

4D-VQ-GAN: A World Model for Synthesizing Medical Scans at Any Time Point for Personalized Disease Progression Modeling of Idiopathic Pulmonary Fibrosis

An Zhao^{*1,2,3} 

AN.ZHAO.19@UCL.AC.UK

¹ *Hawkes Institute, University College London*

² *Department of Computer Science, University College London*

³ *Satsuma Lab, Hawkes Institute, University College London*

Moucheng Xu^{*†1,3,4}

MOUCHENG.XU.18@UCL.AC.UK

⁴ *Department of Medical Physics and Biomedical Engineering, University College London*

Ahmed H. Shahin^{1,2,3}

AHMED.SHAHIN.19@UCL.AC.UK

Wim Wuyts⁵

WIM.WUYTS@UZLEUVEN.BE

⁵ *Department of Respiratory Medicine, University Hospitals Leuven*

Mark G. Jones⁶

MARK.JONES@SOTON.AC.UK

⁶ *NIHR Southampton Biomedical Research Centre and Clinical and Experimental Sciences, University of Southampton*

Joseph Jacob^{†1,3,7}

J.JACOB@UCL.AC.UK

⁷ *UCL Respiratory, University College London*

Daniel C. Alexander^{†1,2}

D.ALEXANDER@UCL.AC.UK

Editors: Accepted for publication at MIDL 2025

Abstract

Understanding the progression trajectories of diseases is crucial for early diagnosis and effective treatment planning. This is especially vital for life-threatening conditions such as Idiopathic Pulmonary Fibrosis (IPF), a chronic, progressive lung disease with a prognosis comparable to many cancers. Computed tomography (CT) imaging has been established as a reliable diagnostic tool for IPF. Accurately predicting future CT scans of early-stage IPF patients can aid in developing better treatment strategies, thereby improving survival outcomes.

As inspired by the recent success of world models in generating video-based virtual physical worlds, we present the first world model for IPF, to synthesize realistic scans of early-stage IPF patients at any time point. We term our model 4D Vector Quantised Generative Adversarial Networks (4D-VQ-GAN). Our model is trained using a two-stage approach. In the first stage, a 3D-VQ-GAN is trained to reconstruct CT volumes. In the second stage, a Neural Ordinary Differential Equation (ODE) model is trained to capture the temporal dynamics of the quantised embeddings, which are generated by the encoder trained in the first stage. For clinical validation, we conduct survival analysis using imaging biomarkers derived from generated CT scans and achieve a C-index either better than or comparable to that of biomarkers derived from the real CT scans. The survival analysis results suggest the potential clinical utility inherent to generated longitudinal CT scans, showing that they can reliably predict survival outcomes. The code is publicly available at <https://github.com/anzhao920/4DVQGAN>.

Keywords: 4D image synthesis, world models, VQ-GAN, neural ODEs, spatial-temporal disease progression modelling, CT, IPF

* Contributed equally

† Work completed at UCL, Moucheng has now moved to Medtronic.

‡ Joint senior authors

1. Introduction

Understanding the disease progression trajectories is vital for understanding diseases’ biological mechanisms and developing better treatments. The traditional methods for understanding the disease progression focus on modelling the progression trajectories using longitudinal, low-dimensional data (e.g., differential equation models (Villemagne et al., 2013; Jack et al., 2013; Oxtoby et al., 2014), self-modelling regression methods (Jedynak et al., 2012; Donohue et al., 2014), event-based models (Wijeratne and Alexander, 2024; Young et al., 2018; Fonteijn et al., 2012)). Those traditional methods normally require strong assumptions of the statistical disease progression patterns, relying on the prior knowledge of the diseases, which are hard to obtain for rare diseases. In addition, the majority of the traditional methods models the progression trajectories at a population level, hindering their applicability on heterogeneous diseases.

To address the aforementioned limitations of the traditional methods to understand the disease progression, we explore a new paradigm of machine learning methods, namely, world models (NVIDIA et al., 2025; Parker-Holder et al., 2024; Bruce et al., 2024). The world models simulate the physical worlds with interactive virtual environments. For example, a recent world model called Genie (Parker-Holder et al., 2024; Bruce et al., 2024) can create game video based environments for the AI agents to interact with. Similarly, in the context of the disease progression, we can adapt temporal medical imaging as the environments, on the analogy as using the videos as environments in physical world models.

In this paper, we explore world models on investigating the progression trajectory of idiopathic pulmonary fibrosis (IPF), a progressive lung condition, with high-resolution CT volumetric scans. As proof of the concept, in this paper, we focus on only one interactive action with the virtual progression trajectories, which is the time. More precisely, we introduce the 4D Vector Quantized Generative Adversarial Network (4D-VQ-GAN). Given two 3D CT scans of an IPF patient at irregular time points, our method can generate synthetic 3D images at any desired time point, effectively modelling a virtual continuous disease progression trajectory for each individual. More importantly, we found that biomarkers derived from the generated CT volumes exhibit a strong clinical correlation with survival outcome, highlighting the potential of our method for personalized treatment planning.

2. Related Works

Our work can be regarded as a type of spatial-temporal disease progression modelling with high-dimensional volumetric imaging data. Previously, a few generative models have been explored to simulate longitudinal magnetic resonance imaging (MRI) scans specifically in the context of Alzheimer’s disease (AD) progression (Couronné et al., 2021; Sauty and Durrleman, 2022; Kim et al., 2021; Martí-Juan et al., 2023; Fan et al., 2022; Puglisi et al., 2024; Ravi et al., 2022; Yoon et al., 2023). For instance, auto-encoder styles model have been used to couple with linear temporal models in (Sauty and Durrleman, 2022; Kim et al., 2021). However, they rely on oversimplified assumptions about evolution trajectories (e.g. linear progression). Other methods (Martí-Juan et al., 2023; Fan et al., 2022) use recurrent neural networks to capture the temporal information. These methods model dynamics in discrete steps, limiting their ability to capture the continuous nature of disease progression. Puglisi et al. (Puglisi et al., 2024) use the latent diffusion model and incorporate prior

knowledge to model the disease progression. However, it also struggles to ensure continuous temporal changes. In addition, existing methods for generating longitudinal MRI scans in AD are not directly applicable to CT lung scans of IPF patients for several reasons. First, IPF is much rarer with shorter patient lifespans than AD resulting in less imaging being acquired. Furthermore, radiation side effects from CT scans discourage repeated scans, resulting in a scarcity of longitudinal CT data and hindering model development. Second, lung CT scans contain vastly more fine textured-structures like vessels, airways, and interstitial tissue compared to the smooth, homogenous brain seen in MRI. Generating these intricate lung structures synthetically is more challenging than replicating brain tissue.

3. Methods

Our 4D-VQ-GAN is a self-supervised generative model trained on temporal CT volumes. As shown in Figure 1, the model consists of two key components: a 3D-VQ-GAN and a temporal model. We train the two components of our model sequentially to make the overall training on high-dimensional spatial-temporal data easier to stabilize. In the first stage, we train a 3D-VQ-GAN to reconstruct each scan. By doing so, the trained encoder of the 3D-VQ-GAN can project the high-dimensional data into low-dimensional code books. In the second stage, we use a Neural ODE to capture the temporal dynamics of the code books. Most importantly, the neural ODE provides us an interactive environment with the latent temporal disease trajectories, so that during the inference, we can simulate the scans at any time point given two scans. In addition, the use of code books as input for temporal modelling avoids overfitting on the temporal data.

