast, FireFlow frequently exhibits over-editing, as shown in the 2nd, 4th and 6th rows. Although the editing instructions are followed, the original image's structure is significantly changed. As for FlowEdit, while the SD3 version of it successfully accomplishes most editing tasks without altering much the original image's structure, it suffers from low visual quality and noticeable over-saturation, as evident in row 1 and row 4. The FLUX version of FlowEdit offers better visual quality, but it has some shortcomings in fidelity and instruction following for some editing tasks. For instance, in row 2, it fails to add a flower, and there is a noticeable change in the dog's ears. Compared to these methods, our proposed DNAEdit method is versatile across various editing tasks and shows superior visual quality. For example, in row 5, our approach successfully applies a global pixel style while preserving the original image's character pose and overall structure. Similarly, in row 6, our method effectively changes the makeup color while retaining facial ID and other details, achieving desired results for both edited and non-edited areas. In summary, DNAEdit effectively balances between editability and fidelity, which is consistent with our quantitative results.

Results on DNA-Bench. Table 3 shows the results of RF-based editing methods on DNA-Bench. Our DNAEdit remains the best, achieving high clip scores while preserving the background. This validates that DNAEdit can be used for image editing with short- and long-text inputs without any change. Comparing the results of the same method under long and short prompts, we can see that inversion-based methods achieve better background preservation with long prompts (*e.g.*, FireFLow achieves a PSNR of 23.33dB on PIE-Bench and a PSNR of 23.57dB on DNA-Bench). This is because long texts provide detailed descriptions that align with image contents, allowing more accurate reconstruction. As shown in Fig. 5, short prompts change a cat into a dog but alter the pose, while long prompts keep the original pose, producing consistent results. In addition, long prompts also result in improved clip similarity scored.

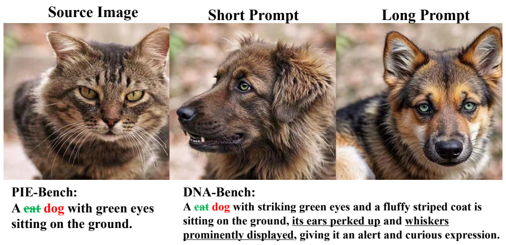

Source Image
Short Prompt
Long Prompt
PIE-Bench:
A ~~eat~~ dog with green eyes sitting on the ground.
DNA-Bench:
A ~~eat~~ dog with striking green eyes and a fluffy striped coat is sitting on the ground, its ears perked up and whiskers prominently displayed, giving it an alert and curious expression.

Figure 5: Visual comparison between editing results using short and long prompt.

4.3 Ablation on Proposed Modules

Baseline. In Table 4, we present the experimental results of our proposed method with different modules. We begin with Exp. ①, which utilizes velocity fields computed on interpolated latents to reverse ODE process. In Exp. ①, we initiate the inversion process by randomly sampling Gaussian noise, which is then used throughout the inversion process. At each step, the Gaussian noise is interpolated with the latent at timestep t to compute the velocity field for timestep $t-1$, facilitating the inversion. During the re-denoise phase, we use the velocity field conditioned on target prompt to generate target image. By employing interpolation to construct the latent of timestep $t-1$, we can mitigate errors caused by approximation. As observed, this setting already achieves relatively good results. However, despite avoiding approximation errors at each step, the use of a fixed Gaussian

Table 4: Ablation study on proposed modules.

Exp.	Component	Structure	Background Preservation				CLIP Similarity	
		Distance ↓	PSNR ↑	LPIPS ↓	MSE ↓	SSIM ↑	Whole ↑	Edited ↑
①	Interpolation	31.90	22.61	147.77	84.60	78.93	25.73	22.47
②	+DNA	32.67	22.18	146.27	89.92	79.73	26.24	23.08
③	+ResOffset	24.93	23.75	120.56	64.81	82.24	26.02	22.79
④	+DNA +ResOffset	33.98	21.97	149.84	95.19	79.32	26.40	23.23
⑤	+DNA+MVG	18.81	24.91	95.44	50.29	85.55	25.78	22.48
⑥	+DNA +ResOffset+MVG	18.87	24.99	95.06	50.45	85.71	25.79	22.87

noise throughout the process can introduce significant errors when approaching pure noise, especially when the initially sampled Gaussian noise deviates much from the desired structure noise.

