

CheXGenBench: A Unified Benchmark For Fidelity, Privacy and Utility of Synthetic Chest Radiographs

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Abstract

We introduce CheXGenBench, a rigorous and multifaceted evaluation framework for synthetic chest radiograph generation that simultaneously assesses fidelity, privacy risks, and clinical utility across state-of-the-art text-to-image generative models. Despite rapid advancements in generative AI for real-world imagery, medical domain evaluations have been hindered by methodological inconsistencies, outdated architectural comparisons, and disconnected assessment criteria that rarely address the practical clinical value of synthetic samples. CheXGenBench overcomes these limitations through standardised data partitioning and a unified evaluation protocol comprising over 20 quantitative metrics that systematically analyse generation quality, potential privacy vulnerabilities, and downstream clinical applicability across 11 leading text-to-image architectures. Our results reveal critical inefficiencies in the existing evaluation protocols, particularly in assessing generative fidelity, leading to inconsistent and uninformative comparisons. Our framework establishes a standardised benchmark for the medical AI community, enabling objective and reproducible comparisons while facilitating seamless integration of both existing and future generative models. Additionally, we release a high-quality, synthetic dataset, *SynthCheX-75K*, comprising 75K radiographs generated by the top-performing model (Sana 0.6B) in our benchmark to support further research in this critical domain. Through CheXGenBench, we establish a new state-of-the-art and release our framework, models, and SynthCheX-75K dataset at <https://raman1121.github.io/CheXGenBench/>

1 Introduction

Recent advances in multi-modal generative models, particularly Text-to-Image (T2I) systems [1, 2, 3, 4], have demonstrated remarkable capabilities in producing high-fidelity synthetic images that closely adhere to natural-language prompts. Central to this progress is the development of comprehensive, well-designed benchmarks that evaluate various aspects of generative performance. These benchmarks drive innovation by establishing standardised evaluation protocols and creating an equitable foundation for model comparison. The natural imaging domain has benefited from numerous such benchmarks, each meticulously assessing specific aspects and identifying limitations that researchers subsequently address in developing next-generation models. For example, MS-COCO dataset [5] has been established as a seminal benchmark for evaluating general performance across multiple tasks, with particular emphasis on text-guided image generation. Building upon this foundation, more specialised benchmarks have emerged to assess specific attributes such as compositional understanding [6, 7, 8], enabling more nuanced analysis of model capabilities. Despite the advancements in the natural imaging domain, there remains a significant gap in medical image analysis, and specifically in terms of benchmarking specialised tasks such as text-to-image generation.

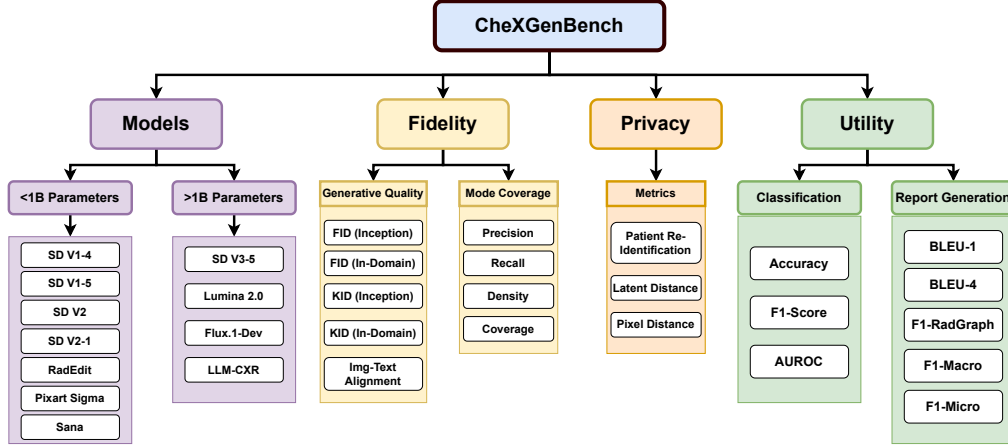


Figure 1: Figure illustrating the overall schematic of the CheXGenBench benchmark for evaluating text-to-image models in synthetic radiograph generation. CheXGenBench organises evaluation into three dimensions: **Fidelity** (measuring generative quality and mode coverage), **Privacy** (assessing memorisation and re-identification risks), and **Utility** (evaluating practical value of synthetic samples through image classification and radiology report generation metrics) through 20+ metrics across 11 widely-adopted **T2I models**.

Benchmarking Medical Imaging AI: Medical image analysis has made significant strides by benefiting from rapid advancements in artificial intelligence; however, its progress faces substantial constraints due to what has been characterised as a benchmarking crisis [9]. The ultimate goal of AI applications in medicine remains the development of intelligent systems capable of supporting and potentially transforming clinical decision-making processes. Progress toward this objective is frequently hindered by insufficient transparency in training and evaluation protocols, coupled with fragmented assessment criteria. Consequently, claims of “state-of-the-art” performance are often premature, non-reproducible, or reflect narrow contextual improvements rather than demonstrating genuine translational capability to clinical practice. The challenges of benchmarking in medical AI diagnostic tasks such as classification, localisation, segmentation and report generation have been discussed, and some improvements have been proposed [10, 11, 12, 13]. However, despite opportunities for impactful societal applications from diagnostic training to rare condition simulation, benchmarking in medical image *generation* remains in an even more nascent and unsatisfactory state. This is exacerbated by unique challenges such as unclear evaluation metrics, data scarcity due to privacy constraints, and long-tailed distributions of rare pathologies.

While medical AI diagnostic tasks have been long studied, the generation of synthetic data through text prompts (medical descriptions) has recently emerged as a critical research focus. Besides being an interesting academic measure of medical AI capability, the ultimate motivation is that progress in diagnostic tasks is usually bottlenecked by *data scarcity* in the medical domain. High-fidelity generative models for synthetic data offer the promise to alleviate this bottleneck and ultimately facilitate clinical impact [14]. Chest radiographs are the most commonly used frontline modality in medical imaging. Although the majority of collected clinical data remain inaccessible behind institutional firewalls and compliances [9], several data repositories have been opened [15, 16, 10, 17], facilitating the development of generative models capable of synthesizing radiographs with potential relevance to downstream clinical utility [18, 19, 20].

Current research on Text-to-Image generation of radiographs can be broadly categorized into two primary streams: (1) studies prioritizing the enhancement of image fidelity and generative performance [21, 22, 20, 23, 19, 24, 25, 26], and (2) investigations focusing on the mitigation of privacy concerns and patient re-identification risks [27, 28, 29, 30, 31] that could undermine synthetic data utility. Despite constituting an active area of research with significant contributions, we have identified several critical benchmarking dimensions in which existing studies demonstrate consistent limitations. **Minimal or Absent Comparative Baselines:** Several notable studies either include minimal (self-

proposed) [23, 30] or no baselines [22] for evaluation. [24, 20] limit their comparative evaluations to only two competing methodologies. **Reporting Inadequate Metrics:** Studies throughout the existing literature predominantly report Fréchet Inception Distance (FID) [32], specifically adopting in-domain image encoders based on primitive architectures [33]. Furthermore, no studies adequately report metrics characterising mode-coverage, a criterion of paramount importance in synthetic image generation for capturing the diversity of the underlying data distribution. Finally and most importantly, all metrics are reported as micro-averages across entire datasets without accounting for conditioning, let alone the long-tailed nature of medical data distributions. For example, excellent *average* generation fidelity could be reflective of the ability to generate more common images of healthy individuals, and the inability to generate images with pathologies of interest. This situation would offer limited clinical utility for pathology diagnosis. **Restriction to Early-Stage Architectures:** Existing studies [19, 22, 23, 34] have predominantly confined themselves to outdated T2I model architectures [35], failing to address the crucial question of how recent advancements in generative modelling [36, 4, 37] from the natural imaging domain translate to the specialised requirements of medical imaging contexts. **Lack of a Unified Evaluation:** Existing studies are fragmented between evaluating generative fidelity [19, 22, 20] or privacy and re-identification risks [27, 29, 31], failing to conduct and provide a unified evaluation of the two key aspects of synthetic radiograph generation research. **Limited Evaluation on Synthetic Data Utility:** Most studies fail to comment on the downstream utility of synthetic radiographs [22, 20] often presenting generation results without rigorously assessing their potential impact on medical image analysis tasks such as classification, segmentation, or diagnostic reasoning.