3D-VQ-GAN As shown in Figure 1, the first stage of training involves a 3D-VQ-GAN (Ge et al., 2022) to reconstruct CT volumes for each case at every time point in the training set. Unlike the original 2D-VQ-GAN (Esser et al., 2021), our 3D-VQ-GAN employs 3D convolutional layers, enabling it to capture spatial structures more effectively in volumetric imaging data. Following the VQ-VAE framework (Van Den Oord et al., 2017), 3D-VQ-GAN compresses high-dimensional volumetric imaging data into a discrete set of latent codes, constrained by a predefined codebook size. Since the model is trained on imaging data, its codebook learns to represent meaningful imaging patterns, with each code acting as a compact and discrete representation of local anatomical structures or texture features. We adapted the original 3D-VQ-GAN loss functions (Ge et al., 2022) for training. Further details can be found in Appendix E.2.

Temporal Model In the second stage of the training, we train a temporal model that can reconstruct the temporal trajectories of the latent embeddings (z) of the imaging data from different time-points, as demonstrated in Figure 1. We realise that generating the future or past latent embeddings from a few observed latent embeddings naturally formulates as an ordinary differential equation. We therefore utilise a neural ODE solver (Chen et al., 2018) to predict the unknown embeddings at new time-points. We found that it is more beneficial to adapt a 3D-ConvGRU (Ballas et al., 2015) as the encoder of the neural ODE solver on our data, with much better computational efficiency. The outputs of the neural ODE are then fed into a light-weight projector, two 3D convolutional layers, to reconstruct the latent embeddings z at inquired time points, with a specified time interval. In practice, We found that adding skip connections to the generated embeddings improves results,

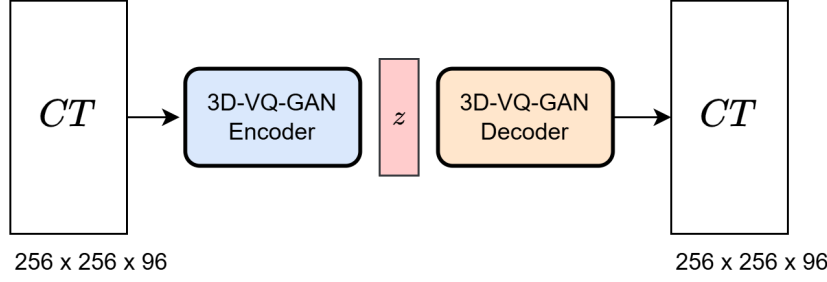
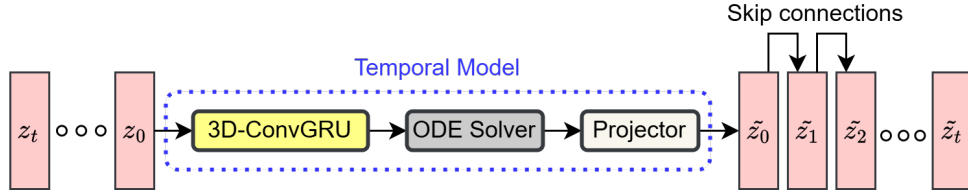
Stage 1: Train the **3D-VQ-GAN** to reconstruct the CT volumes

 Stage 2: Train the **temporal model** to reconstruct the temporal sequence of z from stage 1


Figure 1: The overview of our two-stage training strategies. The first stage trains an encoder-decoder-based 3D-VQ-GAN to reconstruct the CT volumes. The second stage takes the latent embeddings ($z_t, \dots, z_0$) from the first stage, and trains a temporal model to reconstruct them. The temporal model consists of a 3D-ConvGRU, that compresses the temporal latent embeddings to match the dimensionality of the input of the ODE Solver to ease the computational burden. The projector, a light-weight 3D convolutional module reconstructs the temporal latent embeddings from the outputs of the ODE Solver. Those reconstructed latent embeddings are then fed into a frozen 3D-VQ-GAN Decoder from stage 1 for longitudinal CT reconstruction.

offering two key benefits. 1) Training Stability and Efficiency: Skip connections stabilize training and speed up convergence, similar to ResNets, by focusing gradient propagation on meaningful pathological changes rather than both stable anatomy and disease progression. 2) Anatomical Preservation: Skip connections condition predictions on baseline anatomy, preserving stable structures and enabling personalized disease progression modelling. We train the temporal model in a self-supervised manner by using a L2 loss between the input embeddings and the reconstructed embeddings. Please refer to Appendix E.3 for details.

Inference The inference follows the process shown in Figure 2. The trained model needs two CT scans. The user can also input two hyper-parameters for the neural ODE, namely the interval time and the total time duration. For example, as shown in Figure 2, given two initial scans at time point 0 and 1, the interval as 1 year and the total time duration as 3 years, the model will reconstruct the scans at time point 0 and 1, and start to extrapolate future scans at time point 2 and 3.

Survival analysis and biomarker discovery We explore our model’s clinical utility using a survival analysis based approach to mimic the clinical workflows. Radiologists

track prognostic imaging biomarkers in IPF over time to assess disease progression. Though we lack comprehensive visual scores for all cases, we propose a method that mirrors clinical workflows, including selecting key prognostic biomarkers, analyzing their longitudinal changes, and comparing their prognostic value in synthesized vs. real scans. Despite not being pixel-perfect replicas, if synthesized scans maintain consistent biomarker representation and exhibit comparable longitudinal changes to real scans, it would support their clinical utility. The method is as follows:

- **Biomarker Extraction:** The trained 3D-VQGAN encoder is used to project each CT scan into a set of codebook. Each code index represents a distinct imaging pattern in the CT. The frequency of each code index reflects the prevalence of the corresponding imaging pattern. We then use these normalized frequencies of code indices as candidate cross-sectional prognostic biomarkers.
- **Cross-sectional prognostic biomarker selection:** To identify prognostic cross-sectional biomarkers, we perform survival analysis using five-fold cross-validation. The original training dataset is divided into training and validation datasets. In each fold, univariate Cox proportional hazards models (Cox, 1972) are applied to each biomarker, adjusting for age, sex, and smoking status (smoking vs non-smoking). Biomarkers are selected based on three criteria: (1) Hazard Ratio (HR) > 1 (indicating that higher biomarker values are associated with increased mortality risk), (2) p-value < 0.01 (ensuring statistical significance), and (3) Concordance Index (C-index) > 0.5 (demonstrating predictive ability). A biomarker must meet these criteria in all five folds to be considered robust. The top five biomarkers with the highest mean C-index values across the validation sets are selected for further longitudinal biomarker analysis, ensuring that the most predictive biomarkers are prioritized.
- **Longitudinal biomarker analysis:** For each patient in the test dataset, we use their first two available CT scans to synthesize both their second available scan and an additional follow-up scan one year later. The synthetic second scan serves as a predicted version of the actual second scan. We then extract the five selected cross-sectional biomarkers from both real and synthetic scans at two time points: the second scan and the one-year follow-up. The longitudinal biomarker is defined as the change in these biomarkers between the two time points, separately computed for real and synthetic scans. These longitudinal biomarkers, along with the covariates, are input into the Cox model to assess their prognostic value in the test dataset. This analysis evaluates the consistency of biomarker trajectories between real and synthetic scans, and explores the potential utility of synthetic scans in tracking changes over time.