Effectiveness of DNA. In Exp. ②, we introduce DNA by adjusting the initially sampled Gaussian noise during the inversion process. By comparing ① and ②, we can observe that as the structural and background preservation metrics remain nearly unchanged, the Clip Whole and Clip Edited similarity significantly increase, improving from 25.73 and 22.47 to 26.24 and 23.08, respectively. This improvement is attributed to the DNA process, where the noise is continuously moved by the difference between the linear velocity and the velocity conditioned on the source prompt. This movement injects the original image structure and gradually aligns the random noise with the structured noise corresponding to source prompt, enabling the generated results to better match the target prompt during editing.

Effectiveness of ResOffset. Comparing Exp. ① and ③, we see that the introduction of ResOffset during the re-denoising process significantly improves the metrics for image structure and background preservation. For instance, the Structure Distance improves from 31.90 to 24.93, and the PSNR increases from 22.61 dB to 23.75 dB. By incorporating the latent calculated with ResOffset, we shift Z_t^{edit} to Z_t^{*edit}, enhancing the consistency between the intended preserved regions in the noisy latent Z_t^* during the DNA process and those Z_t^{*edit} during re-denoising. This ensures that the velocity field during denoising accordingly tends to preserve these regions.

Effectiveness of MVG. Comparing Exp. ④ and ⑥, we observe that the introduction of MVG results in a decrease in structure similarity from 33.98 to 18.87, while PSNR increases from 21.97 dB to 24.99 dB, indicating a significant improvement in editing fidelity. As a trade-off for faithfulness to the original image, there is a decrease in CLIP similarity. Since MVG ensures that the overall structure of the edited image undergoes minimal changes, it imposes greater limitations on whole image editing, leading to a decrease in the whole image metric from 26.40 to 25.79 (-0.61). However, because MVG distinguishes between edited and non-edited regions and uses the evolved image to guide the editing of specific areas, the restriction on edited regions is greatly reduced, resulting in only a slight decrease of 0.36 in Edited CLIP similarity. This demonstrates that under the guidance of MVG, fidelity can be significantly enhanced while avoiding the constraints on edited regions that could lead to unchanged results. Please refer to **Appendix** for detailed ablation studies on the setting of the MVG coefficient.

5 Conclusion

We presented a novel RF-based method, namely DNAEdit, for text-guided image editing. By utilizing RF's property of linear trajectory, we proposed a method to estimate accurate latents by calculating the velocity fields at specific timesteps through random sampling and linear interpolation. By analyzing the expected and predicted velocity fields, we presented DNA to align the image to the ideal noise directly in the Gaussian noise domain. We then introduced MVG to maintain background areas while guiding effective changes in editing regions. Theoretical analyses were provided to explain the effectiveness of DNA and MVG and their connections with existing RF-based editing methods. Experiments were conducted on the commonly used PIE-Bench and our newly improved long-text DNA-Bench. Both qualitative and quantitative results showed that our DNAEdit approach performed well on various editing tasks, producing high-quality edits faithful to the original image.

Limitations. As a training-free editing method, DNAEdit utilizes the strong priors of pre-trained T2I models by converting images into structured noise aligned with the given text. Therefore, it may fall short in achieving desired editing results for cases that lie outside the foundation T2I model's prior.

References

[1] Mingdeng Cao, Xintao Wang, Zhongang Qi, Ying Shan, Xiaohu Qie, and Yinqiang Zheng. Masactrl: Tuning-free mutual self-attention control for consistent image synthesis and editing. In *Proceedings of the IEEE/CVF International Conference on Computer Vision*, pages 22560–22570, 2023.

