

# Replay-free Sequential Fine-tuning of Medical VLMs

He Li

*Tsinghua University, People's Republic of China*

LIHE22@MAILS.Tsinghua.EDU.CN

Yuhui Zhang

Xiaohan Wang

Serena Yeung-Levy

*Stanford University, United States*

YUHUIZ@STANFORD.EDU

XHANWANG@STANFORD.EDU

SYYEUNG@STANFORD.EDU

## Abstract

Catastrophic forgetting severely limits the adaptation of Vision Language Models (VLMs) for medical applications, where sequential learning on private data is often necessary. We propose that this issue stems from insufficient regularization and demonstrate that regularizing parameter updates during fine-tuning effectively mitigates forgetting without harming new task performance. To validate our method in a clinical context, we introduce **Medical-CL**, a new continual learning benchmark spanning pathology, cell microscopy, radiology, and surgery. Our streamlined, replay-free approach proves highly effective on this benchmark, offering a practical path toward building comprehensive, continually-learning medical VLMs and advancing the development of medical AI.

**Keywords:** Vision Language Models, Continual Learning, Catastrophic Forgetting.

**Data and Code Availability** We use publicly available datasets: MLLM-CL Benchmark, BSBCM, PitVis-2023, PathVQA, ROCov2. We will make code and data publicly available.

**Institutional Review Board (IRB)** Our research does not require IRB approval.

## 1. Introduction

The emergence of Vision Language Models (VLMs) represents a significant milestone in artificial intelligence (Alayrac et al., 2022; Liu et al., 2023; Achiam et al., 2023). Building upon this foundational success, the field has increasingly focused on fine-tuning these powerful models for specialized medical applications, aiming to create robust medical VLMs.

However, the catastrophic forgetting phenomenon (Zhai et al., 2024; Shuttleworth et al., 2024) is an un-

avoidable issue for the development of medical VLM. This issue manifests as a severe degradation in a model's performance on previously learned tasks after it has been fine-tuned for a new specialization (McCloskey and Cohen, 1989). Within the context of medical VLMs, fine-tuning on a specific dataset could inadvertently compromise its general reasoning abilities or diminish its acquired knowledge pertinent to other medical fields. Furthermore, given that a significant volume of medical data is private or sensitive and cannot be easily shared, sequential learning on different datasets is an unavoidable necessity for building comprehensive medical VLMs under current constraints.

Drawing inspiration from prior research into the loss landscapes of Large Language Models (Chen et al., 2025) and the significance of orthogonal subspaces during fine-tuning (Wang et al., 2023), we hypothesize that the forgetting phenomenon arises from insufficient regularization during the adaptation process. Based on reasonable assumptions derived from landscape and subspace theory, we present the rationale for the efficacy of *regularizing parameter updates*.

Our experimental results demonstrate that *regularization applied to parameter updates can effectively mitigate forgetting without compromising performance on the fine-tuning task*. This holds true across multiple sequential fine-tuning scenarios, including domain-continual learning (Zhao et al., 2025). Empirical evaluations reveal that our simple approach surpasses the performance of existing methods, particularly those that depend on a data replay buffer. This outcome highlights the strong, inherent capacity of Vision-Language Models for continual learning.

Subsequently, we extend our investigation to various medical domains, curating a novel medical continual learning benchmark, which we term **Medical-**