To address these critical limitations, we introduce CheXGenBench, a comprehensive benchmark designed for rigorous evaluation of frontier generative models across a diverse spectrum of metrics encompassing: (1) generation fidelity and mode coverage, (2) privacy and re-identification risk assessment, and (3) downstream clinical utility through an extensive suite of 20+ quantitative and interpretable metrics. We establish standardised training and evaluation protocols to enable equitable comparison between diverse model architectures. CheXGenBench prioritises usability and adaptability, facilitating seamless plug-and-play integration of both existing and emerging generative frameworks. Through systematic evaluation, we present several T2I models previously **unexplored** for radiograph generation and establish new state-of-the-art (SoTA) performance. Furthermore, we release a synthetic dataset, *SynthCheX-75K*, comprising 75K high-quality radiographs generated by our benchmark-leading model to facilitate advancement in medical image analysis research.

2 CheXGenBench Design

CheXGenBench is designed to evaluate each text-to-image model across three dimensions comprehensively: (1) generative fidelity and mode coverage (Sec 2.2), (2) privacy and patient re-identification risks (Sec 2.2), and (3) synthetic data utility for downstream tasks (Sec 2.4), which we elucidate in detail in the following sub-sections.

Design Principles: CheXGenBench is designed for usability, featuring decoupled training and evaluation pipelines. This allows researchers to use preferred training frameworks (Hugging Face Diffusers [38], ai-toolkit¹, etc.) while adhering to a standardised evaluation. Users only need to provide synthetic images and a metadata file for the benchmark for automatic assessment using over 20 metrics. Pre-defined data splits further simplify adoption, balancing comprehensive assessment with practical use for medical imaging research.

2.1 Training Dataset and Protocol

Criteria for Model Inclusion: Our model selection was guided by two main criteria. First, we included models previously used for synthetic radiograph generation in existing literature [35, 19, 20, 39] to provide continuity and comparability with prior work. Second, we incorporated recent state-of-the-art models (both diffusion and auto-regressive) [36, 40, 4, 41, 37] from the natural imaging domain that had not yet been evaluated for chest X-ray synthesis. Thus we both benchmark established methods and assess the potential of newer architectures for medical image generation.

¹<https://github.com/ostris/ai-toolkit>

Training Dataset with Enhanced Captions: We conduct all evaluations on the MIMIC-CXR dataset [15], which has emerged as the de-facto data repository for chest radiograph text-to-image generation [19, 22, 39, 20, 23]. While each CXR image in the dataset is associated with a corresponding free-text radiology report, conventional approaches have relied on rule-based methods to derive abbreviated descriptions for T2I model training [39, 19]. These traditional approaches, however, prove inadequate due to inconsistencies in report structure and clinical terminology [42].

Recent advances have shifted toward deep learning-based techniques that generate more comprehensive and clinically accurate summaries from radiology reports, contributing to state-of-the-art medical foundation models [42]. Building on evidence that more descriptive captions enhance generative fidelity [43], we adopt the “LLaVA-Rad” annotations in place of the traditional captions available in MIMIC-CXR. Fig. 2 illustrates the distribution of character lengths in the two annotations. To our knowledge, this represents the first study to use enhanced descriptive captions for the generation of synthetic radiographs with MIMIC-CXR data. In Appendix Sec. A, we empirically show that “LLaVA-Rad” annotations improve fidelity and reduce re-identification risks, and strongly recommend for future research in this domain.

Training Protocol: Our analysis revealed that prior studies employed inconsistent training budgets, undermining valid cross-model comparison. To establish a level evaluation framework, we implemented a standardised training protocol across all T2I models. Each architecture was trained for precisely 20 epochs on an identical training split of 237,388 samples annotated with “LLaVA-Rad” annotations. We release the training and evaluation data splits along with the benchmark.

The models in our benchmark were stratified into two categories based on parameter count: (1) models with fewer than 1B parameters, and (2) models exceeding 1B parameters. For the smaller models, we employed full fine-tuning (FFT) of all parameters. For larger architectures, we implemented Low-Rank Adaptation (LoRA) [44] with rank 32 on standard query, key, and value layers in the attention blocks to address both computational constraints and reflect realistic training scenarios.

2.2 Evaluation Protocol: Generative Fidelity, Mode Coverage, and Conditional Analysis

Limitations of Current Fidelity Assessment: The Fréchet Inception Distance (FID) score [32] is widely used for evaluating synthetic radiograph fidelity. Standard FID uses InceptionV3 [45] features trained on natural images, creating domain mismatch for medical images [46]. While some research employs domain-specific encoders like DenseNet-121 [47] trained on radiographs [33], we argue these adaptations remain inadequate. DenseNet-121, despite domain alignment, represents an outdated backbone that fails to capture critical nuances, reducing FID reliability for radiograph quality assessment. We perform an extensive ablation on this in Appendix Section B. Additionally, studies using natural image-text pre-trained CLIP [48, 19] further compromise evaluation integrity due to high domain misalignment.

Improving metric Reliability in CheXGenBench : We address the aforementioned limitations and enable a more nuanced evaluation of synthetic radiographs in CheXGenBench . For robust image fidelity assessment using Fréchet Inception Distance (FID), CheXGenBench employs features from *RadDino* [49], a model with SoTA performance on radiology classification and report generation tasks. To evaluate image-text alignment, we integrate *BioViL-T* [50], a vision-language model specialized in the biomedical domain.

Expanding the Metric Suite with Density and Mode Coverage: All prior studies have reported generation fidelity without a systematic evaluation of how effectively generated samples capture critical distributional characteristics, notably the density of the resulting sample distribution and coverage of distinct modes from the true data. This is of particular importance in medical datasets since not all pathologies are distributed equally. To address this, CheXGenBench also supports Precision, Recall, Density and Coverage [51].

Precision, Recall, Density, and Coverage (PRDC) metrics are essential for evaluating mode coverage, particularly in long-tailed distributions where FID scores can be skewed by majority classes. This is evident in the MIMIC-CXR dataset, where “No Finding” radiographs, representing healthy X-rays, predominate despite pathological images offering greater clinical value for synthesis. Within the PRDC framework, **Precision** quantifies generated sample realism, **Recall** measures how well the real distribution is captured, **Density** assesses feature space concentration, and **Coverage** determines the

proportion of modes of real data successfully generated, together providing a more comprehensive assessment than global metrics alone.

Conditional Analysis for Individual Pathologies: CheXGenBench extends evaluation capabilities through pathology-specific conditional analysis, wherein we compute each generation fidelity metric independently across individual pathologies in the MIMIC-CXR dataset. This granular assessment approach provides critical insights that enable developers to precisely evaluate generative performance for specific medical conditions. Such an analysis becomes particularly valuable in scenarios requiring selective augmentation of underrepresented pathologies through a generative model, which is the most desired use case. Our framework calculates FID, KID, image-text alignment, and PRDC metrics for each distinct pathology, facilitating comprehensive performance evaluation at the condition-specific level. To the best of our knowledge, we are the first study to include pathology-conditional evaluation.