[2] Yingying Deng, Xiangyu He, Changwang Mei, Peisong Wang, and Fan Tang. Fireflow: Fast inversion of rectified flow for image semantic editing. *arXiv preprint arXiv:2412.07517*, 2024.

[3] Patrick Esser, Sumith Kulal, Andreas Blattmann, Rahim Entezari, Jonas Müller, Harry Saini, Yam Levi, Dominik Lorenz, Axel Sauer, Frederic Boesel, et al. Scaling rectified flow transformers for high-resolution image synthesis. In *Forty-first International Conference on Machine Learning*, 2024.

[4] Ayaan Haque, Matthew Tancik, Alexei A Efros, Aleksander Holynski, and Angjoo Kanazawa. Instruct-nerf2nerf: Editing 3d scenes with instructions. In *Proceedings of the IEEE/CVF International Conference on Computer Vision*, pages 19740–19750, 2023.

[5] Amir Hertz, Ron Mokady, Jay Tenenbaum, Kfir Aberman, Yael Pritch, and Daniel Cohen-or. Prompt-to-prompt image editing with cross-attention control. In *The Eleventh International Conference on Learning Representations*, 2023.

[6] Xuan Ju, Ailing Zeng, Yuxuan Bian, Shaoteng Liu, and Qiang Xu. Direct inversion: Boosting diffusion-based editing with 3 lines of code. *arXiv preprint arXiv:2310.01506*, 2023.

[7] Vladimir Kulikov, Matan Kleiner, Inbar Huberman-Spiegelglas, and Tomer Michaeli. Flowedit: Inversion-free text-based editing using pre-trained flow models. *arXiv preprint arXiv:2412.08629*, 2024.

[8] Black Forest Labs. Flux. `https://github.com/black-forest-labs/flux`, 2024. Accessed: 2024-11-14.

[9] Black Forest Labs. Official weights of FLUX.1 dev. `https://huggingface.co/black-forest-labs/FLUX.1-dev`, 2024. Accessed: 2024-11-14.

[10] Shanglin Li, Bohan Zeng, Yutang Feng, Sicheng Gao, Xiuhui Liu, Jiaming Liu, Lin Li, Xu Tang, Yao Hu, Jianzhuang Liu, et al. Zone: Zero-shot instruction-guided local editing. In *Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition*, pages 6254–6263, 2024.

[11] Yaron Lipman, Ricky T. Q. Chen, Heli Ben-Hamu, Maximilian Nickel, and Matthew Le. Flow matching for generative modeling. In *The Eleventh International Conference on Learning Representations*, 2023.

[12] Xingchao Liu, Chengyue Gong, and qiang liu. Flow straight and fast: Learning to generate and transfer data with rectified flow. In *The Eleventh International Conference on Learning Representations*, 2023.

[13] Yongjia Ma, Donglin Di, Xuan Liu, Xiaokai Chen, Lei Fan, Wei Chen, and Tonghua Su. Adams bashforth moulton solver for inversion and editing in rectified flow. *arXiv preprint arXiv:2503.16522*, 2025.

[14] Daiki Miyake, Akihiro Iohara, Yu Saito, and Toshiyuki Tanaka. Negative-prompt inversion: Fast image inversion for editing with text-guided diffusion models. *arXiv preprint arXiv:2305.16807*, 2023.

[15] Ron Mokady, Amir Hertz, Kfir Aberman, Yael Pritch, and Daniel Cohen-Or. Null-text inversion for editing real images using guided diffusion models. In *Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition*, pages 6038–6047, 2023.

[16] Gaurav Parmar, Krishna Kumar Singh, Richard Zhang, Yijun Li, Jingwan Lu, and Jun-Yan Zhu. Zero-shot image-to-image translation. In *ACM SIGGRAPH 2023 Conference Proceedings*, pages 1–11, 2023.