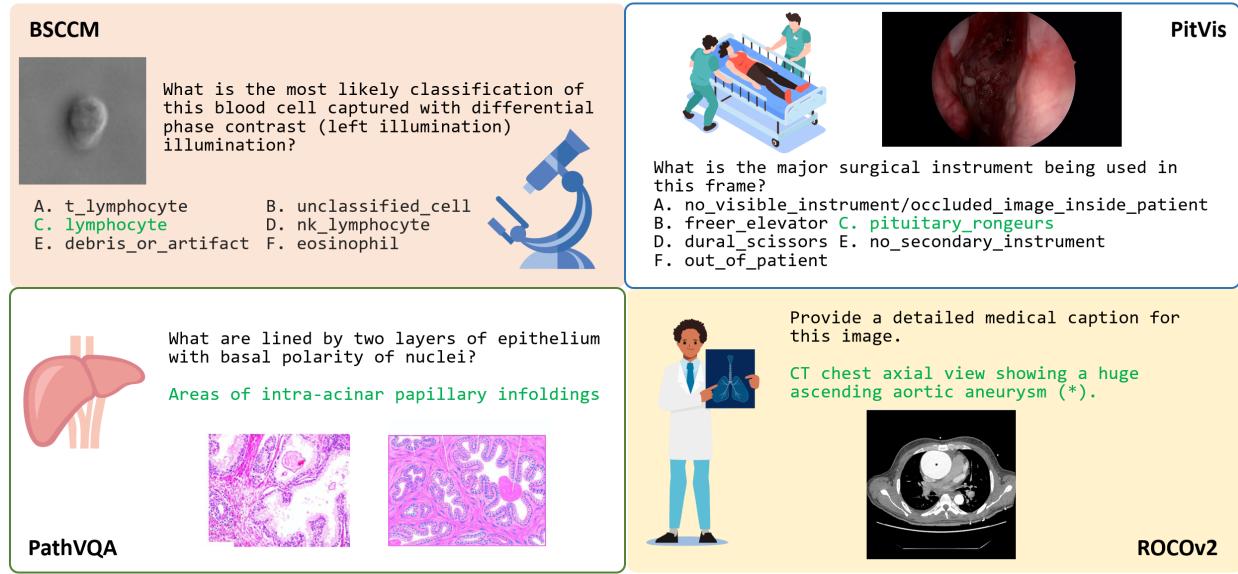


Figure 1: An Illustration of the Proposed Medical-CL Benchmark

75 **CL**, from a collection of public datasets (Pinkard  
76 et al., 2024; Das et al., 2025; He et al., 2020; Rückert  
77 et al., 2024). The **Medical-CL** benchmark in-  
78 corporates a variety of question formats, including  
79 àmultiple-choice, short-answer, and image caption-  
80 ing, to ensure a comprehensive evaluation. Adhering  
81 to a protocol similar to the **MLLM-CL** continual  
82 learning benchmark (Zhao et al., 2025), we confirm  
83 that our proposed method remains highly effective on  
84 this new benchmark.

85 In summary, this paper contributes a com-  
86 prehensive experimental investigation and correspond-  
87 ing theoretical analysis of the catastrophic forgetting  
88 phenomenon during VLM fine-tuning. Our work of-  
89 fers practical guidance for adapting these models to  
90 medical domains while preserving their previous ca-  
91 pabilities. This facilitates the sequential fine-tuning  
92 of VLMs on new medical data with minimal per-  
93 formance loss on previously learned tasks. We anticipate  
94 that this research will benefit practitioners in the field  
95 and advance the development of more robust and the-  
96oretically grounded VLMs. Code, checkpoints and  
97 data are available through anonymous links in Ap-  
98 pendix A.

## 2. Challenge: Sequentially Fine-tuning of VLMs

### 2.1. MLLM-CL Benchmark for General Continual Learning

The challenge of general sequential fine-tuning is  
103 analogous to the continual learning problem. Accord-  
104 ingly, we adopt the MLLM-CL benchmark and  
105 its evaluation protocols as proposed in a recent study  
106 (Zhao et al., 2025). This sequential learning bench-  
107 mark comprises five distinct domains: Remote Sens-  
108 ing (**RSVQA**), Medicine (**PathVQA**), Autonomous  
109 Driving (**DriveLM**), Science (**AI2D**, **SciVerse**,  
110 **MapQA**, **TQA**), and Finance (**StockQA**).  
111

For simplicity, these tasks are denoted as **RS**,  
112 **Med**, **AD**, **Sci**, and **Fin**, respectively. In our ex-  
113 periments, we follow the sequential fine-tuning order  
114 established in the original MLLM-CL study: **RS** →  
115 **Med** → **AD** → **Sci** → **Fin**. Training Details are  
116 provided in Appendix C.  
117

### 2.2. Evaluation Metrics

To ensure a fair and direct comparison, our evaluation  
119 protocol strictly adheres to the methodology outlined  
120 in MLLM-CL (Zhao et al., 2025). We report two  
121 primary metrics: *Last* and *Average*. The *Last* metric  
122 represents the average accuracy across all previously  
123