2.3 Evaluation Protocol: Privacy and Patient Re-Identification

Deep generative models can inadvertently memorise distinctive training examples, allowing an attacker to reverse-engineer sensitive patient information from seemingly “synthetic” images [52, 53]. In the medical domain, even coarse anatomical cues may be enough to link a generated radiograph back to an individual, breaching data-protection regulations such as HIPAA² and the EU GDPR³. Consequently, to assess clinical relevance claims, a benchmark that **must** characterise (i) how much a model memorises, and (ii) how easily a real patient can be re-identified from its outputs.

Re-identification risk formulation. To evaluate privacy and patient re-identification risks, we implement established metrics from the existing literature [27, 29, 30, 31]. Let $\mathcal{D}_{\text{real}} = \{x_i, c_i\}_{i=1}^N$ be the training set of chest radiographs x_i with corresponding captions c_i , and let G_θ denote a text-to-image model producing synthetic images $\hat{x} = G_\theta(c)$. We assess whether a generated sample \hat{x} memorizes any training image x_i via a learned similarity function $\ell(\hat{x}, x_i)$ with $\text{Memorised}(x_i) \Leftrightarrow \ell(\hat{x}, x_i) > \delta$, where δ is a fixed safety margin. We evaluate similarity through three distinct lenses: (i) **Pixel distance** (ℓ_{pix}): $\|\hat{x} - x_i\|_2$, to detect near-duplicates [52]. (ii) **Latent distance** (ℓ_{lat}): Normalized Euclidean distance in the embedding space of *RadDino* [49]. (iii) **Re-identification score** (s_{reid}): Probability that \hat{x} and x_i are from the same patient, as estimated by a Siamese neural network [54].

Assessing re-identification. Instead of relying solely on pixel-based [52] or structural-based [55] similarity, we adopt the deep learning-based metric $\ell = f_\theta^{\text{re-id}}$ [54]. The model $f_\theta^{\text{re-id}}$ is a Siamese network with a ResNet-50 [56] backbone trained to classify whether two chest X-ray images originate from the same patient. For any pair (\hat{x}, x) of a generated and real image, $f_\theta^{\text{re-id}}$ outputs a re-identification score $s_{\text{reid}} \in [0, 1]$ after a sigmoid layer. A synthetic image \hat{x} is considered re-identified if $s_{\text{reid}} \geq \delta$ for any training image x .

Privacy metrics summary. Given a dataset of M generated images $\{\hat{x}^{(j)}\}_{j=1}^M$ (across M different random seeds), let $s_{\text{reid}}^{(j)}$, $\ell_{\text{lat}}^{(j)}$, and $\ell_{\text{pix}}^{(j)}$ denote, respectively, the Re-ID score, latent-space distance, and pixel-space distance of sample j to its closest training image. We report the following dataset-level statistics:

$$\begin{aligned}
\text{Avg. Re-ID Score } (\downarrow) : \bar{s}_{\text{reid}} &= \frac{1}{M} \sum_{j=1}^M s_{\text{reid}}^{(j)}, & \text{Avg. Latent Distance } (\uparrow) : \bar{\ell}_{\text{lat}} &= \frac{1}{M} \sum_{j=1}^M \ell_{\text{lat}}^{(j)}, \\
\text{Avg. Pixel Distance } (\uparrow) : \bar{\ell}_{\text{pix}} &= \frac{1}{M} \sum_{j=1}^M \ell_{\text{pix}}^{(j)}, & \text{Max. Re-ID Score } (\downarrow) : s_{\text{reid}}^{\max} &= \max_{1 \leq j \leq M} s_{\text{reid}}^{(j)}, \\
\text{Count}[s_{\text{reid}} > \delta] (\downarrow) : C_\delta &= \sum_{j=1}^M \mathbf{1}[s_{\text{reid}}^{(j)} > \delta].
\end{aligned}$$

²<https://www.hhs.gov/hipaa/for-professionals/privacy/index.htm>

³<http://gdpr.eu/what-is-gdpr/>

Table 1: Table comparing the results for generative fidelity for 11 different T2I models in the benchmark. The best result for each metric is indicated with **bold**, while the second-best result is underlined. The overall best performing model (See Appendix Tab. 8) is **highlighted in green**.

Model	Size	Default Resolution	Prev. Available For CXR?	Fine-Tuning	FID ↓ (RadDino)	KID ↓ (RadDino)	Alignment Score ↑	Precision ↑	Recall ↑	Density ↑	Coverage ↑
SD V1-4 [35]	0.86B	512	✓	FFT	125.186	0.172	0.357	0.488	0.301	0.236	0.217
SD V1-5 [35]	0.86B	512	✓	FFT	118.932	0.147	0.326	0.536	0.473	0.242	0.256
SD V2 [35]	0.86B	512	✓	FFT	194.724	0.376	0.311	0.480	0.086	0.166	0.057
SD V2-1 [35]	0.86B	512	✓	FFT	186.530	0.413	0.197	0.530	0.049	0.180	0.038
RadEdit [39]	0.86B	512	✓	N/A	69.695	0.033	0.677	0.397	<u>0.544</u>	0.150	0.285
Pixart Sigma [36]	0.60B	512	✗	FFT	<u>60.154</u>	<u>0.023</u>	0.697	0.666	0.522	0.506	<u>0.506</u>
Sana [4]	0.60B	512	✗	FFT	54.225	0.016	<u>0.695</u>	<u>0.674</u>	0.614	<u>0.520</u>	0.548
SD V3.5 Medium [40]	2.50B	1024	✗	LoRA(r=32)	91.302	0.103	0.044	0.632	0.205	0.401	0.244
Lumina 2.0 [41]	2.60B	1024	✗	LoRA(r=32)	101.198	0.110	0.121	0.574	0.014	0.256	0.170
Flux.1-Dev [37]	12B	1024	✗	LoRA(r=32)	122.400	0.144	0.036	0.420	0.008	0.125	0.326
LLM-CXR [20]	12B	256	✓	N/A	71.243	0.061	0.319	0.782	0.041	0.671	0.459

2.4 Evaluation Protocol: Synthetic Data Utility for Downstream Tasks

A significant application of synthetic data in radiology lies in enhancing downstream model performance, potentially circumventing the stringent sharing restrictions imposed on medical datasets. For our utility assessment framework, we have strategically selected two prevalent downstream tasks previously established in radiological evaluation [19]: **(1) Image Classification** and **(2) Radiology Report Generation (RRG)**. These tasks were deliberately chosen for their distinct complexities. Image classification serves as a unimodal assessment, directly evaluating the intrinsic quality of synthetic radiographs, while RRG functions as a more demanding multimodal evaluation, assessing the factual correctness between synthetic images and their corresponding clinical descriptions.

Downstream Image Classification: We adopt the experimental setting previously utilised [19] and measure classification performance when a classifier [56] is trained *exclusively* on synthetic data (20K samples) (\mathcal{D}_{syn}) (for 20 epochs). This provides us with an idea of the stand-alone clinical value of the synthetic data from a generative model. The performance metrics are calculated on a held-out real test set (\mathcal{D}_{test}) to ensure clinical relevance and generalizability of our findings. We quantify classification performance through standard accuracy, F1-Score, and AUROC metrics.