[17] Litu Rout, Yujia Chen, Nataniel Ruiz, Constantine Caramanis, Sanjay Shakkottai, and Wen-Sheng Chu. Semantic image inversion and editing using rectified stochastic differential equations. *arXiv preprint arXiv:2410.10792*, 2024.

[18] Jiaming Song, Chenlin Meng, and Stefano Ermon. Denoising diffusion implicit models. In *International Conference on Learning Representations*, 2021.

[19] StablityAI. Official weights of SD3 medium diffusers. `https://huggingface.co/stabilityai/stable-diffusion-3-medium-diffusers`, 2024. Accessed: 2024-11-14.

[20] OpenAI Team. Gpt-4o system card, 2024.

[21] Narek Tumanyan, Michal Geyer, Shai Bagon, and Tali Dekel. Plug-and-play diffusion features for text-driven image-to-image translation. In *Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition*, pages 1921–1930, 2023.

[22] Jiangshan Wang, Junfu Pu, Zhongang Qi, Jiayi Guo, Yue Ma, Nisha Huang, Yuxin Chen, Xiu Li, and Ying Shan. Taming rectified flow for inversion and editing. *arXiv preprint arXiv:2411.04746*, 2024.

[23] Z. Wang, A.C. Bovik, H.R. Sheikh, and E.P. Simoncelli. Image quality assessment: From error visibility to structural similarity. *IEEE Transactions on Image Processing*, page 600–612, 2004.

[24] Chengdong Wu, Ling-Qiao Huang, Qianxi Zhang, Binyang Li, Lei Ji, Fan Yang, Guillermo Sapiro, and Nan Duan. Godiva: Generating open-domain videos from natural descriptions. 2021.

[25] Pengcheng Xu, Boyuan Jiang, Xiaobin Hu, Donghao Luo, Qingdong He, Jiangning Zhang, Chengjie Wang, Yunsheng Wu, Charles Ling, and Boyu Wang. Unveil inversion and invariance in flow transformer for versatile image editing. *arXiv preprint arXiv:2411.15843*, 2024.

[26] Sihan Xu, Yidong Huang, Jiayi Pan, Ziqiao Ma, and Joyce Chai. Inversion-free image editing with language-guided diffusion models. In *Proceedings of the IEEE/CVF Conference on Computer Vision and Pattern Recognition*, pages 9452–9461, 2024.

[27] Zexuan Yan, Yue Ma, Chang Zou, Wenteng Chen, Qifeng Chen, and Linfeng Zhang. Eedit: Rethinking the spatial and temporal redundancy for efficient image editing. *arXiv preprint arXiv:2503.10270*, 2025.

[28] Zhen Yang, Ganggui Ding, Wen Wang, Hao Chen, Bohan Zhuang, and Chunhua Shen. Object-aware inversion and reassembly for image editing. *arXiv preprint arXiv:2310.12149*, 2023.

[29] Richard Zhang, Phillip Isola, Alexei A. Efros, Eli Shechtman, and Oliver Wang. The unreasonable effectiveness of deep features as a perceptual metric. In *2018 IEEE/CVF Conference on Computer Vision and Pattern Recognition*, 2018.

[30] Tianrui Zhu, Shiyi Zhang, Jiawei Shao, and Yansong Tang. Kv-edit: Training-free image editing for precise background preservation. *arXiv preprint arXiv:2502.17363*, 2025.

NeurIPS Paper Checklist

1. **Claims**

   Question: Do the main claims made in the abstract and introduction accurately reflect the paper's contributions and scope?

   Answer: [Yes]

   Justification: Yes, the main claims in the abstract and introduction accurately reflect the paper's contributions and scope.