Method	Last					Average				
	RS (%)	Med (%)	AD (%)	Sci (%)	Fin (%)	RS (%)	Med (%)	AD (%)	Sci (%)	Fin (%)
Zero-shot	32.29	28.28	15.59	35.55	62.56	-	-	-	-	-
<i>w/ replay buffer</i>										
LoRA	29.57	29.19	7.09	19.55	63.60	80.87	58.60	38.95	36.41	36.78
MoELoRA	40.23	23.58	5.19	18.35	74.89	80.00	56.91	34.69	31.70	31.36
O-LoRA	76.21	51.34	36.50	42.64	90.20	80.13	70.23	61.35	53.34	59.38
L2P	75.21	38.50	32.31	41.05	88.05	80.09	68.64	54.79	48.68	55.02
ModalPrompt	64.77	38.60	20.61	29.98	88.22	80.11	60.99	50.67	41.97	48.44
HiDe-LLaVA	75.36	39.23	37.17	45.02	81.89	<b>81.51</b>	62.37	49.37	50.61	55.73
MR-LoRA	<b>79.87</b>	<b>62.71</b>	<u>51.89</u>	<b>52.48</b>	89.69	80.82	<b>72.19</b>	<u>65.41</u>	<b>62.52</b>	<b>67.31</b>
IncLoRA (Ours)	77.43	<u>62.57</u>	<b>52.00</b>	<b>52.48</b>	<u>90.41</u>	78.30	71.93	65.38	62.12	66.98
SeqFull (Ours)	<b>78.94</b>	62.45	51.50	<u>52.08</u>	<b>91.21</b>	75.62	<b>72.16</b>	<b>65.77</b>	<u>62.32</u>	<b>67.24</b>
<i>w/o replay buffer</i>										
LoRA	26.75	25.76	0.79	18.69	70.44	80.72	59.68	40.51	18.64	28.49
MoELoRA	21.42	25.29	0.79	17.01	60.34	80.05	57.26	37.03	19.65	24.97
O-LoRA	62.68	35.17	16.93	34.44	92.16	80.22	67.56	51.51	44.28	48.28
L2P	63.82	34.63	22.96	38.58	<b>92.98</b>	80.02	68.86	51.57	45.12	50.59
ModalPrompt	65.99	37.35	23.27	37.61	87.60	80.11	59.66	46.86	42.97	50.36
HiDe-LLaVA	41.17	30.33	18.73	37.08	<u>92.21</u>	<b>80.91</b>	65.47	39.78	32.92	43.90
IncLoRA (Ours)	<b>77.20</b>	<b>58.97</b>	<u>51.43</u>	<u>47.44</u>	90.24	77.59	<u>71.59</u>	<u>64.40</u>	<u>60.22</u>	<u>65.06</u>
SeqFull (Ours)	<b>79.10</b>	<b>61.22</b>	<b>52.36</b>	<b>50.52</b>	91.29	77.06	<b>72.75</b>	<b>66.09</b>	<b>62.49</b>	<b>67.44</b>

Table 1: Results for domain continual learning in MLLM-CL benchmark. We highlight **the best result** and the second best result separately for *w/ replay buffer* and *w/o replay buffer*.

124 learned tasks after the model has completed training  
 125 on the final task in the sequence. The *Average* metric  
 126 captures performance throughout the entire training  
 127 process, defined as the mean of the average accuracies  
 128 calculated after each sequential task is learned.

range of scenarios from cellular-level analysis and surgical procedures to high-level pathology and radiology interpretation. This diversity provides a robust framework for evaluating sequential learning capabilities in specialized medical contexts.

### 129 2.3. Medical-CL Benchmark for Medical 130 Continual Learning

131 To specifically evaluate sequential fine-tuning within  
 132 the medical domain, we introduce a novel benchmark,  
 133 termed **Medical-CL**. This benchmark is curated from several publicly available datasets, including  
 134 BSCCM (Pinkard et al., 2024), PitVis (Das et al.,  
 135 2025), PathVQA (He et al., 2020), and ROCOv2  
 136 (Rückert et al., 2024).

137 These tasks are denoted as **Cell**, **Sur**, **Path**, and  
 138 **Rad**, respectively. We follow MLLM-CL and use a  
 139 randomized order of **Path** → **Sur** → **Cell** → **Rad**.  
 140 For **Cell**, **Sur** and **Path**, we use answer accuracy as  
 141 the metric, while for **Rad**, we adapt BLEU (Papineni  
 142 et al., 2002) and rescale it to 0-100 to fit the regular  
 143 percentage accuracy. Training Details are provided  
 144 in Appendix D.