Downstream Report Generation: We choose an existing multimodal model *LLaVA-Rad* [42] with SoTA radiograph understanding abilities and continue to fine-tune it with 20,000 synthetic samples. The performance is reported on a real test set (\mathcal{D}_{test}). We quantify RRG performance using the standard metrics adopted in literature [19, 42]: BLEU [57], ROUGE-L [58], F1-RadGraph [59], and F1-Score. BLEU-1 and BLEU-4 measure word and short phrase overlap with reference reports to gauge basic fluency and word choice. ROUGE-L focuses on sentence-level structure and recall of important, potentially non-contiguous, phrases. F1-RadGraph evaluates for factual correctness, while F1-Scores (F1-5 and F1-14) assess the accuracy of identifying the presence or absence of a predefined set of 5 or 14 specific radiological findings within the generated report.

3 Experiments and Results

Training Setting: Our evaluation used various T2I models with different training approaches. We used existing radiograph generation models (RadEdit [39], LLM-CXR [20]) unmodified. For models under 1B parameters, we performed full fine-tuning (FFT), while larger models used Parameter-Efficient Fine-Tuning (PEFT) with LoRA [44] (rank 32) on query, key, and value layers. Stable-Diffusion variants utilised Huggingface Diffusers [38], while Sana and Pixart-Sigma were trained using their official repositories. Larger models employed the ai-toolkit package⁴. Training followed officially recommended hyperparameters with a consistent total batch size of 128 across 4 Nvidia H200 GPUs, using 237,388 training samples and 5,034 test samples. Downstream evaluation experiments were conducted on Nvidia A100 GPUs.

3.1 Fidelity of Synthetic Generations

Results on Global Assessment

⁴<https://github.com/ostris/ai-toolkit>

Table 2: Comparison of FID (RadDino) scores (\downarrow) across individual pathologies in the MIMIC-CXR dataset. Lower values indicate superior performance, with the best results for each pathology highlighted in **bold**. The most challenging pathology (highest average FID across models) is highlighted in red, while the best-performing model overall is highlighted in green. We also highlight the best performing pathology for each model in blue.

Model	Atelectasis	Cardiomegaly	Consolid.	Edema	EC	Fracture	LL	LO	NF	PE	PO	PN	PT	SD
SD V1-4	134.11	131.04	184.30	144.84	217.75	238.78	225.99	129.38	106.34	128.16	255.84	163.82	212.48	135.10
SD V1-5	125.67	124.75	181.25	139.94	213.94	243.17	123.13	255.64	167.81	193.75	243.17	101.08	119.91	123.64
SD V2	188.72	193.91	241.24	214.40	214.40	253.91	268.28	280.11	193.99	299.48	223.43	250.96	183.34	193.99
SD V2-1	179.20	181.79	228.43	193.62	242.65	263.01	260.15	185.00	192.30	178.84	287.27	213.26	242.60	176.99
RadEdit	63.38	62.79	136.59	76.94	155.97	197.58	184.11	61.90	67.88	60.60	215.92	114.66	151.34	53.10
Pixart Sigma	59.27	60.39	133.96	73.93	155.53	179.44	174.63	56.83	48.74	59.05	210.90	108.42	150.55	51.61
Sana	51.03	54.68	127.46	67.84	147.00	172.32	163.14	49.23	44.60	49.80	199.45	99.52	141.99	46.51
SD V3.5 Medium	94.94	94.84	149.05	111.94	168.48	184.75	173.37	86.72	89.60	91.92	203.62	124.07	163.27	86.99
Lumina 2.0	109.39	111.11	162.36	131.18	182.35	191.83	182.22	99.53	95.66	105.25	213.50	134.58	165.09	102.78
Flux.1-Dev	137.10	133.60	176.76	152.91	191.48	191.02	194.97	133.37	100.58	137.66	221.23	156.59	190.93	127.03
LLM-CXR	71.57	71.37	136.65	83.18	148.28	168.50	163.22	66.93	64.62	67.83	200.84	108.04	147.52	67.54

The results are presented in Tab. 1, where we showcase both fidelity and mode coverage metrics. Sana [4] delivers superior overall performance across key metrics, achieving the lowest FID and KID scores, indicating exceptional generation fidelity, while simultaneously attaining the highest Recall and Coverage, demonstrating its capacity to capture diverse modes (distributions) throughout the dataset. Pixart Sigma [36] emerges as a strong contender, exhibiting the highest image-text alignment alongside second-best FID, KID, and Coverage scores. LLM-CXR [20] exhibits specialised capabilities, substantially outperforming all other models in Precision; however, its notably low Recall suggests limited generative scope, primarily effective for specific distributions (pathologies). This also highlights that conventional fidelity metrics like FID do not present a complete picture of the model performance. Earlier Stable-Diffusion variants (SD V-1.x, V2-x) demonstrate consistently suboptimal scores across all metrics despite full fine-tuning, a particularly significant finding given their prevalent adoption in the synthetic radiograph generation literature [19, 34, 27, 23]. Larger architectural models (SD V3-5 [40], Lumina 2.0 [41], Flux.1-Dev [37]), with the exception of LLM-CXR, yield predominantly inferior performance across evaluation metrics. SD V3-5 exhibits high Precision but low Recall, Density, and Coverage scores, mirroring trends observed in LLM-CXR. We hypothesise that this stems from the inability of LoRA to provide sufficient adaptation for the medical domain, a limitation previously observed in [23]. Performance improvements might be achievable by extending LoRA to other linear layers beyond attention (Q,K,V) layers, however, we leave this exploration to future work. Overall, Sana achieves the optimal performance-efficiency trade-off among all evaluated models. **Notably**, Sana has been adapted for synthetic radiograph generation for the first time through this work.

Results on Conditional Assessment

Results for conditional analysis on individual pathologies are presented in Tab. 2. Consistent with trends observed in Tab. 1, Sana demonstrates superior performance, achieving the lowest FID scores across 12 of the 14 pathology categories. This indicates Sana’s robust capability to generate high-fidelity radiographs across diverse pathological conditions. Pixart Sigma maintains its position as the second-best performing model, while RadEdit frequently secures the third-best scores across multiple categories. LLM-CXR demonstrates competitive performance for specific pathologies, notably achieving strong results for Edema (83.18) and No Finding (64.62), frequently outperforming both earlier Stable Diffusion models and certain large-scale models (SD V3.5, Lumina, Flux.1-Dev).

Concerning Observations: This analysis reveals concerning patterns. Substantial performance variation exists across pathologies for each model, regardless of overall performance. For instance, Sana exhibits FID scores ranging from 44.60 for “No Finding (NF)” to 199.45 for “Pleural Other (PO)”. Notably, five of the eleven models achieve optimal performance on “No Finding” cases, which represent healthy radiographs with limited clinical utility from synthetic X-rays, while all models consistently perform poorly on “Pleural Other (PO)” pathology. In Appendix D and Tab. 10, we empirically demonstrate that model performance strongly correlates with pathology prevalence in the training dataset (correlation coefficient: 0.947), suggesting that current models primarily

¹**Note:** EC = Enlarged Cardiomeastinum, LL = Lung Lesion, LO = Lung Opacity, NF = No Finding, PE = Pleural Effusion, PO = Pleural Other, PN = Pneumonia, PT = Pneumothorax, SD = Support Devices.

Table 3: Results on Re-Identification Risk and Patient Privacy Metrics. We present the average scores across 2000 samples and individual scores with maximum privacy risks.