   Guidelines:

   - The answer NA means that the abstract and introduction do not include the claims made in the paper.
   - The abstract and/or introduction should clearly state the claims made, including the contributions made in the paper and important assumptions and limitations. A No or NA answer to this question will not be perceived well by the reviewers.
   - The claims made should match theoretical and experimental results, and reflect how much the results can be expected to generalize to other settings.
   - It is fine to include aspirational goals as motivation as long as it is clear that these goals are not attained by the paper.

2. **Limitations**

   Question: Does the paper discuss the limitations of the work performed by the authors?

   Answer: [Yes]

   Justification: We discuss limitations in the final section (after the conclusion).

   Guidelines:

   - The answer NA means that the paper has no limitation while the answer No means that the paper has limitations, but those are not discussed in the paper.
   - The authors are encouraged to create a separate "Limitations" section in their paper.
   - The paper should point out any strong assumptions and how robust the results are to violations of these assumptions (e.g., independence assumptions, noiseless settings, model well-specification, asymptotic approximations only holding locally). The authors should reflect on how these assumptions might be violated in practice and what the implications would be.
   - The authors should reflect on the scope of the claims made, e.g., if the approach was only tested on a few datasets or with a few runs. In general, empirical results often depend on implicit assumptions, which should be articulated.
   - The authors should reflect on the factors that influence the performance of the approach. For example, a facial recognition algorithm may perform poorly when image resolution is low or images are taken in low lighting. Or a speech-to-text system might not be used reliably to provide closed captions for online lectures because it fails to handle technical jargon.
   - The authors should discuss the computational efficiency of the proposed algorithms and how they scale with dataset size.
   - If applicable, the authors should discuss possible limitations of their approach to address problems of privacy and fairness.
   - While the authors might fear that complete honesty about limitations might be used by reviewers as grounds for rejection, a worse outcome might be that reviewers discover limitations that aren't acknowledged in the paper. The authors should use their best judgment and recognize that individual actions in favor of transparency play an important role in developing norms that preserve the integrity of the community. Reviewers will be specifically instructed to not penalize honesty concerning limitations.

3. **Theory assumptions and proofs**

   Question: For each theoretical result, does the paper provide the full set of assumptions and a complete (and correct) proof?

   Answer: [Yes]

Justification: Yes, the paper provides a full set of assumptions and a proof for each theoretical result.

Guidelines:

- The answer NA means that the paper does not include theoretical results.
- All the theorems, formulas, and proofs in the paper should be numbered and cross-referenced.
- All assumptions should be clearly stated or referenced in the statement of any theorems.
- The proofs can either appear in the main paper or the supplemental material, but if they appear in the supplemental material, the authors are encouraged to provide a short proof sketch to provide intuition.
- Inversely, any informal proof provided in the core of the paper should be complemented by formal proofs provided in appendix or supplemental material.
- Theorems and Lemmas that the proof relies upon should be properly referenced.

4. **Experimental result reproducibility**

   Question: Does the paper fully disclose all the information needed to reproduce the main experimental results of the paper to the extent that it affects the main claims and/or conclusions of the paper (regardless of whether the code and data are provided or not)?

   Answer: [Yes]

   Justification: Yes, the paper fully discloses all necessary information to reproduce the main experimental results, supporting the main claims and conclusions.

   Guidelines:

   - The answer NA means that the paper does not include experiments.
   - If the paper includes experiments, a No answer to this question will not be perceived well by the reviewers: Making the paper reproducible is important, regardless of whether the code and data are provided or not.
   - If the contribution is a dataset and/or model, the authors should describe the steps taken to make their results reproducible or verifiable.
   - Depending on the contribution, reproducibility can be accomplished in various ways. For example, if the contribution is a novel architecture, describing the architecture fully might suffice, or if the contribution is a specific model and empirical evaluation, it may be necessary to either make it possible for others to replicate the model with the same dataset, or provide access to the model. In general. releasing code and data is often one good way to accomplish this, but reproducibility can also be provided via detailed instructions for how to replicate the results, access to a hosted model (e.g., in the case of a large language model), releasing of a model checkpoint, or other means that are appropriate to the research performed.
   - While NeurIPS does not require releasing code, the conference does require all submissions to provide some reasonable avenue for reproducibility, which may depend on the nature of the contribution. For example
     (a) If the contribution is primarily a new algorithm, the paper should make it clear how to reproduce that algorithm.
     (b) If the contribution is primarily a new model architecture, the paper should describe the architecture clearly and fully.
     (c) If the contribution is a new model (e.g., a large language model), then there should either be a way to access this model for reproducing the results or a way to reproduce the model (e.g., with an open-source dataset or instructions for how to construct the dataset).
     (d) We recognize that reproducibility may be tricky in some cases, in which case authors are welcome to describe the particular way they provide for reproducibility. In the case of closed-source models, it may be that access to the model is limited in some way (e.g., to registered users), but it should be possible for other researchers to have some path to reproducing or verifying the results.

5. **Open access to data and code**

Question: Does the paper provide open access to the data and code, with sufficient instructions to faithfully reproduce the main experimental results, as described in supplemental material?

Answer: [Yes]

Justification: All data are publicly available. We will release the codes and new data if the paper is accepted.

Guidelines:

- The answer NA means that paper does not include experiments requiring code.
- Please see the NeurIPS code and data submission guidelines (`https://nips.cc/public/guides/CodeSubmissionPolicy`) for more details.
- While we encourage the release of code and data, we understand that this might not be possible, so "No" is an acceptable answer. Papers cannot be rejected simply for not including code, unless this is central to the contribution (e.g., for a new open-source benchmark).
- The instructions should contain the exact command and environment needed to run to reproduce the results. See the NeurIPS code and data submission guidelines (`https://nips.cc/public/guides/CodeSubmissionPolicy`) for more details.
- The authors should provide instructions on data access and preparation, including how to access the raw data, preprocessed data, intermediate data, and generated data, etc.
- The authors should provide scripts to reproduce all experimental results for the new proposed method and baselines. If only a subset of experiments are reproducible, they should state which ones are omitted from the script and why.
- At submission time, to preserve anonymity, the authors should release anonymized versions (if applicable).
- Providing as much information as possible in supplemental material (appended to the paper) is recommended, but including URLs to data and code is permitted.

6. **Experimental setting/details**

Question: Does the paper specify all the training and test details (e.g., data splits, hyperparameters, how they were chosen, type of optimizer, etc.) necessary to understand the results?

Answer: [Yes]

Justification: Yes, the paper provides all necessary details, including hyperparameters, evaluation metrics and *etc.* to fully understand the results.

Guidelines:

- The answer NA means that the paper does not include experiments.
- The experimental setting should be presented in the core of the paper to a level of detail that is necessary to appreciate the results and make sense of them.
- The full details can be provided either with the code, in appendix, or as supplemental material.

7. **Experiment statistical significance**

Question: Does the paper report error bars suitably and correctly defined or other appropriate information about the statistical significance of the experiments?

Answer: [No]

Justification: We do not report error bars.

Guidelines:

- The answer NA means that the paper does not include experiments.
- The authors should answer "Yes" if the results are accompanied by error bars, confidence intervals, or statistical significance tests, at least for the experiments that support the main claims of the paper.
- The factors of variability that the error bars are capturing should be clearly stated (for example, train/test split, initialization, random drawing of some parameter, or overall run with given experimental conditions).

- The method for calculating the error bars should be explained (closed form formula, call to a library function, bootstrap, etc.)
- The assumptions made should be given (e.g., Normally distributed errors).
- It should be clear whether the error bar is the standard deviation or the standard error of the mean.
- It is OK to report 1-sigma error bars, but one should state it. The authors should preferably report a 2-sigma error bar than state that they have a 96% CI, if the hypothesis of Normality of errors is not verified.
- For asymmetric distributions, the authors should be careful not to show in tables or figures symmetric error bars that would yield results that are out of range (e.g. negative error rates).
- If error bars are reported in tables or plots, The authors should explain in the text how they were calculated and reference the corresponding figures or tables in the text.