145 As illustrated in Figure 1, each dataset was  
 146 adapted for VLM evaluation. Our benchmark com-  
 147 prises four distinct medical datasets, spanning a

### 154 3. Analysis: Why the Forgetting is 155 Happening?

156 Research indicates that pretrained Large Language  
 157 Models (LLMs) have loss landscapes with wide, flat,  
 158 and anisotropic basins, where model performance is  
 159 stable (Chen et al., 2025; Xu et al., 2024). The pre-  
 160 training on web-scale data creates a general founda-  
 161 tional basin. The process of fine-tuning can be seen  
 162 as optimizing a more specialized sub-basin within this  
 163 foundational one to adapt the model to a specific tar-  
 164 get task.

165 For a pretrained model  $f_\theta$  and a task  $\mathcal{T}$ , the loss  
 166 landscape  $\mathcal{L}_{f_\theta, \mathcal{T}}$  contains a task-specific sub-basin.  
 167 Catastrophic forgetting occurs when subsequent pa-  
 168 rameter updates push the model outside of this spe-  
 169 cialized sub-basin. To analyze this, we can decom-  
 170 pose the parameter space into two orthogonal sub-  
 171 spaces: a **robust subspace**  $\mathcal{R}_{f_\theta, \mathcal{T}}$ , characterized  
 172 by low loss curvature where parameter changes have

<b>IncLoRA</b>	Path	Sur	Cell	Rad	Average
Zero-shot	36.01	31.45	4.99	12.86	21.11
Path	68.85				68.84
Sur	63.83	53.43			58.63
Cell	59.93	51.62	84.34		65.30
Rad	53.58	47.12	75.58	18.12	48.57

Table 2: Performance of **IncLoRA** on the Medical-CL benchmark without a replay buffer.

173 minimal impact, and a **sensitive subspace**  $\mathcal{S}_{f_\theta, \mathcal{T}}$ ,  
 174 defined by high loss curvature where performance is  
 175 acutely sensitive to changes.

176 The key to preventing catastrophic forgetting is to  
 177 regularize parameter updates to avoid disrupting the  
 178 sensitive subspace  $\mathcal{S}_{f_\theta, \mathcal{T}}$  of previously learned tasks.  
 179 Common fine-tuning strategies achieve this through  
 180 two primary forms of regularization:

- 181 • **Low Learning Rates** act as a *soft regularization*. By discouraging large steps, this approach  
 182 biases the optimization process to remain within  
 183 the robust subspace  $\mathcal{R}_{f_\theta, \mathcal{T}}$ , reducing the likelihood  
 184 of venturing into the sensitive subspace.
- 185 • **Parameter-Efficient Fine-Tuning (PEFT)**  
 186 methods like LoRA impose a *structural regularization*. They restrict all updates to a predefined,  
 187 low-dimensional parameter subspace. This inherently limits the dimensionality of the sensitive  
 188 subspace that can be altered, thereby preserving  
 189 knowledge from prior tasks by design.

193 In essence, both strategies mitigate forgetting by  
 194 constraining parameter updates, either in magnitude  
 195 or direction, to protect the sensitive dimensions critical  
 196 for retaining previously acquired knowledge.

## 197 4. Solution: Limiting the Parameter 198 Update

### 199 4.1. Ablation Study on General MLLM-CL

200 As presented in Table 2, we conduct a comprehensive  
 201 evaluation of our proposed methods, **IncLoRA** and  
 202 **SeqFull**, on the general-purpose MLLM-CL benchmark.  
**IncLoRA** will reinitialize a new LoRA for  
 203 each task and merge the LoRA weight into the model  
 204 after learning each task. Then, the next task in  
 205 stream will use this merged model as the new base  
 206 model and repeat the process. **SeqFull** as its name,

<b>SeqFull</b>	Path	Sur	Cell	Rad	Average
Zero-shot	36.01	31.45	4.99	12.86	21.11
Path	61.17				61.17
Sur	59.85	58.03			58.94
Cell	59.24	56.47	82.09		65.94
Rad	54.54	57.54	80.27	16.20	52.09

Table 3: Performance of **SeqFull** on the Medical-CL benchmark without a replay buffer.

208 will sequentially train the all the LLM Backbone pa-  
 209 rameters without any trick.