4. Experiments

Datasets Our data comes from a longitudinal dataset comprising 681 volumetric CT scans from 219 IPF patients, obtained from University Hospitals Leuven, Belgium, a single centre in Leuven. We randomly divided the dataset into 80% for training (552 CT scans from 175 patients) and 20% for testing (129 CT scans from 44 patients). Different patients have varying numbers of scans, reflecting the natural variations in imaging availability in real

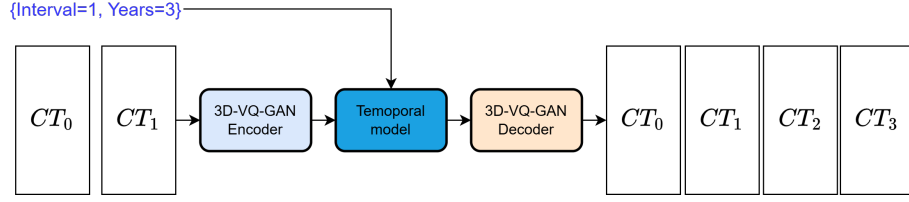


Figure 2: The inference of the trained model. Given two scans, the model can generate more scans up to the specified year at a specific interval.

clinical practice. The CT scans were acquired with varying slice thicknesses, ranging from 0.75 mm to 1 mm, and in-plane resolution varied with pixel spacing ranging from 0.38 mm to 0.98 mm. Additionally, we use an external cross-sectional dataset of 98 IPF patients from the University Hospital Southampton NHS Foundation Trust, UK, to evaluate the generalizability of the 3D-VQ-GAN trained in Stage 1 and more details can be found in Appendix D.1. For survival analysis, patients must have complete data on death status, censoring information, and all relevant covariates (age, sex and smoking status). In the training dataset, 71 out of 141 patients have observed deaths. For the cross-sectional biomarker analysis test dataset, patients must have at least three time points, with 10 out of 17 patients having observed deaths. For the longitudinal biomarker analysis test dataset, patients are required to have at least three time points and a one-year follow-up for the second available data point, with 9 out of 14 patients having observed deaths.

Preprocessing We focus on modelling changes within the lung areas. We segment the lung regions using a pre-trained U-Net (Ronneberger et al., 2015; Hofmanninger et al., 2020) for all CT scans of IPF patients and visually inspect the lung masks. Subsequently, we register the longitudinal lung scans to remove extraneous artifacts caused by lung motion or incorrect body positioning. Our lung scan registration method is a faster version (implemented in (Hansen and Heinrich, 2021)) of the CorrField method (Heinrich et al., 2015). Visualizations of the segmentation and registration outcomes can be found in Appendix C.

Training Our models are trained on an NVIDIA A100 80GB GPU. The first training stage used a batch size of 1, with an accumulated batch size of 6, and lasted 20,000 steps, equivalent to 10 days. The second training stage also used a batch size of 1 and lasted 15 hours. The hyperparameters of the training can be found in Appendix A.

Evaluation Metrics To evaluate the image quality of the reconstructed CT scans in the first stage of training, we use Mean Squared Error (MSE). For assessing the image quality of the generated temporal CT scans in the second stage, we use Peak Signal-to-Noise Ratio (PSNR) and Structural Similarity Index (SSIM). For survival analysis, we use C-index, a metric that measures the predictive accuracy of a model by evaluating the agreement between predicted risk scores and actual survival outcomes.

5. Results

In this section, we present the results of our model on the following tasks: 1) interpolation, for imputing missing CT scans between the two input scans; 2) extrapolation, for predicting

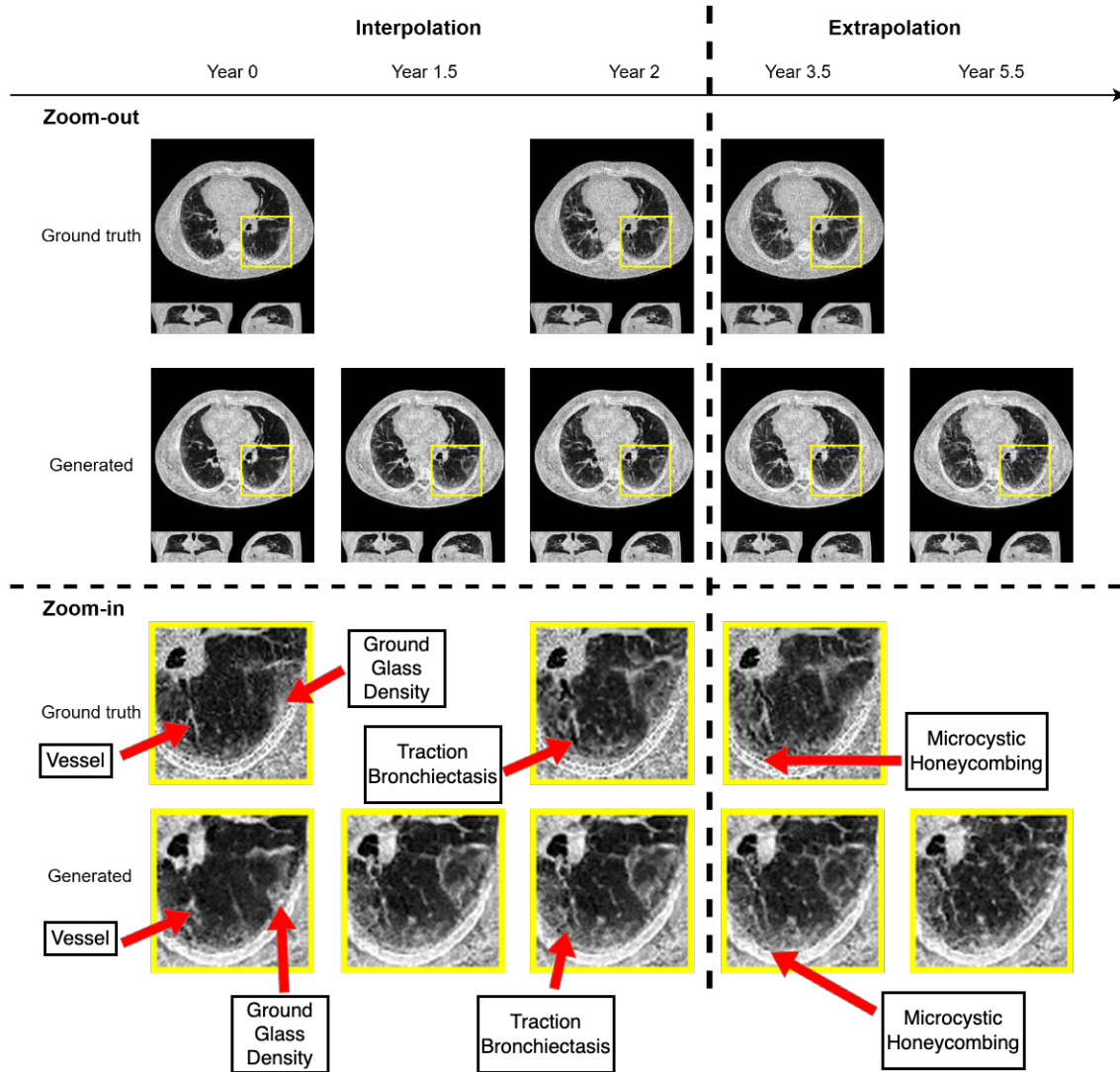


Figure 3: Three real CT scans of an IPF patient are shown in the upper panel, representing axial, coronal, and sagittal sections. Using two scans from year 0 and year 2, the trained model can generate CT scans at any arbitrary time points. The below panel shows the generated CT images at five different time points, with three corresponding to the real scans. A zoomed region of the left lower lobe (yellow box) in the real and generated CT scans show comparable amounts of architectural distortion, patterned ground glass opacification and reticulation, all hallmarks of lung fibrosis. The availability of our scans are not uniform across time and across patients, the model is trained on scans at irregular time points.

the future CT scans beyond the time span of the two given input scans; 3) survival outcome prediction, for evaluating of the clinical utility of the proposed method.

Table 1: Ablation Study on Interpolation and Extrapolation Tasks.