8. **Experiments compute resources**

   Question: For each experiment, does the paper provide sufficient information on the computer resources (type of compute workers, memory, time of execution) needed to reproduce the experiments?

   Answer: [Yes]

   Justification: We detail the type of compute resources in appendix.

   Guidelines:

   - The answer NA means that the paper does not include experiments.
   - The paper should indicate the type of compute workers CPU or GPU, internal cluster, or cloud provider, including relevant memory and storage.
   - The paper should provide the amount of compute required for each of the individual experimental runs as well as estimate the total compute.
   - The paper should disclose whether the full research project required more compute than the experiments reported in the paper (e.g., preliminary or failed experiments that didn't make it into the paper).

9. **Code of ethics**

   Question: Does the research conducted in the paper conform, in every respect, with the NeurIPS Code of Ethics `https://neurips.cc/public/EthicsGuidelines`?

   Answer: [Yes]

   Justification: Yes, the research in the paper fully conforms to the NeurIPS Code of Ethics in every respect.

   Guidelines:

   - The answer NA means that the authors have not reviewed the NeurIPS Code of Ethics.
   - If the authors answer No, they should explain the special circumstances that require a deviation from the Code of Ethics.
   - The authors should make sure to preserve anonymity (e.g., if there is a special consideration due to laws or regulations in their jurisdiction).

10. **Broader impacts**

    Question: Does the paper discuss both potential positive societal impacts and negative societal impacts of the work performed?

    Answer: [Yes]

    Justification: Yes, we analyze the potential social impact in appendix.

    Guidelines:

    - The answer NA means that there is no societal impact of the work performed.
    - If the authors answer NA or No, they should explain why their work has no societal impact or why the paper does not address societal impact.

- Examples of negative societal impacts include potential malicious or unintended uses (e.g., disinformation, generating fake profiles, surveillance), fairness considerations (e.g., deployment of technologies that could make decisions that unfairly impact specific groups), privacy considerations, and security considerations.
- The conference expects that many papers will be foundational research and not tied to particular applications, let alone deployments. However, if there is a direct path to any negative applications, the authors should point it out. For example, it is legitimate to point out that an improvement in the quality of generative models could be used to generate deepfakes for disinformation. On the other hand, it is not needed to point out that a generic algorithm for optimizing neural networks could enable people to train models that generate Deepfakes faster.
- The authors should consider possible harms that could arise when the technology is being used as intended and functioning correctly, harms that could arise when the technology is being used as intended but gives incorrect results, and harms following from (intentional or unintentional) misuse of the technology.
- If there are negative societal impacts, the authors could also discuss possible mitigation strategies (e.g., gated release of models, providing defenses in addition to attacks, mechanisms for monitoring misuse, mechanisms to monitor how a system learns from feedback over time, improving the efficiency and accessibility of ML).

11. **Safeguards**

    Question: Does the paper describe safeguards that have been put in place for responsible release of data or models that have a high risk for misuse (e.g., pretrained language models, image generators, or scraped datasets)?

    Answer: [NA]

    Justification: The paper poses no such risks.

    Guidelines:

    - The answer NA means that the paper poses no such risks.
    - Released models that have a high risk for misuse or dual-use should be released with necessary safeguards to allow for controlled use of the model, for example by requiring that users adhere to usage guidelines or restrictions to access the model or implementing safety filters.
    - Datasets that have been scraped from the Internet could pose safety risks. The authors should describe how they avoided releasing unsafe images.
    - We recognize that providing effective safeguards is challenging, and many papers do not require this, but we encourage authors to take this into account and make a best faith effort.