210 In the setting where a replay buffer (details in Ap-  
 211 pendix B) is utilized, many contemporary methods  
 212 employ sophisticated mechanisms to mitigate forget-  
 213 ting. As evidenced by the results, our simple, trick-  
 214 free methods achieve performance that is highly com-  
 215 parable to the state-of-the-art. For instance, our **Se-**  
 216 **qFull** method achieves 78.94% on the **RS** task un-  
 217 der the **Last** metric, closely trailing the 79.87% of  
 218 the more complex **MR-LoRA**, while simultaneously  
 219 outperforming it in the **Fin** domain.

220 The advantages of our methodology become even  
 221 more pronounced in the more challenging and real-  
 222 istic scenario without a replay buffer, since medi-  
 223 cal data involves privacy and any possible leakage  
 224 from replay buffer is unacceptable. In this setting,  
 225 **IncLoRA** and **SeqFull** consistently outperforms all  
 226 other competing methods, establishing new bench-  
 227 marks across most domains.

## 228 4.2. Application on Medical-CL

229 To evaluate the effectiveness of our proposed methods  
 230 in a specialized and privacy-sensitive domain, we ap-  
 231 plied IncLoRA and SeqFull to the Medical-CL bench-  
 232 mark, as shown in Table 2 and Table 3. The results  
 233 demonstrate strong performance in this challenging,  
 234 buffer-free setting.

235 Both methods significantly outperform the zero-  
 236 shot baseline across all medical subdomains (Pathol-  
 237 ogy, Surgery, Cell, and Radiology). For instance, af-  
 238 ter being trained on the full sequence of tasks, **Se-**  
 239 **qFull** achieves a final average score of 52.09, while  
 240 **IncLoRA** achieves 48.57, both substantial improve-  
 241 ments over the 21.11 baseline. Notably, both models  
 242 show a strong ability to acquire new knowledge, with  
 243 Cell performance reaching 84.34 for **IncLoRA** and  
 244 82.09 for **SeqFull**. These results highlight the via-  
 245 bility of our simple yet effective continual learning

246 strategies for specialized applications where data pri-  
 247 vacy is paramount.

## 248 5. Discussion

249 Our findings have significant implications for medical  
 250 AI, offering a replay-free continual learning method  
 251 that addresses data privacy by enabling institutions  
 252 to fine-tune VLMs on local datasets. Future work  
 253 could focus on optimizing regularization strategies  
 254 for diverse medical modalities or assessing long-term  
 255 performance. These next steps are vital for developing  
 256 theoretically grounded, adaptable, and scalable  
 257 VLMs that can safely learn across the vast landscape  
 258 of medical knowledge.