Model Variant	Interpolation			Extrapolation		
	MSE↓	SSIM↑	PSNR↑	MSE↓	SSIM↑	PSNR↑
3D-VQ-GAN+ODE encoder (ConvGRU)	0.018	0.500	17.913	0.023	0.472	16.974
3D-VQ-GAN+ODE encoder (ConvGRU)+embeddings skip connections (proposed)	0.020	0.469	17.387	0.019	0.489	17.816
3D-VQ-GAN+ODE encoder (ODE-ConvGRU)+embeddings skip connections	0.018	0.508	17.900	0.026	0.440	16.913
3D-VQ-GAN+ODE encoder (ConvGRU)+embeddings skip connections+masked out inputs	0.035	0.343	15.366	0.036	0.340	15.24

Interpolation and extrapolation In this experiment, we evaluate the performance of the proposed method in reconstructing latent dynamics from sparse, irregularly sampled data. The model is trained to reconstruct the given input sequence of 3D imaging data and is then tested on both interpolation and extrapolation tasks. Figure 3 illustrates example qualitative results. The patient’s year 0 and year 2 scans were used for inference, with the year 3.5 scan serving as ground truth for the extrapolation experiment. Inference was performed with a 0.5-year interval, extending up to 5.5 years from the baseline (year 0). As shown in the zoomed-in section, both real and generated CT scans exhibit comparable architectural distortion, ground glass opacification, and reticulation—key features of lung fibrosis. The quantitative results are shown in Table 1.

Ablation study The proposed method uses Neural ODE to predict the difference embeddings for each time point relative to the previous one, incorporating skip connections. In the ablation experiments (Table 1), we remove the skip connections and allow the model to directly predict the latent embeddings of all time points using Neural ODE. However, this modification resulted in significantly poorer extrapolation performance. We also replaced ConvGRU with ODE-ConvGRU (Park et al., 2021) as the ODE solver encoder. While ODE-ConvGRU is designed for irregularly sampled longitudinal data, it leads to notably worse extrapolation performance compared to the model using standard ConvGRU. Additionally, we experiment with randomly masking time points (excluding the baseline) and task the model with reconstructing the unseen time points. This approach also results in significantly worse extrapolation performance. Overall, the proposed model demonstrates balanced performance in both interpolation and extrapolation tasks.

Survival outcome prediction Following the method in Section 3, the top five most significant cross-sectional imaging biomarkers are selected for survival analysis. The selected five biomarkers exhibit weak to moderate correlation, with pairwise correlation coefficients all below 0.64 and an average correlation of 0.41. In the test dataset, we extrapolate the third CT scan using the first two available CT scans. For the cross-sectional imaging biomarker, the C-index using the generated third scans is 0.943. In comparison, using biomarkers derived from real CT scans for survival prediction yields a slightly lower C-index of 0.914. Next, we compute the longitudinal biomarker by evaluating the change in these top five significant biomarkers over the course of one year, both for real and generated CT scans. By inputting these longitudinal biomarkers along with covariates into the Cox model, we obtain C-indices of 1.0 for both real and generated CT scans. However, these results may be overestimated due to the limited sample size. The C-index of survival analysis using generated scans is comparable to that of real scans, further highlighting the strong clinical potential of our method.

Table 2: Survival outcome prediction results on biomarkers selected from 5-fold cross-validation.

Biomarker type	C-Index	
	Real CT scans	Generated CT scans (ours)
Cross-sectional biomarker	0.914	0.943
Longitudinal biomarkers	1	1

6. Discussion

We aim to understand disease progression by interacting with a virtual disease progression trajectory, which is physically visualized through a medical imaging modality that both clinicians and patients can intuitively perceive. This is a key aspect that distinguishes our approach from previous methods in disease progression modeling, which build mathematical models to explicitly describe disease progression based on a limited set of variables derived from medical images. Our approach enables clinicians to perform direct virtual diagnoses on the generated future scans, thereby avoiding information loss that occurs during the extraction of variables from the scans. Our model is also designed to be scalable, allowing future work to explore larger-scale implementations, with more potential interactions (e.g. interventions) with the progression trajectories. We hope that our work will interest the community in further exploration of disease progression trajectories through the lens of world models, extending beyond IPF. This approach could as well potentially improve existing screening and prevention technologies for different diseases.

Beyond disease progression analysis, the model has the potential for applications like data augmentation. However, the proposed method exhibits certain limitations. Firstly, the current approach utilizes a deterministic Neural ODE in the latent space, which assumes a shared disease dynamic across all patients. This might not be ideal for heterogeneous diseases with diverse subtypes and distinct progression patterns. Secondly, a crucial limitation of the current validation process is its reliance on a single dataset for evaluating the model. Finally, the study relies on a single training/validation split due to limited training resource, preventing an assessment of performance variability.

7. Conclusion

This paper presents a generative environment to simulate the progression trajectories of IPF patients based on CT imaging. The proposed generative environment can be seen as a world model. Our world model for IPF can realistically synthesize CT images of IPF patients that contain visual hallmarks of lung fibrosis comparable to those in real scans. Most importantly, the generated CT images can yield survival outcomes that are sometimes even more accurate than those derived from the real images.

Acknowledgments

AZ was supported by CSC-UCL Joint Research Scholarship. MCX was supported by GSK, United Kingdom (BIDS3000034123) and UCL Engineering Dean’s Prize. AHS was supported by the Open Source Imaging Consortium (OSIC) <https://www.osicild.org>. DCA is supported by UK EPSRC grants M020533, R006032, R014019, V034537, Wellcome Trust, United Kingdom UNS113739, Wellcome Trust 221915/Z/20/Z. JJ was supported by the Wellcome Trust 209553/Z/17/Z and 227835/Z/23/Z, the Chan Zuckerberg Initiative CZIF2024-009938. JJ is Radiology co-lead for the Open Source Imaging Consortium (OSIC). DCA, and JJ are supported by the NIHR UCLH Biomedical Research Centre, UK. This research was funded in whole or in part by the Wellcome Trust [209553/Z/17/Z and 227835/Z/23/Z]. For the purpose to support future research, the author has applied a CC BY-NC 4.0 copyright licence to any author accepted manuscript version arising from this submission.

References

- Nicolas Ballas, Li Yao, Chris Pal, and Aaron Courville. Delving deeper into convolutional networks for learning video representations. *arXiv preprint arXiv:1511.06432*, 2015.
- David Bau, Jun-Yan Zhu, Jonas Wulff, William Peebles, Hendrik Strobelt, Bolei Zhou, and Antonio Torralba. Seeing what a gan cannot generate. In *Proceedings of the IEEE/CVF international conference on computer vision*, pages 4502–4511, 2019.
- Yoshua Bengio, Nicholas Léonard, and Aaron Courville. Estimating or propagating gradients through stochastic neurons for conditional computation. *arXiv preprint arXiv:1308.3432*, 2013.
- Jake Bruce, Michael D Dennis, Ashley Edwards, Jack Parker-Holder, Yuge Shi, Edward Hughes, Matthew Lai, Aditi Mavalankar, Richie Steigerwald, Chris Apps, Yusuf Aytar, Sarah Maria Elisabeth Bechtle, Feryal Behbahani, Stephanie C.Y. Chan, Nicolas Heess, Lucy Gonzalez, Simon Osindero, Sherjil Ozair, Scott Reed, Jingwei Zhang, Konrad Zolna, Jeff Clune, Nando De Freitas, Satinder Singh, and Tim Rocktäschel. Genie: Generative interactive environments. In Ruslan Salakhutdinov, Zico Kolter, Katherine Heller, Adrian Weller, Nuria Oliver, Jonathan Scarlett, and Felix Berkenkamp, editors, *Proceedings of the 41st International Conference on Machine Learning*, volume 235 of *Proceedings of Machine Learning Research*, pages 4603–4623. PMLR, 21–27 Jul 2024. URL <https://proceedings.mlr.press/v235/bruce24a.html>.
- Ricky TQ Chen, Yulia Rubanova, Jesse Bettencourt, and David K Duvenaud. Neural ordinary differential equations. In *Advances in neural information processing systems*, volume 31, 2018.
- Raphaël Couronné, Paul Vernhet, and Stanley Durrleman. Longitudinal self-supervision to disentangle inter-patient variability from disease progression. In *International Conference on Medical image computing and computer-assisted intervention*, pages 231–241. Springer, 2021.