12. **Licenses for existing assets**

    Question: Are the creators or original owners of assets (e.g., code, data, models), used in the paper, properly credited and are the license and terms of use explicitly mentioned and properly respected?

    Answer: [Yes]

    Justification: Yes, we clearly indicate the baseline methods and testing data used in the paper. Their licenses permit use with academic scope.

    Guidelines:

    - The answer NA means that the paper does not use existing assets.
    - The authors should cite the original paper that produced the code package or dataset.
    - The authors should state which version of the asset is used and, if possible, include a URL.
    - The name of the license (e.g., CC-BY 4.0) should be included for each asset.
    - For scraped data from a particular source (e.g., website), the copyright and terms of service of that source should be provided.

- If assets are released, the license, copyright information, and terms of use in the package should be provided. For popular datasets, `paperswithcode.com/datasets` has curated licenses for some datasets. Their licensing guide can help determine the license of a dataset.
- For existing datasets that are re-packaged, both the original license and the license of the derived asset (if it has changed) should be provided.
- If this information is not available online, the authors are encouraged to reach out to the asset's creators.

13. **New assets**

    Question: Are new assets introduced in the paper well documented and is the documentation provided alongside the assets?

    Answer: [Yes]

    Justification: Code and dataset will be release if the paper is accepted.

    Guidelines:

    - The answer NA means that the paper does not release new assets.
    - Researchers should communicate the details of the dataset/code/model as part of their submissions via structured templates. This includes details about training, license, limitations, etc.
    - The paper should discuss whether and how consent was obtained from people whose asset is used.
    - At submission time, remember to anonymize your assets (if applicable). You can either create an anonymized URL or include an anonymized zip file.

14. **Crowdsourcing and research with human subjects**

    Question: For crowdsourcing experiments and research with human subjects, does the paper include the full text of instructions given to participants and screenshots, if applicable, as well as details about compensation (if any)?

    Answer: [NA]

    Justification: The paper does not involve crowd sourcing nor research with human subjects.

    Guidelines:

    - The answer NA means that the paper does not involve crowdsourcing nor research with human subjects.
    - Including this information in the supplemental material is fine, but if the main contribution of the paper involves human subjects, then as much detail as possible should be included in the main paper.
    - According to the NeurIPS Code of Ethics, workers involved in data collection, curation, or other labor should be paid at least the minimum wage in the country of the data collector.

15. **Institutional review board (IRB) approvals or equivalent for research with human subjects**

    Question: Does the paper describe potential risks incurred by study participants, whether such risks were disclosed to the subjects, and whether Institutional Review Board (IRB) approvals (or an equivalent approval/review based on the requirements of your country or institution) were obtained?

    Answer: [NA]

    Justification: The paper does not involve crowd sourcing nor research with human subjects.

    Guidelines:

    - The answer NA means that the paper does not involve crowdsourcing nor research with human subjects.
    - Depending on the country in which research is conducted, IRB approval (or equivalent) may be required for any human subjects research. If you obtained IRB approval, you should clearly state this in the paper.

- We recognize that the procedures for this may vary significantly between institutions and locations, and we expect authors to adhere to the NeurIPS Code of Ethics and the guidelines for their institution.
- For initial submissions, do not include any information that would break anonymity (if applicable), such as the institution conducting the review.

16. **Declaration of LLM usage**

    Question: Does the paper describe the usage of LLMs if it is an important, original, or non-standard component of the core methods in this research? Note that if the LLM is used only for writing, editing, or formatting purposes and does not impact the core methodology, scientific rigorousness, or originality of the research, declaration is not required.

    Answer: [NA]

    Justification: Our core method focuses on image editing and does not involve LLMs as part.

    Guidelines:

    - The answer NA means that the core method development in this research does not involve LLMs as any important, original, or non-standard components.
    - Please refer to our LLM policy (`https://neurips.cc/Conferences/2025/LLM`) for what should or should not be described.