## 259 References

- 260 Josh Achiam, Steven Adler, Sandhini Agarwal, Lama  
 261 Ahmad, Ilge Akkaya, Florencia Leoni Aleman,  
 262 Diogo Almeida, Janko Altenschmidt, Sam Altman,  
 263 Shyamal Anadkat, et al. Gpt-4 technical report.  
 264 *arXiv preprint arXiv:2303.08774*, 2023.
- 265 Jean-Baptiste Alayrac, Jeff Donahue, Pauline Luc,  
 266 Antoine Miech, Iain Barr, Yana Hasson, Karel  
 267 Lenc, Arthur Mensch, Katherine Millican, Malcolm  
 268 Reynolds, et al. Flamingo: a visual language model  
 269 for few-shot learning. *Advances in neural informa-*  
 270 *tion processing systems*, 35:23716–23736, 2022.
- 271 Huanran Chen, Yinpeng Dong, Zeming Wei, Yao  
 272 Huang, Yichi Zhang, Hang Su, and Jun Zhu.  
 273 Understanding pre-training and fine-tuning from  
 274 loss landscape perspectives. *arXiv preprint*  
 275 *arXiv:2505.17646*, 2025.
- 276 Adrito Das, Danyal Z Khan, Dimitrios Psychogios,  
 277 Yitong Zhang, John G Hanrahan, Francisco Vas-  
 278 concelos, You Pang, Zhen Chen, Jinlin Wu, Xi-  
 279 aoyang Zou, et al. Pitvis-2023 challenge: Work-  
 280 flow recognition in videos of endoscopic pituitary  
 281 surgery. *Medical Image Analysis*, page 103716,  
 282 2025.
- 283 Xuehai He, Yichen Zhang, Luntian Mou, Eric Xing,  
 284 and Pengtao Xie. Pathvqa: 30000+ questions for  
 285 medical visual question answering. *arXiv preprint*  
 286 *arXiv:2003.10286*, 2020.
- 287 Haotian Liu, Chunyuan Li, Qingyang Wu, and  
 288 Yong Jae Lee. Visual instruction tuning. *Ad-*  
 289 *vances in neural information processing systems*,  
 290 36:34892–34916, 2023.
- 291 Michael McCloskey and Neal J Cohen. Catastrophic  
 292 interference in connectionist networks: The se-  
 293 quential learning problem. In *Psychology of learn-  
 294 ing and motivation*, volume 24, pages 109–165. El-  
 295 sevier, 1989.
- 296 Kishore Papineni, Salim Roukos, Todd Ward, and  
 297 Wei-Jing Zhu. Bleu: a method for automatic eval-  
 298 uation of machine translation. In *Proceedings of the*  
 299 *40th annual meeting of the Association for Compu-  
 300 tational Linguistics*, pages 311–318, 2002.
- 301 Henry Pinkard, Cherry Liu, Fanice Nyatigo, Daniel A  
 302 Fletcher, and Laura Waller. The berkeley sin-  
 303 gle cell computational microscopy (bsccm) dataset.  
 304 *arXiv preprint arXiv:2402.06191*, 2024.
- 305 Johannes Rückert, Louise Bloch, Raphael Brügel,  
 306 Ahmad Idrissi-Yaghir, Henning Schäfer, Cynthia S  
 307 Schmidt, Sven Koitka, Obioma Pelka, Asma Ben  
 308 Abacha, Alba G. Seco de Herrera, et al. Rocov2:  
 309 Radiology objects in context version 2, an updated  
 310 multimodal image dataset. *Scientific Data*, 11(1):  
 311 688, 2024.
- 312 Reece Shuttleworth, Jacob Andreas, Antonio Tor-  
 313 rralba, and Pratyusha Sharma. Lora vs full finetun-  
 314 ing: An illusion of equivalence. *arXiv preprint*  
 315 *arXiv:2410.21228*, 2024.
- 316 Xiao Wang, Tianze Chen, Qiming Ge, Han Xia, Rong  
 317 Bao, Rui Zheng, Qi Zhang, Tao Gui, and Xu-  
 318 anjing Huang. Orthogonal subspace learning for  
 319 language model continual learning. *arXiv preprint*  
 320 *arXiv:2310.14152*, 2023.
- 321 Yichu Xu, Xin-Chun Li, Lan Li, and De-Chuan Zhan.  
 322 Visualizing, rethinking, and mining the loss land-  
 323 scape of deep neural networks. *arXiv preprint*  
 324 *arXiv:2405.12493*, 2024.
- 325 Yuexiang Zhai, Shengbang Tong, Xiao Li, Mu Cai,  
 326 Qing Qu, Yong Jae Lee, and Yi Ma. Investigat-  
 327 ing the catastrophic forgetting in multimodal large  
 328 language model fine-tuning. In *Conference on Par-  
 329 simony and Learning*, pages 202–227. PMLR, 2024.
- 330 Hongbo Zhao, Fei Zhu, Rundong Wang, Gaofeng  
 331 Meng, and Zhaoxiang Zhang. Mllm-cl: Contin-  
 332 ual learning for multimodal large language models.  
 333 *arXiv preprint arXiv:2506.05453*, 2025.

334 Yaowei Zheng, Richong Zhang, Junhao Zhang,  
 335 Yanhan Ye, Zheyuan Luo, Zhangchi Feng, and  
 336 Yongqiang Ma. Llamafactory: Unified efficient  
 337 fine-tuning of 100+ language models. *arXiv*  
 338 preprint *arXiv:2403.13372*, 2024.