- David R Cox. Regression models and life-tables. *Journal of the Royal Statistical Society: Series B (Methodological)*, 34(2):187–202, 1972.
- Antonia Creswell, Tom White, Vincent Dumoulin, Kai Arulkumaran, Biswa Sengupta, and Anil A Bharath. Generative adversarial networks: An overview. *IEEE signal processing magazine*, 35(1):53–65, 2018.
- Florinel-Alin Croitoru, Vlad Hondru, Radu Tudor Ionescu, and Mubarak Shah. Diffusion models in vision: A survey. *IEEE Transactions on Pattern Analysis and Machine Intelligence*, 45(9):10850–10869, 2023.
- Michael C Donohue, Hélène Jacqmin-Gadda, Mélanie Le Goff, Ronald G Thomas, Rema Raman, Anthony C Gamst, Laurel A Beckett, Clifford R Jack Jr, Michael W Weiner, Jean-François Dartigues, et al. Estimating long-term multivariate progression from short-term data. *Alzheimer’s & Dementia*, 10:S400–S410, 2014.
- Patrick Esser, Robin Rombach, and Bjorn Ommer. Taming transformers for high-resolution image synthesis. In *Proceedings of the IEEE/CVF conference on computer vision and pattern recognition*, pages 12873–12883, 2021.
- Chen-Chen Fan, Liang Peng, Tian Wang, Hongjun Yang, Xiao-Hu Zhou, Zhen-Liang Ni, Sheng Chen, Yan-Jie Zhou, Zeng-Guang Hou, et al. Tr-gan: multi-session future mri prediction with temporal recurrent generative adversarial network. *IEEE Transactions on Medical Imaging*, 41(8):1925–1937, 2022.
- Chen-Chen Fan, Hongjun Yang, Liang Peng, Xiao-Hu Zhou, Sheng Chen, and Zeng-Guang Hou. Tr-transgan: Temporal recurrent transformer generative adversarial network for longitudinal mri dataset expansion. *IEEE Transactions on Cognitive and Developmental Systems*, pages 1–10, 2024.
- André Ferreira, Jianning Li, Kelsey L Pomykala, Jens Kleesiek, Victor Alves, and Jan Egger. Gan-based generation of realistic 3d data: A systematic review and taxonomy. *arXiv preprint arXiv:2207.01390*, 2022.
- André Ferreira, Jianning Li, Kelsey L Pomykala, Jens Kleesiek, Victor Alves, and Jan Egger. Gan-based generation of realistic 3d volumetric data: A systematic review and taxonomy. *Medical Image Analysis*, page 103100, 2024.
- Hubert M. Fonteijn, Marc Modat, Matthew J. Clarkson, Josephine Barnes, Manja Lehmann, Nicola Z. Hobbs, Rachael I. Scahill, Sarah J. Tabrizi, Sebastien Ourselin, Nick C. Fox, and Daniel C. Alexander. An event-based model for disease progression and its application in familial alzheimer’s disease and huntington’s disease. *NeuroImage*, 60(3):1880–1889, 2012. ISSN 1053-8119. doi: <https://doi.org/10.1016/j.neuroimage.2012.01.062>. URL <https://www.sciencedirect.com/science/article/pii/S1053811912000791>.
- Wolfgang Förstner and Eberhard Gülch. A fast operator for detection and precise location of distinct points, corners and centres of circular features. In *Proc. ISPRS intercommission conference on fast processing of photogrammetric data*, volume 6, pages 281–305, 1987.

- Songwei Ge, Thomas Hayes, Harry Yang, Xi Yin, Guan Pang, David Jacobs, Jia-Bin Huang, and Devi Parikh. Long video generation with time-agnostic vqgan and time-sensitive transformer. In *European Conference on Computer Vision*, pages 102–118. Springer, 2022.
- Lasse Hansen and Mattias P Heinrich. Graphregnet: Deep graph regularisation networks on sparse keypoints for dense registration of 3d lung cts. *IEEE Transactions on Medical Imaging*, 40(9):2246–2257, 2021.
- Mattias P Heinrich, Heinz Handels, and Ivor JA Simpson. Estimating large lung motion in copd patients by symmetric regularised correspondence fields. In *International Conference on Medical Image Computing and Computer-Assisted Intervention*, pages 338–345. Springer, 2015.
- Alessa Hering, Lasse Hansen, Tony CW Mok, Albert CS Chung, Hanna Siebert, Stephanie Häger, Annkristin Lange, Sven Kuckertz, Stefan Heldmann, Wei Shao, et al. Learn2reg: comprehensive multi-task medical image registration challenge, dataset and evaluation in the era of deep learning. *IEEE Transactions on Medical Imaging*, 42(3):697–712, 2022.
- Jonathan Ho, Ajay Jain, and Pieter Abbeel. Denoising diffusion probabilistic models. In *Advances in neural information processing systems*, volume 33, pages 6840–6851, 2020.
- Jonathan Ho, William Chan, Chitwan Saharia, Jay Whang, Ruiqi Gao, Alexey Gritsenko, Diederik P Kingma, Ben Poole, Mohammad Norouzi, David J Fleet, et al. Imagen video: High definition video generation with diffusion models. *arXiv preprint arXiv:2210.02303*, 2022.
- Johannes Hofmanninger, Forian Prayer, Jeanny Pan, Sebastian Röhrich, Helmut Prosch, and Georg Langs. Automatic lung segmentation in routine imaging is primarily a data diversity problem, not a methodology problem. *European Radiology Experimental*, 4(1): 1–13, 2020.
- Kazuki Irie, Róbert Csordás, and Jürgen Schmidhuber. Topological neural discrete representation learning\à la kohonen. *arXiv preprint arXiv:2302.07950*, 2023.
- Clifford R Jack, Heather J Wiste, Timothy G Lesnick, Stephen D Weigand, David S Knopman, Prashanthi Vemuri, Vernon S Pankratz, Matthew L Senjem, Jeffrey L Gunter, Michelle M Mielke, et al. Brain β -amyloid load approaches a plateau. *Neurology*, 80(10): 890–896, 2013.
- Bruno M Jedynak, Andrew Lang, Bo Liu, Elyse Katz, Yanwei Zhang, Bradley T Wyman, David Raunig, C Pierre Jedynak, Brian Caffo, Jerry L Prince, et al. A computational neurodegenerative disease progression score: method and results with the alzheimer’s disease neuroimaging initiative cohort. *Neuroimage*, 63(3):1478–1486, 2012.
- David Kanaa, Vikram Voleti, Samira Ebrahimi Kahou, and Christopher Pal. Simple video generation using neural odes. *arXiv preprint arXiv:2109.03292*, 2021.