Model	SD V1-4	SD V1-5	SD V2	SD V2-1	RadEdit	Sana	Pixart- Σ	SD V3-5	Lum. 2.0	Flux	LLM-CXR
Avg. Re-ID Score (\downarrow)	0.539	0.572	0.533	0.503	0.481	0.551	0.548	0.365	0.513	0.404	0.537
Avg. Latent Distance (\uparrow)	0.592	0.583	0.588	0.592	0.560	0.540	0.561	0.601	0.591	0.595	0.557
Avg. Pixel Distance (\uparrow)	143.441	143.634	143.936	145.652	145.272	162.901	159.864	147.098	145.612	155.926	149.626
Max. Re-ID Score (\downarrow)	0.996	0.996	0.996	0.997	0.992	0.996	0.994	0.997	0.993	0.992	0.994
Count Re-ID $> \delta$ (\downarrow)	434	498	454	392	380	442	442	236	223	196	419

reflect dataset distribution characteristics rather than achieving balanced clinical utility. We hope this analysis encourages model developers to incorporate training strategies tailored for long-tailed distributions [60].

3.2 Results on Privacy and Re-Identification Risks

Experimental Setting: To quantify re-identification risks, we select a subset of 2000 image-text pairs (x_i^{img}, x_i^{txt}) from the training set and generate $N(= 10)$ synthetic samples $\hat{x}_i^{img,1}, \hat{x}_i^{img,2}, \dots, \hat{x}_i^{img,N}$ using 10 different random seeds for each training prompt. Next, we calculate Re-ID scores, Pixel and Latent Distances between each real-synthetic pair $(x_i^{img}, \hat{x}_i^{img,n})$ for all $n \in \{1, 2, \dots, N\}$. Finally, we report the maximum Re-ID score $\max_j s_{reid}^{(j)}$, minimum pixel distance $\min_j \ell_{pix}^{(j)}$ and minimum latent distance $\min_j \ell_{lat}^{(j)}$ across N generations for each sample. This approach enables us to identify the greatest privacy risk posed for each training sample across multiple generations.

The privacy risk assessment results are detailed in Tab. 3. Most models exhibit Average Re-ID scores within a comparable range, with SD V3-5 notably achieving the lowest (most favorable) score. For latent and pixel distances, a similar pattern emerges, where SD V3-5 and Sana demonstrate superior performance (i.e., lower average distances), respectively. **Concerning Observations:**

We conducted a detailed analysis of *individual* scores across 2,000 samples, with particular attention to two key metrics: (1) the maximum Re-ID score, which represents the highest potential for re-identification, and (2) the frequency of samples exceeding a high-risk threshold ($\delta = 0.85$). Our results reveal that all models, regardless of their fidelity performance, generate samples that can be re-identified with high confidence. The proportion of samples presenting significant re-identification risk remains substantial across all models, ranging from 10% to 25%. Notably, models trained with LoRA demonstrate a relatively lower incidence of high-risk samples, potentially due to their reduced capacity for memorization [30]. These findings underscore a critical insight: **generative models pose substantial privacy risks irrespective of their generative capabilities.**

3.3 Utility of Synthetic Samples for Downstream Tasks

Downstream Task: Image Classification

Results: We present the results in Tab. 4. Sana emerges as exceptionally effective, with its synthetic images enabling classifiers to match or exceed the original data baseline on an impressive 10 out of 13 pathologies. Interestingly, it surpasses the baseline on *Fracture*, an underrepresented class in MIMIC-CXR. Other models, such as RadEdit, Pixart-Sigma, and LLM-CXR, show limited success by matching the baseline for at most two pathologies, failing to surpass it. Models like SD V1-4, SD V3-5, Lumina 2.0, and Flux.1-Dev generally produce synthetic data that leads to classifiers significantly underperforming the Original Data baseline across most or all pathologies. **Viability:**

The results from Sana strongly suggest that high-quality synthetic data can, in some cases, be a viable standalone replacement for real data for training medical image classifiers. This is a powerful finding with implications for data privacy, scarcity, and augmentation. In Appendix C, we expand on the correlation between generative fidelity and downstream utility for classification.

Downstream Task: Radiology Report Generation

The results are presented in Tab. 5. Firstly, we observe that *additional* fine-tuning with synthetic data, irrespective of the model, leads to a performance degradation as compared to the original baseline (trained with real data). In terms of the models, RadEdit and Sana emerge as leading performers.

Table 4: Performance Comparison (AUC \uparrow) of a ResNet50 classifier trained **only on synthetic data** vs. Original (Real) Data Baseline for all pathologies in the MIMIC dataset. Results matching or exceeding the Original Data baseline are **bolded** and within 0.01 AUC are underlined.

Model	Atel-ectasis	Cardio-megaly	Consol-idation	Edema	EC	Fracture	LL	LO	NF	PE	PO	PN	PT	SD
Original (Real)	0.75	0.76	0.72	0.85	0.61	0.58	0.63	0.70	0.84	0.84	0.74	0.67	0.71	0.83
SD V1-4	0.70	0.70	0.67	0.81	0.56	<u>0.57</u>	0.63	0.67	0.80	0.77	0.65	0.60	0.65	0.80
SD V1-5	0.72	0.72	0.69	0.81	<u>0.60</u>	0.53	0.66	0.67	0.82	0.79	0.68	0.62	<u>0.70</u>	0.83
SD V2	0.66	0.69	0.66	0.78	0.61	0.53	0.55	0.63	0.75	0.76	0.50	0.61	0.64	0.78
SD V2-1	0.63	0.67	0.65	0.71	0.55	0.59	<u>0.62</u>	0.62	0.75	0.74	0.57	0.56	0.61	0.75
RadEdit	0.73	0.73	0.72	<u>0.84</u>	0.61	0.56	0.60	<u>0.69</u>	0.81	0.82	0.72	<u>0.66</u>	0.66	0.77
Pixart Sigma	<u>0.74</u>	0.73	0.70	<u>0.84</u>	0.61	0.58	0.61	<u>0.69</u>	<u>0.83</u>	0.81	0.68	0.63	<u>0.70</u>	0.80
Sana	<u>0.74</u>	0.76	0.72	0.85	0.61	0.62	0.63	0.70	<u>0.83</u>	0.84	<u>0.73</u>	0.64	0.72	0.83
SD V3-5	0.55	0.55	0.56	0.55	0.47	0.47	0.47	0.53	0.60	0.54	0.58	0.49	0.55	0.71
Lumina 2.0	0.46	0.48	0.52	0.51	0.46	<u>0.57</u>	0.53	0.52	0.59	0.55	0.57	0.49	0.50	0.71
Flux.1-Dev	0.41	0.41	0.44	0.40	0.44	0.52	0.48	0.42	0.40	0.38	0.50	0.48	0.44	0.67
LLM-CXR	0.70	0.69	0.70	0.81	0.61	<u>0.57</u>	0.54	0.65	0.80	0.77	0.66	0.61	0.63	0.73

Table 5: Radiology Report Generation (RRG) performance metrics for various generative models.

Metric	Original	SD V1-4	SD V1-5	SD V2	SD V2-1	RadEdit	Pixart- Σ	Sana	SD V3-5	Lumina 2.0	Flux.1-Dev	LLM-CXR
BLEU-1 (\uparrow)	38.16	25.85	26.02	26.62	26.76	30.55	31.25	31.11	23.49	17.96	18.19	29.78
BLEU-4 (\uparrow)	15.38	6.76	7.50	7.35	7.38	8.36	7.91	7.70	4.91	4.27	3.36	7.93
ROUGE-L (\uparrow)	0.31	0.23	0.24	0.24	0.24	0.24	0.23	0.24	0.20	0.20	0.18	0.23
F1-RadGraph (\uparrow)	0.29	0.21	0.24	0.23	0.22	0.24	0.22	0.23	0.17	0.18	0.14	0.21
Micro F1-5 (\uparrow)	0.57	0.56	0.54	0.57	0.57	0.55	0.50	0.57	0.31	0.41	0.32	0.55
Micro F1-14 (\uparrow)	0.57	0.53	0.51	0.55	0.53	0.55	0.52	0.55	0.35	0.41	0.36	0.53

RadEdit excels in BLEU-4 (fluency) and is a top contender in F1-RadGraph (semantic accuracy of clinical entities) and Micro F1-14 (specific findings detection), while Sana demonstrates strengths in ROUGE-L (sentence structure) and Micro F1 scores for identifying specific findings. LLM-CXR also gives a strong performance, often giving second- or third-best scores. Pixart Sigma shows the best individual word usage (BLEU-1), and models like SD V2 also perform well in Micro F1 scores. Overall, no single model dominates in all metrics. These results reflect that current T2I models might show high fidelity, but their utility for multimodal tasks such as report generation is still limited under the current setting. Potentially, generations with stronger image-text alignment or training VQA models on a collection of real and synthetic data from scratch can alleviate this.