## Appendix A. Annoymous Links

We provide fully annoymous links to our supplemen-	340
tary materials here.	341
Code	342
<a href="https://anonymous.4open.science/r/replay-free-finetuning-medical-vlm-BB37">https://anonymous.4open.science/r/ replay-free-finetuning-medical-vlm-BB37</a>	343
Model Checkpoints	345
<a href="https://huggingface.co/Replay-Free-Finetuning-Medical-VLM/checkpoints">https://huggingface.co/ Replay-Free-Finetuning-Medical-VLM/ checkpoints</a>	346
Medical-CL Dataset	349
<a href="https://huggingface.co/datasets/Replay-Free-Finetuning-Medical-VLM/Medical-CL">https://huggingface.co/datasets/ Replay-Free-Finetuning-Medical-VLM/ Medical-CL</a>	350
	351
	352

## Appendix B. Fine-tuning Protocol

**Base Model.** For all the evaluations in this paper, we adapt LLaVA-7B as our base model for fine-tuning. The checkpoint could be downloaded from <https://huggingface.co/llava-hf/llava-1.5-7b-hf>.

**Fine-tuning Settings.** For **IncLoRA** fine-tuning, we set the LLM backbone as the LoRA target and unfreeze the projector. For **SeqFull** fine-tuning, we all the paramters of LLM backbone and projector to be trainable.

**Training Framework.** Our experimental framework is built upon the LLaMA-Factory repository (Zheng et al., 2024). The training configurations adhere to the official guidelines provided in the LLaVA model repositories (Liu et al., 2023).

**Prompt Templates.** For the LLaVA model, we utilized the corresponding system prompt templates provided within the LLaMA-Factory framework. For all the evaluations except the image captioning for **Radiology**, we turn all the questions into multiple-choice and add format instruction in prompt to avoid the influence of the mismatch of output format.

**Replay Buffer.** We exactly follow the setting in **MLLM-CL** Zhao et al. (2025), specifically, for each task, we collect a replay data buffer of size 20 samples. Then, for every downstream sequential fine-tuning, we directly hybrid the all the replay data into the training data. No over-sampling is implemented.

381 **Appendix C. MLLM-CL Fine-tuning**  
 382 **Hyperparameters**

383 The training length for every task is aligned to  
 384 MLLM-CL (Zhao et al., 2025) for fair comparison.

Config	Value
optimizer	AdamW
batch size	64
lr schedule	cosine decay
lr warmup ratio	0.1
base lr	$8 \times 10^{-5}$
epoch for RS	1
epoch for Med	3
epoch for AD	1
epoch for Sci	2
epoch for Fin	1
LoRA rank	8

Table 4: Hyperparameters of **IncLoRA** in MLLM-CL Benchmark *w/o replay buffer*.

Config	Value
optimizer	AdamW
batch size	64
lr schedule	cosine decay
lr warmup ratio	0.1
base lr	$8 \times 10^{-5}$
epoch for RS	1
epoch for Med	3
epoch for AD	1
epoch for Sci	2
epoch for Fin	1
LoRA rank	16

Table 5: Hyperparameters of **IncLoRA** in MLLM-CL Benchmark *w/ replay buffer*.

Config	Value
optimizer	AdamW
batch size	16
lr schedule	cosine decay
lr warmup ratio	0.1
base lr	$1 \times 10^{-6}$
epoch for RS	1
epoch for Med	3
epoch for AD	1
epoch for Sci	2
epoch for Fin	1

Table 6: Hyperparameters of **SeqFull** in MLLM-CL Benchmark *w/o replay buffer*.

Config	Value
optimizer	AdamW
batch size	16
lr schedule	cosine decay
lr warmup ratio	0.1
base lr	$1 \times 10^{-6}$
epoch for RS	1
epoch for Med	3
epoch for AD	1
epoch for Sci	2
epoch for Fin	1

Table 7: Hyperparameters of **SeqFull** in MLLM-CL Benchmark *w/ replay buffer*.

<sup>385</sup> **Appendix D. Medical-CL Fine-tuning**  
<sup>386</sup> **Hyperparameters**

<sup>387</sup> All the experiment in this part is *w/o replay buffer*.

Config	Value
optimizer	AdamW
batch size	64
lr schedule	cosine decay
lr warmup ratio	0.1
base lr	$1 \times 10^{-6}$
step for Path	2000
step for Sur	2000
step for Cell	2000
step for Rad	2000
LoRA rank	16

Table 8: Hyperparameters of **IncLoRA** in Medical-CL Benchmark.

Config	Value
optimizer	AdamW
batch size	16
lr schedule	cosine decay
lr warmup ratio	0.1
base lr	$1 \times 10^{-6}$
step for Path	2000
step for Sur	2000
step for Cell	2000
step for Rad	2000

Table 9: Hyperparameters of **SeqFull** in Medical-CL Benchmark.