- Amirhossein Kazerooni, Ehsan Khodapanah Aghdam, Moein Heidari, Reza Azad, Mohsen Fayyaz, Ilker Hacihaliloglu, and Dorit Merhof. Diffusion models in medical imaging: A comprehensive survey. *Medical Image Analysis*, 88:102846, 2023.
- Firas Khader, Gustav Mueller-Franzes, Soroosh Tayebi Arasteh, Tianyu Han, Christoph Haarbuerger, Maximilian Schulze-Hagen, Philipp Schad, Sandy Engelhardt, Bettina Baessler, Sebastian Foersch, et al. Medical diffusion–denoising diffusion probabilistic models for 3d medical image generation. *arXiv preprint arXiv:2211.03364*, 2022.
- Firas Khader, Gustav Müller-Franzes, Tianyu Han, Sven Nebelung, Christiane Kuhl, Johannes Stegmaier, and Daniel Truhn. Transformers for ct reconstruction from monoplanar and biplanar radiographs. In *International Workshop on Simulation and Synthesis in Medical Imaging*, pages 1–10. Springer, 2023.
- Seong Tae Kim, Umut Küçükaskan, and Nassir Navab. Longitudinal brain mr image modeling using personalized memory for alzheimer’s disease. *IEEE Access*, 9:143212–143221, 2021.
- Diederik P Kingma and Jimmy Ba. Adam: A method for stochastic optimization. *arXiv preprint arXiv:1412.6980*, 2014.
- Diederik P Kingma and Max Welling. Auto-encoding variational bayes. *arXiv preprint arXiv:1312.6114*, 2013.
- Guillaume Le Moing, Jean Ponce, and Cordelia Schmid. Ccvs: context-aware controllable video synthesis. In *Advances in Neural Information Processing Systems*, volume 34, pages 14042–14055, 2021.
- Yikuan Li, Mohammad Mamouei, Gholamreza Salimi-Khorshidi, Shishir Rao, Abdelaali Hassaine, Dexter Canoy, Thomas Lukasiewicz, and Kazem Rahimi. Hi-behrt: Hierarchical transformer-based model for accurate prediction of clinical events using multimodal longitudinal electronic health records. *IEEE Journal of Biomedical and Health Informatics*, 27(2):1106–1117, 2022.
- Yanbin Liu, Girish Dwivedi, Farid Boussaid, and Mohammed Bennamoun. 3d brain and heart volume generative models: A survey. *ACM Computing Surveys*, 56(6):1–37, 2024.
- Marco Lorenzi, Xavier Pennec, Giovanni B Frisoni, Nicholas Ayache, Alzheimer’s Disease Neuroimaging Initiative, et al. Disentangling normal aging from alzheimer’s disease in structural magnetic resonance images. *Neurobiology of aging*, 36:S42–S52, 2015.
- Ilya Loshchilov and Frank Hutter. Decoupled weight decay regularization. *arXiv preprint arXiv:1711.05101*, 2017.
- Gerard Martí-Juan, Marco Lorenzi, Gemma Piella, Alzheimer’s Disease Neuroimaging Initiative, et al. Mc-rvae: Multi-channel recurrent variational autoencoder for multimodal alzheimer’s disease progression modelling. *NeuroImage*, 268:119892, 2023.

- NVIDIA, :, Niket Agarwal, Arslan Ali, Maciej Bala, Yogesh Balaji, Erik Barker, Tiffany Cai, Prithvijit Chattopadhyay, Yongxin Chen, Yin Cui, Yifan Ding, Daniel Dworakowski, Jiaojiao Fan, Michele Fenzi, Francesco Ferroni, Sanja Fidler, Dieter Fox, Songwei Ge, Yunhao Ge, Jinwei Gu, Siddharth Gururani, Ethan He, Jiahui Huang, Jacob Huffman, Pooya Jannaty, Jingyi Jin, Seung Wook Kim, Gergely Klár, Grace Lam, Shiyi Lan, Laura Leal-Taixe, Anqi Li, Zhaoshuo Li, Chen-Hsuan Lin, Tsung-Yi Lin, Huan Ling, Ming-Yu Liu, Xian Liu, Alice Luo, Qianli Ma, Hanzi Mao, Kaichun Mo, Arsalan Mousavian, Seungjun Nah, Sriharsha Niverty, David Page, Despoina Paschalidou, Zeeshan Patel, Lindsey Pavao, Morteza Ramezanali, Fitsum Reda, Xiaowei Ren, Vasanth Rao Naik Sabavat, Ed Schmerling, Stella Shi, Bartosz Stefaniak, Shitao Tang, Lyne Tchaptmi, Przemek Tredak, Wei-Cheng Tseng, Jibin Varghese, Hao Wang, Haoxiang Wang, Heng Wang, Ting-Chun Wang, Fangyin Wei, Xinyue Wei, Jay Zhangjie Wu, Jiashu Xu, Wei Yang, Lin Yen-Chen, Xiaohui Zeng, Yu Zeng, Jing Zhang, Qinsheng Zhang, Yuxuan Zhang, Qingqing Zhao, and Artur Zolkowski. Cosmos world foundation model platform for physical ai, 2025. URL <https://arxiv.org/abs/2501.03575>.
- Neil P Oxtoby, Alexandra L Young, Nick C Fox, Alzheimer’s Disease Neuroimaging Initiative, Pankaj Daga, David M Cash, Sebastien Ourselin, Jonathan M Schott, and Daniel C Alexander. Learning imaging biomarker trajectories from noisy alzheimer’s disease data using a bayesian multilevel model. In *Bayesian and graphical Models for Biomedical Imaging: First International Workshop, BAMBI 2014, Cambridge, MA, USA, September 18, 2014, Revised Selected Papers*, pages 85–94. Springer, 2014.
- Sunghyun Park, Kangyeol Kim, Junsoo Lee, Jaegul Choo, Joonseok Lee, Sookyoung Kim, and Edward Choi. Vid-ode: Continuous-time video generation with neural ordinary differential equation. In *Proceedings of the AAAI Conference on Artificial Intelligence*, volume 35, pages 2412–2422, 2021.
- Jack Parker-Holder, Philip Ball, Jake Bruce, Vibhavari Dasagi, Kristian Holsheimer, Christos Kaplanis, Alexandre Moufarek, Guy Scully, Jeremy Shar, Jimmy Shi, Stephen Spencer, Jessica Yung, Michael Dennis, Sultan Kenjeyev, Shangbang Long, Vlad Mnih, Harris Chan, Maxime Gazeau, Bonnie Li, Fabio Pardo, Luyu Wang, Lei Zhang, Frederic Besse, Tim Harley, Anna Mitenkova, Jane Wang, Jeff Clune, Demis Hassabis, Raia Hadsell, Adrian Bolton, Satinder Singh, and Tim Rocktäschel. Genie 2: A large-scale foundation world model. 2024. URL <https://deepmind.google/discover/blog/genie-2-a-large-scale-foundation-world-model/>.
- Lemuel Puglisi, Daniel C Alexander, and Daniele Ravi. Enhancing spatiotemporal disease progression models via latent diffusion and prior knowledge. In *International Conference on Medical Image Computing and Computer-Assisted Intervention*, pages 173–183. Springer, 2024.
- Daniele Ravi, Stefano B Blumberg, Silvia Ingala, Frederik Barkhof, Daniel C Alexander, Neil P Oxtoby, Alzheimer’s Disease Neuroimaging Initiative, et al. Degenerative adversarial neuroimage nets for brain scan simulations: Application in ageing and dementia. *Medical Image Analysis*, 75:102257, 2022.