4 The SynthCheX-75K Dataset

We introduce *SynthCheX-75K*, a comprehensive synthetic dataset for medical image analysis research. We generated this dataset using Sana [4], our benchmark’s top-performing model, after additional fine-tuning from 20 to 50 epochs. Analysis in Appendix Fig. 4 shows that extended fine-tuning yields modest FID improvements and more significant Recall improvements across all pathologies. Using a highly-capable medical VLM, HealthGPT [61], we first filter out all the low-quality generations (0.83%), and include only images with high (39%) or medium quality (60.16%). The dataset is publicly available [here](#). Data filtration is further discussed in Appendix F.

5 Conclusion

We identified critical gaps in synthetic radiograph generation research and introduced CheXGenBench to assess generation fidelity, privacy preservation, re-identification risk, and downstream utility in a single framework. Our findings reveal that: (1) models, *even SoTA*, struggle with long-tailed medical data distributions significantly limiting their potential utility, (2) models, *even with poor fidelity*, pose high privacy risks, and (3) synthetic data offers limited utility in downstream multimodal tasks. These limitations highlight substantial opportunities for improvement in future research. With our benchmark-leading Sana (0.6B) model, we produced *SynthCheX-75K*, a high-quality synthetic radiograph dataset. We have open-sourced our benchmark, model checkpoints, and dataset to provide a standard evaluation protocol for a comprehensive assessment of medical image generation models and expect the benchmark to grow with new generative models and paradigms.

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A Benefits of Adopting LLaVA-Rad Annotations

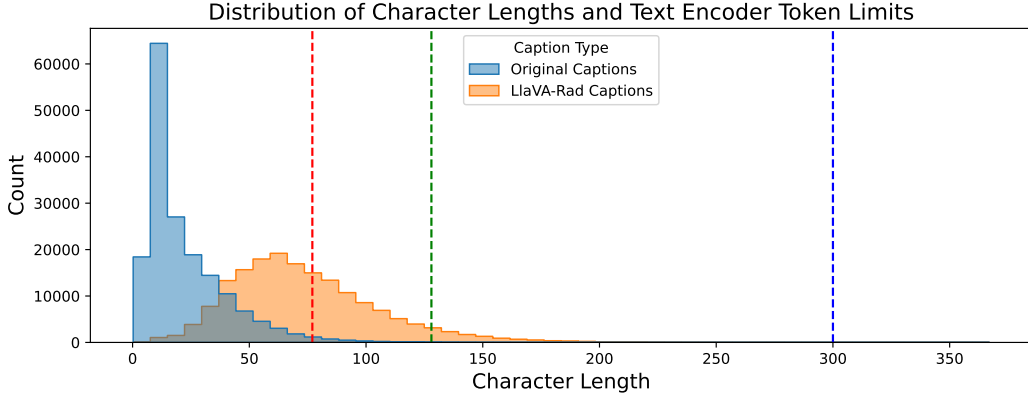


Figure 2: Figure depicting distribution of character lengths for original MIMIC captions and LLaVA-Rad annotations. We also illustrate the text-encoder token length limits for all **SD variants** and **Flux (77 tokens)**, **RadEdit (128 tokens)**, and **Pixart Sigma (300 tokens)**.

Note: We treat 1 token \approx 4 characters²

Table 6: Comparison of generation fidelity (left) and privacy preservation (right) metrics across different stable diffusion models. LLaVA-Rad annotations consistently outperform original MIMIC impressions, yielding improved image quality (FID/KID (\downarrow), higher alignment (\uparrow)) and enhanced privacy protection (Re-ID (\downarrow), latent/pixel distances (\uparrow)).

Model	Prompt Type	FID (RadDino)	KID (RadDino)	Alignment Score
SD-V1-4	Original MIMIC	147.298	0.198	0.272
SD-V1-4	LlaVA-Rad	125.186	0.172	0.357
SD-V1-5	Original MIMIC	144.661	0.201	0.257
SD-V1-5	LlaVA-Rad	118.932	0.147	0.326
SD-V2	Original MIMIC	214.202	0.496	0.145
SD-V2	LlaVA-Rad	194.724	0.376	0.311

Model	Prompt Type	Max. Re-ID Distance \downarrow	Min Latent Distance \uparrow	Min. Pixel Distance \uparrow
SD-V1-4	Original MIMIC	0.725 ± 0.71	0.482 ± 0.66	132.24 ± 4.6
SD-V1-4	LlaVA-Rad	0.539 ± 0.31	0.592 ± 0.05	143.44 ± 4.6
SD-V1-5	Original MIMIC	0.721 ± 0.47	0.476 ± 0.41	131.44 ± 4.2
SD-V1-5	LlaVA-Rad	0.572 ± 0.29	0.583 ± 0.04	143.634 ± 4.2
SD-V2	Original MIMIC	0.687 ± 0.23	0.483 ± 0.34	132.64 ± 4.3
SD-V2	LlaVA-Rad	0.533 ± 0.32	0.588 ± 0.05	143.936 ± 4.3

(a) Generation fidelity metrics.

(b) Privacy and memorisation risk metrics.

In this section, we demonstrate that LLaVA-Rad Annotations lead to substantial improvements in both fidelity performance and reduction of re-identification risks (Table 6). We attribute these improvements to two key factors: the enhanced descriptiveness of the annotations and the removal of certain tokens from the original MIMIC annotations known to increase privacy risks [31]. Figure 2 displays the distribution of average character lengths across both annotation types. MIMIC annotations cluster around significantly smaller values, while LLaVA-Rad Annotations exhibit a wider distribution, indicating greater descriptive detail. Table 6a reveals that LLaVA-Rad Annotations significantly enhance all three fidelity metrics (FID, KID, and Image-Text Alignment) compared to the original MIMIC annotations. Additionally, in Tab. 6b, we observe a substantial improvement in privacy risk mitigation, further validating the superiority of the LLaVA-Rad annotation approach.

²<https://help.openai.com/en/articles/4936856-what-are-tokens-and-how-to-count-them>

B Unreliability in Fidelity Estimates with Outdated Backbones

Table 7: Comparison of FID and KID metrics across models using two distinct in-domain encoders. While the conventional DenseNet-121 encoder [33] exhibits minimal variance (0.001 - 0.075) across models, indicating limited discriminative power, the RadDino encoder [49] demonstrates substantially greater metric differentiation (54.22 - 194.72), providing more meaningful evaluation of model performance.

Metric	SD V1-4	SD V1-5	SD V2	SD V2-1	RadEdit	Pixart Sigma	Sana	SD V3-5	Lumina 2.0	Flux.1-Dev	LLM-CXR
FID	DenseNet	0.025	0.075	0.053	0.056	0.001	0.001	0.001	0.002	0.001	0.025
	RadDino	125.180	118.930	194.720	186.530	69.690	60.150	54.220	91.300	101.190	71.240
KID	DenseNet	0.004	0.004	0.005	0.005	0.001	0.001	0.001	0.004	0.003	0.003
	RadDino	0.172	0.147	0.376	0.413	0.033	0.023	0.016	0.103	0.110	0.061

We demonstrate that existing protocols for evaluating generative fidelity in radiographic imaging are unreliable. Current approaches [19, 23, 20] calculate image fidelity (FID Score) using an in-domain DenseNet-121 model trained on the MIMIC-CXR dataset. We argue this model lacks sufficient discriminative power, resulting in less meaningful fidelity assessments.

In our CheXGenBench benchmark, we address this limitation by leveraging features from RadDino, a state-of-the-art model specifically designed for radiographs. As shown in Table 7, FID evaluation with DenseNet-121 shows minimal variance across models, often ranking several models at the same position. In contrast, the RadDino encoder significantly enhances evaluation quality by providing more meaningful feature representations that better differentiate between model performances.

C Correlation between Fidelity and Downstream Tasks

Image Fidelity: We present the rank for each T2I model across each individual fidelity and mode coverage metric in Tab. 8. We also present the combined rank averaged across all the metrics resulting in Sana [4], Pixart Sigma [36], and LLM-CXR [20] as the top-three performers across all models.

Downstream Image Classification: We present the rank for each T2I model across each individual pathology in Tab. 9.

The Pearson correlation between fidelity and classification rank is **0.70**. Based on the correlation coefficient of 0.70 between image fidelity and downstream classification performance, we can derive several important conclusions:

1. **Strong Positive Correlation:** A correlation of 0.70 indicates a strong positive relationship between image fidelity and downstream classification performance. This means that as image fidelity increases, classification performance tends to increase substantially as well. This also supports the value of developing high-fidelity synthetic image generators for medical applications.
2. **Substantial Explained Variance:** The coefficient of determination (r^2) would be approximately 0.49, suggesting that about 49% of the variance in classification performance can be explained by image fidelity.
3. **Model Selection Guidance:** When choosing models for generating synthetic medical images for training purposes, prioritizing those with higher fidelity metrics would be a data-driven approach that’s likely to yield better downstream performance.
4. **Not a Perfect Relationship:** While strong, the correlation of 0.70 still leaves about 51% of the variance unexplained. This suggests other factors beyond simple image fidelity also influence classification performance, such as:
 - (a) Diversity of the generated images
 - (b) Representation of edge cases
 - (c) Specific features that are diagnostically relevant but might not contribute heavily to overall fidelity metrics

For medical imaging applications specifically, this correlation supports the hypothesis that realistic-looking synthetic images translate to better diagnostic model performance, though the relationship

isn't perfect. This finding could help justify investments in more sophisticated image generation techniques that prioritize visual fidelity.

Table 8: Performance ranking of generative models for image fidelity across multiple evaluation metrics (lower rank indicates better performance). The top-3 performers are (1) Sana [4], (2) Pixart Sigma [36], and (3) LLM-CXR [20].

Model	FID		KID		Alignment Score	Precision	Recall	Density	Coverage	Average Rank	Normalized Rank
	Inception	RadDino	Inception	RadDino							
SD V1-4	9	9	9	9	4	8	5	7	8	7.55	8
SD V1-5	8	7	8	8	5	6	4	6	6	6.44	6
SD V2	10	11	10	10	7	9	6	9	10	9.11	10
SD V2-1	11	10	11	11	8	7	7	8	11	9.33	11
RadEdit	3	3	3	3	3	11	2	10	5	4.78	4
SD V3-5	5	5	5	5	10	2	11	4	7	6.00	5
Lumina 2.0	6	6	6	6	9	5	9	5	9	6.78	7
Flux.1-Dev	7	8	7	7	11	10	10	11	4	8.33	9
LLM-CXR	4	4	4	4	6	1	8	1	3	3.89	3
Pixart Sigma	2	2	2	2	1	4	3	3	2	2.33	2
Sana	1	1	1	1	2	3	1	2	1	1.44	1

Note: Lower rank numbers indicate better performance. Top three models highlighted based on normalized rank.

Table 9: Ranking each T2I Model for synthetic data utility (image classification) across all 14 pathologies.

Model	Atel.	Card.	Cons.	Edema	EC	Fract.	LL	LO	NF	PE	PO	PN	PT	SD	Avg.
SD V1-4	5.5	5.0	6.0	5.0	7.0	5.0	2.5	4.5	5.5	5.5	6.0	7.0	5.0	3.5	5.0
SD V1-5	4.0	4.0	5.0	5.0	6.0	8.5	1.0	4.5	3.0	4.0	3.5	4.0	2.5	1.5	4.0
SD V2	7.0	6.5	7.0	7.0	3.0	8.5	7.0	7.0	7.5	7.0	10.5	5.5	6.0	5.0	7.0
SD V2-1	8.0	8.0	8.0	8.0	8.0	2.0	4.0	8.0	7.5	8.0	8.5	8.0	8.0	7.0	7.0
RadEdit	3.0	2.5	1.5	2.5	3.0	7.0	6.0	2.5	4.0	2.0	2.0	1.0	4.0	6.0	3.0
Pixart Sigma	1.5	2.5	3.5	2.5	3.0	3.0	5.0	2.5	1.5	3.0	3.5	3.0	2.5	3.5	3.0
Sana	1.5	1.0	1.5	1.0	3.0	1.0	2.5	1.0	1.5	1.0	1.0	2.0	1.0	1.5	1.0
SD V3-5	9.0	9.0	9.0	9.0	9.0	11.0	11.0	9.0	9.0	10.0	7.0	9.5	9.0	9.5	9.0
Lumina 2.0	10.0	10.0	10.0	10.0	10.0	5.0	9.0	10.0	10.0	9.0	8.5	9.5	10.0	9.5	9.0
Flux.1-Dev	11.0	11.0	11.0	11.0	11.0	10.0	10.0	11.0	11.0	11.0	10.5	11.0	11.0	11.0	11.0
LLM-CXR	5.5	6.5	3.5	5.0	3.0	5.0	8.0	6.0	5.5	5.5	5.0	5.5	7.0	8.0	6.0

Legend: Atel. = Atelectasis, Card. = Cardiomegaly, Cons. = Consolidation, EC = Enlarged Cardiomeastinum, Fract. = Fracture, LL = Lung Lesion, LO = Lung Opacity, NF = No Finding, PE = Pleural Effusion, PO = Pleural Other, PN = Pneumonia, PT = Pneumothorax, SD = Support Devices, Avg. = Average Ranks

D Correlation Between Fidelity and Disease Distribution

In this section, we examine whether generative fidelity performance for individual pathologies, as reported in Tab. 2, correlates with the frequency of pathology occurrence in the training dataset. Fig. 3 illustrates the occurrence frequency distribution of 14 distinct pathologies in the training set. Conditions such as “No Finding (NF)”, “Pleural Effusion (PE)”, “Support Devices (SD)”, and “Lung Opacity (LO)” represent the most frequently observed pathologies in the training data. Conversely, “Fracture” and “Pleural Other” exhibit significantly lower occurrence frequencies.

Tab. 10 presents the comparative rankings according to occurrence frequency and FID scores. Analysis reveals a remarkably strong positive correlation coefficient of **0.947** between these rankings, providing compelling evidence that generative fidelity demonstrates substantial dependence on pathology occurrence frequency in the training distribution.