- Ali Razavi, Aaron Van den Oord, and Oriol Vinyals. Generating diverse high-fidelity images with vq-vae-2. In *Advances in neural information processing systems*, volume 32, 2019.
- Olaf Ronneberger, Philipp Fischer, and Thomas Brox. U-net: Convolutional networks for biomedical image segmentation. In *International Conference on Medical image computing and computer-assisted intervention*, pages 234–241. Springer, 2015.
- Yulia Rubanova, Ricky TQ Chen, and David K Duvenaud. Latent ordinary differential equations for irregularly-sampled time series. In *Advances in neural information processing systems*, volume 32, 2019.
- Benoît Sauty and Stanley Durrleman. Progression models for imaging data with longitudinal variational auto encoders. In *International Conference on Medical image computing and computer-assisted intervention*, pages 3–13. Springer, 2022.
- Yujun Shen, Ceyuan Yang, Xiaoou Tang, and Bolei Zhou. Interfacegan: Interpreting the disentangled face representation learned by gans. *IEEE transactions on pattern analysis and machine intelligence*, 44(4):2004–2018, 2020.
- Karen Simonyan and Andrew Zisserman. Very deep convolutional networks for large-scale image recognition. *arXiv preprint arXiv:1409.1556*, 2014.
- Nripendra Kumar Singh and Khalid Raza. Medical image generation using generative adversarial networks: A review. *Health informatics: A computational perspective in healthcare*, pages 77–96, 2021.
- Raphaël Sivera, Hervé Delingette, Marco Lorenzi, Xavier Pennec, Nicholas Ayache, Alzheimer’s Disease Neuroimaging Initiative, et al. A model of brain morphological changes related to aging and alzheimer’s disease from cross-sectional assessments. *NeuroImage*, 198:255–270, 2019.
- Li Sun, Junxiang Chen, Yanwu Xu, Mingming Gong, Ke Yu, and Kayhan Batmanghelich. Hierarchical amortized gan for 3d high resolution medical image synthesis. *IEEE journal of biomedical and health informatics*, 26(8):3966–3975, 2022.
- Petru-Daniel Tudosiu, Thomas Varsavsky, Richard Shaw, Mark Graham, Parashkev Nachev, Sebastien Ourselin, Carole H Sudre, and M Jorge Cardoso. Neuromorphologically-preserving volumetric data encoding using vq-vae. *arXiv preprint arXiv:2002.05692*, 2020.
- Hristina Uzunova, Jan Ehrhardt, Fabian Jacob, Alex Frydrychowicz, and Heinz Handels. Multi-scale gans for memory-efficient generation of high resolution medical images. In *International Conference on Medical image computing and computer-assisted intervention*, pages 112–120. Springer, 2019.
- Aaron Van Den Oord, Oriol Vinyals, et al. Neural discrete representation learning. In *Advances in neural information processing systems*, volume 30, 2017.
- Victor L Villemagne, Samantha Burnham, Pierrick Bourgeat, Belinda Brown, Kathryn A Ellis, Olivier Salvado, Cassandra Szoeki, S Lance Macaulay, Ralph Martins, Paul Maruff,

- et al. Amyloid β deposition, neurodegeneration, and cognitive decline in sporadic alzheimer’s disease: a prospective cohort study. *The Lancet Neurology*, 12(4):357–367, 2013.
- Vikram Voleti, Alexia Jolicoeur-Martineau, and Chris Pal. Mcvd-masked conditional video diffusion for prediction, generation, and interpolation. In *Advances in Neural Information Processing Systems*, volume 35, pages 23371–23385. Curran Associates, Inc., 2022.
- Peter A. Wijeratne and Daniel C. Alexander. Unscrambling disease progression at scale: fast inference of event permutations with optimal transport. In A. Globerson, L. Mackey, D. Belgrave, A. Fan, U. Paquet, J. Tomczak, and C. Zhang, editors, *Advances in Neural Information Processing Systems*, volume 37, pages 63316–63341. Curran Associates, Inc., 2024. URL https://proceedings.neurips.cc/paper_files/paper/2024/file/73c362193e3e23188b2a74de7824cc4c-Paper-Conference.pdf.
- Weihao Xia, Yujiu Yang, and Jing-Hao Xue. Modelling latent dynamics of stylegan using neural odes. *arXiv preprint arXiv:2208.11197*, 2022.
- Wilson Yan, Yunzhi Zhang, Pieter Abbeel, and Aravind Srinivas. Videogpt: Video generation using vq-vae and transformers. *arXiv preprint arXiv:2104.10157*, 2021.
- Jee Seok Yoon, Chenghao Zhang, Heung-Il Suk, Jia Guo, and Xiaoxiao Li. Sadm: Sequence-aware diffusion model for longitudinal medical image generation. In *International Conference on Information Processing in Medical Imaging*, pages 388–400. Springer, 2023.
- Alexandra L. Young, Razvan V. Marinescu, Neil P. Oxtoby, Martina Bocchetta, Keir Yong, Nicholas C. Firth, David M. Cash, David L. Thomas, Katrina M. Dick, Jorge Cardoso, John van Swieten, Barbara Borroni, Daniela Galimberti, Mario Masellis, Maria Carmela Tartaglia, James B. Rowe, Caroline Graff, Fabrizio Tagliavini, Giovanni B. Frisoni, Robert Laforce, Elizabeth Finger, Alexandre de Mendonça, Sandro Sorbi, Jason D. Warren, Sebastian Crutch, Nick C. Fox, Sebastien Ourselin, Jonathan M. Schott, Jonathan D. Rohrer, Daniel C. Alexander, Christin Andersson, Silvana Archetti, Andrea Arighi, Luisa Benussi, Giuliano Binetti, Sandra Black, Maura Cosseddu, Marie Fallström, Carlos Ferreira, Chiara Fenoglio, Morris Freedman, Giorgio G. Fumagalli, Stefano Gazzina, Roberta Ghidoni, Marina Grisoli, Vesna Jelic, Lize Jiskoot, Ron Keren, Gemma Lombardi, Carolina Maruta, Lieke Meeter, Simon Mead, Rick van Minkelen, Benedetta Nacmias, Linn Öijerstedt, Alessandro Padovani, Jessica Panman, Michela Pievani, Cristina Polito, Enrico Premi, Sara Prioni, Rosa Rademakers, Veronica Redaelli, Ekaterina Rogaeva, Giacomina Rossi, Martin Rossor, Elio Scarpini, David Tang-Wai, Hakan Thonberg, Pietro Tiraboschi, Ana Verdelho, Michael W. Weiner, Paul Aisen, Ronald Petersen, Clifford R. Jack, William Jagust, John Q. Trojanowki, Arthur W. Toga, Laurel Beckett, Robert C. Green, Andrew J. Saykin, John Morris, Leslie M. Shaw, Zaven Khachaturian, Greg Sorensen, Lew Kuller, Marc Raichle, Steven Paul, Peter Davies, Howard Fillit, Franz Hefti, Davie Holtzman, M. Marcel Mesulam, William Potter, Peter Snyder, Adam Schwartz, Tom Montine, Ronald G. Thomas, Michael Donohue, Sarah Walter, Devon Gessert, Tamie Sather, Gus Jiminez, Danielle Harvey, Matthew Bernstein, Paul Thompson, Norbert Schuff, Bret Borowski, Jeff Gunter, Matt Senjem, Prashanthi Vemuri, David