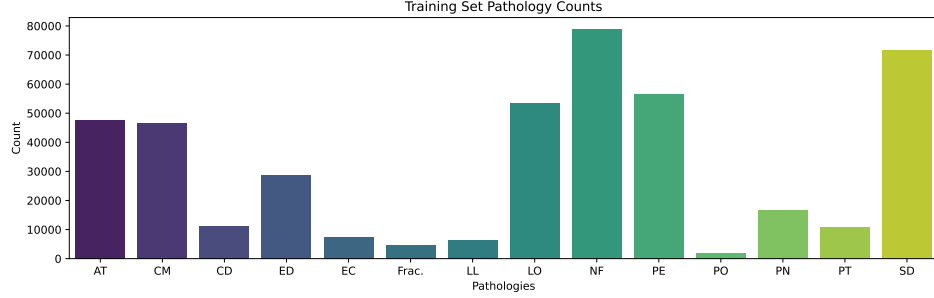


Figure 3: Figure depicting the distribution of pathology counts for the 14 different conditions present in the MIMIC dataset. We indicate pathologies with there abbreviations.

Note: **AT** (Atelectasis), **CM** (Cardiomegaly), **CD** (Consolidation), **ED** (Edema), **EC** (Enlarged Cardiome-diastinum), **Frac.** (Fracture), **LL** (Lung Lesion), **LO** (Lung Opacity), **NF** (No Finding), **PE** (Pleural Effusion), **PO** (Pleural Other), **PN** (Pneumonia), **PT** (Pneumothorax), **SD** (Support Devices).

Table 10: Occurrence Frequency and Generative Fidelity for Different Pathologies with rankings. We calculate the "Fidelity Rank" across models from Tab. 2

Pathology Code	Count (n)	Prevalence Rank	FID (RadDino)	Fidelity Rank
NF	78,939	1	110.75	2
SD	71,537	2	109.77	1
PE	56,433	3	130.45	5
LO	53,513	4	133.77	7
AT	47,704	5	114.28	3
CM	46,602	6	114.89	4
ED	28,601	7	130.75	6
PN	16,832	8	146.69	8
CD	11,290	9	172.14	9
PT	10,971	10	172.15	10
EC	7,454	11	188.95	11
LL	6,491	12	194.99	12
Frac.	4,671	13	211.58	13
PO	2,024	14	227.43	14

Note: Lower FID (Fréchet Inception Distance) scores indicate better generative fidelity. The table shows a correlation between pathology prevalence and generative quality. Pathology codes: NF = No Finding, SD = Support Devices, PE = Pleural Effusion, LO = Lung Opacity, AT = Atelectasis, CM = Cardiomegaly, ED = Edema, PN = Pneumonia, CD = Consolidation, PT = Pneumothorax, EC = Enlarged Cardiome-diastinum, LL = Lung Lesion, Frac. = Fracture, PO = Pleural Other.

E Effect of Additional Fine-Tuning of Sana

In this section, we analyze the impact of extended fine-tuning on our benchmark-leading model, Sana (0.6B), by increasing training from 20 epochs (as reported in the main benchmark) to 50 epochs. Our analysis reveals a nuanced picture of how prolonged training affects different performance dimensions. In Tab. 11, we show the improvements from the 20 epoch checkpoint on Report Generation task.

Fidelity Improvements: As illustrated in Figure 4a, extended fine-tuning yields modest but consistent improvements in FID scores across all pathologies. The most significant gains were observed in *No Finding*, which stands as the class with the most number of samples in the MIMIC dataset.

Improvement in Recall Scores: Fig. 4b demonstrates that recall scores show more substantial improvements than fidelity metrics. This pattern indicates that extended training primarily enhances the model’s ability to reproduce a larger spectrum of pathological variations rather than incrementally

improving visual quality. Interestingly, in this scenario, all classes (majority and minority) show significant improvement.

Takeaway: Despite the additional training epochs, performance improvements on rare pathologies remain disproportionately small compared to common conditions. This observation shows that addressing long-tailed distribution challenges cannot be solved through extended fine-tuning alone and would require specialised algorithmic changes.

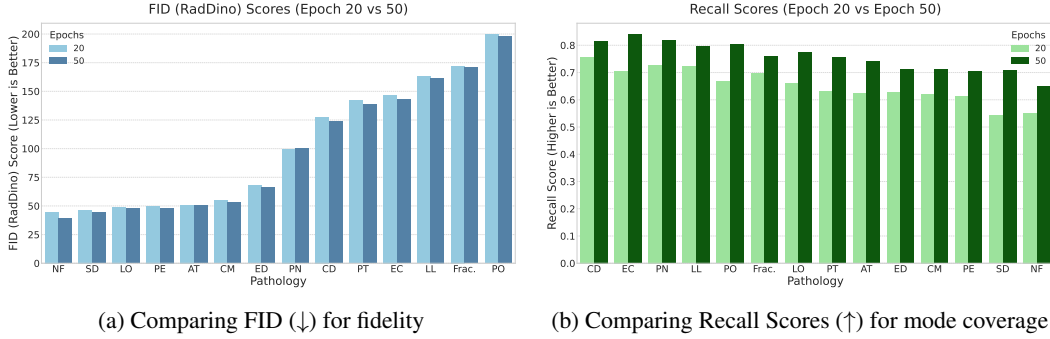


Figure 4: Extended Training Impact on Sana Model Performance. Comparison of generative quality metrics after standard (20 epochs) and extended (50 epochs) fine-tuning of the Sana model. While FID scores show modest improvement, the Recall metric exhibits substantial enhancement across all pathologies, indicating significantly improved sample diversity without compromising fidelity.

E.1 Training Settings and Hyperparameters

The hyperparameters (learning rates) for Text-to-Image model training are provided in Tab. ?? . Existing foundation models (RadEdit, LLM-CXR) were not re-trained and used as is.

For evaluating downstream utility, the learning rates are provided in Tab. ?? .

Hyper-Params	SD V1-4	SD V1-5	SD V2	SD V2-1	RadEdit	Pixart Sigma	Sana	SD V3-5	Lumina 2.0	Flux.1-Dev	LLM-CXR
Fine-Tuning	FFT	FFT	FFT	FFT	N/A	FFT	FFT	LoRA (r-32)	LoRA (r-32)	LoRA (r-32)	N/A
Learning Rate	5e-6	5e-6	5e-6	5e-6	-	2e-5	1e-4	1e-4	1e-4	1e-4	-

Model	ResNet-50 (Classification)	LLaVA-Rad (RRG)
Fine-Tuning	FFT	LoRA
Learning Rate	1e-4	1e-4

F Data Filtration for SynthCheX-75K

Generative models can lead to both high and low-fidelity generations on different subsets of the dataset. In order to keep the sample quality high in SynthCheX-75K, a stringent filtration process was adopted using HealthGPT [61], a highly-capable medical VLM with advanced understanding, reasoning and generation.

The VLM was provided with the following meta-prompt to classify the quality of each generated sample.

META PROMPT: "You are an expert radiologist and medical annotator. Your task is to assess the quality of an image given its description and classify the image as either 'High Quality', 'Medium Quality', or 'Low Quality'. Keep your responses limited to only these three options. If the image is not relevant to the description, respond with 'Not Relevant'."

After quality label assignment, images with "Low Quality" and "Not Relevant" labels were removed from the dataset leading to 75,649 samples of high-quality radiographs with pathological annotations.

Table 11: Comparing the performance of fine-tuning Sana from 20 to 50 epochs for the RRG task. Additional fine-tuning does provide benefits, however, they are marginal.

Model	BLEU-1	BLEU-4	ROUGE-L	F1-RadGraph	Micro F1-5	Micro F1-14
Original	38.16	15.38	0.31	0.29	0.57	0.57
Sana (Epoch 20)	29.83	7.70	0.24	0.23	0.57	0.55
Sana (Epoch 50)	30.80 (+0.97)	7.91 (+0.21)	0.25 (+0.01)	0.24 (+0.01)	0.58 (+0.01)	0.57 (+0.02)

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