Jones, Kejal Kantarci, Chad Ward, Robert A. Koeppe, Norm Foster, Eric M. Reiman, Kewei Chen, Chet Mathis, Susan Landau, Nigel J. Cairns, Erin Householder, Lisa Taylor-Reinwald, Virginia Lee, Magdalena Korecka, Michal Figurski, Karen Crawford, Scott Neu, Tatiana M. Foroud, Steven Potkin, Li Shen, Kelley Faber, Sungeun Kim, Kwangsik Nho, Leon Thal, Neil Buckholtz, Marylyn Albert, Richard Frank, John Hsiao, Jeffrey Kaye, Joseph Quinn, Betty Lind, Raina Carter, Sara Dolen, Lon S. Schneider, Sonia Pawluczyk, Mauricio Beccera, Liberty Teodoro, Bryan M. Spann, James Brewer, Helen Vanderswag, Adam Fleisher, Judith L. Heidebrink, Joanne L. Lord, Sara S. Mason, Colleen S. Albers, David Knopman, Kris Johnson, Rachelle S. Doody, Javier Villanueva-Meyer, Munir Chowdhury, Susan Rountree, Mimi Dang, Yaakov Stern, Lawrence S. Honig, Karen L. Bell, Beau Ances, Maria Carroll, Sue Leon, Mark A. Mintun, Stacy Schneider, Angela Oliver, Daniel Marson, Randall Griffith, David Clark, David Geldmacher, John Brockington, Erik Roberson, Hillel Grossman, Effie Mitsis, Leyla de Toledo-Morrell, Raj C. Shah, Ranjan Duara, Daniel Varon, Maria T. Greig, Peggy Roberts, Marilyn Albert, Chiadi Onyike, Daniel D’Agostino, Stephanie Kielb, James E. Galvin, Brittany Cerbone, Christina A. Michel, Henry Rusinek, Mony J. de Leon, Lidia Glodzik, Susan De Santi, P. Murali Doraiswamy, Jeffrey R. Petrella, Terence Z. Wong, Steven E. Arnold, Jason H. Karlawish, David Wolk, Charles D. Smith, Greg Jicha, Peter Hardy, Partha Sinha, Elizabeth Oates, Gary Conrad, Oscar L. Lopez, MaryAnn Oakley, Donna M. Simpson, Anton P. Porsteinsson, Bonnie S. Goldstein, Kim Martin, Kelly M. Makino, M. Saleem Ismail, Connie Brand, Ruth A. Mulnard, Gaby Thai, Catherine Mc-Adams-Ortiz, Kyle Womack, Dana Mathews, Mary Quiceno, Ramon Diaz-Arrastia, Richard King, Myron Weiner, Kristen Martin-Cook, Michael DeVous, Allan I. Levey, James J. Lah, Janet S. Cellar, Jeffrey M. Burns, Heather S. Anderson, Russell H. Swerdlow, Liana Apostolova, Kathleen Tingus, Ellen Woo, Daniel Hs Silverman, Po H. Lu, George Bartzokis, Neill R. Graff-Radford, Francine Parfitt, Tracy Kendall, Heather Johnson, Martin R. Farlow, Ann Marie Hake, Brandy R. Matthews, Scott Herring, Cynthia Hunt, Christopher H. van Dyck, Richard E. Carson, Martha G. MacAvoy, Howard Chertkow, Howard Bergman, Chris Hosein, Bojana Stefanovic, Curtis Caldwell, Ging-Yuek Robin Hsiung, Howard Feldman, Benita Mudge, Michele Assaly, Andrew Kertesz, John Rogers, Charles Bernick, Donna Munic, Diana Kerwin, Marek-Marsel Mesulam, Kristine Lipowski, Chuang-Kuo Wu, Nancy Johnson, Carl Sadowsky, Walter Martinez, Teresa Villena, Raymond Scott Turner, Kathleen Johnson, Brigid Reynolds, Reisa A. Sperling, Keith A. Johnson, Gad Marshall, Meghan Frey, Barton Lane, Allyson Rosen, Jared Tinklenberg, Marwan N. Sabagh, Christine M. Belden, Sandra A. Jacobson, Sherye A. Sirrel, Neil Kowall, Ronald Killiany, Andrew E. Budson, Alexander Norbash, Patricia Lynn Johnson, Joanne Allard, Alan Lerner, Paula Ogrocki, Leon Hudson, Evan Fletcher, The Genetic FTD Initiative (GENFI), and The Alzheimer’s Disease Neuroimaging Initiative (ADNI). Uncovering the heterogeneity and temporal complexity of neurodegenerative diseases with subtype and stage inference. *Nature Communications*, 9(1):4273, Oct 2018. ISSN 2041-1723. doi: 10.1038/s41467-018-05892-0. URL <https://doi.org/10.1038/s41467-018-05892-0>.

Richard Zhang, Phillip Isola, Alexei A Efros, Eli Shechtman, and Oliver Wang. The unreasonable effectiveness of deep features as a perceptual metric. In *Proceedings of the IEEE conference on computer vision and pattern recognition*, pages 586–595, 2018.

Appendix A. Training and implementation details

We train the model for two stages, 3D-VQ-GAN and latent disease ODE. All models are trained on a NVIDIA A100 80GB GPU.

A.1. 3D-VQ-GAN

In line with recommendations from (Ge et al., 2022; Esser et al., 2021), the training of 3D-VQ-GAN begins on all CT scans in the training set using the reconstruction loss. Subsequently, the GAN loss is introduced after 10,000 steps. Hyperparameters are set as follows: $\lambda_{\text{perc}} = \lambda_{\text{rec}} = 4$ and $\lambda_{\text{GAN}} = 1$. The Adam optimizer (Kingma and Ba, 2014) is employed with a learning rate of 3×10^{-4} and $\beta_1 = 0.5, \beta_2 = 0.9$. Training the 3D-VQ-GAN spans 20,000 steps, and the best model, determined by the smallest training loss after adding the GAN loss, is selected. The batch size is set at 1, and the accumulated batch size is 6. Training the first-stage model takes approximately 10 days.

A.2. Disease ODE

After completing the training of 3D-VQ-GAN, we proceed to train the latent disease ODE using the AdamW optimizer (Loshchilov and Hutter, 2017). The training spans 100 epochs, employing a batch size of 1, a learning rate of 2×10^{-4} , and $\beta_1 = 0.5, \beta_2 = 0.9$. To enhance the model’s performance at later time points, we implement a linearly increasing weights strategy, assigning higher loss weights for later time points. The best model, identified by the smallest training loss, is selected. Training the latent disease ODE takes approximately 15 hours.

A.3. Implementation details

For the implementation of 3D-VQ-GAN, we adopt a similar network structure as outlined in (Ge et al., 2022). The codebook size is set to $M = 256$ with an embedding size of $c = 16$. We employ a compression rate $r = 4$, calculated as the ratio between D, H, W and d, h, w . All input 3D CT scans are resized to $D = 96, H = 256, W = 256$ before being fed into the model. In the latent disease ODE, the neural ODE solver is implemented by stacking three 3D convolution layers. The code is implemented using PyTorch 1.8.

Appendix B. Pseudo code for the algorithm for biomarker extraction and selection

Input: Baseline CT scans, time-to-death, censoring status, age, gender, smoking status
Output: A ranked list of prognostically significant biomarkers, with corresponding HR, p-value, and C-index values.

Feature Extraction:

Use a trained 3D-VQGAN encoder to extract codebook indices from each CT scan.

Compute a normalized histogram of these indices to obtain proportional representations of imaging patterns (biomarkers).

Biomarker selection via Five-Fold Cross-Validation:

for *fold* **do**

 Split the dataset into training (80%) and validation (20%) sets.

for *biomarker candidate* **do**

 Fit a univariate Cox proportional hazards model, adjusting for covariates (age, sex, smoking status).

 Compute p-value, hazard ratio (HR) from the trained Cox model, and compute C-index on the validation set.

 Retain biomarkers that satisfy $HR > 1$, $p\text{-value} < 0.01$, and $C\text{-index} > 0.5$ on all five folds.

Among the shortlisted biomarkers, select the top 5 with the highest mean validation-set C-index across folds.

Appendix C. Pre-processing

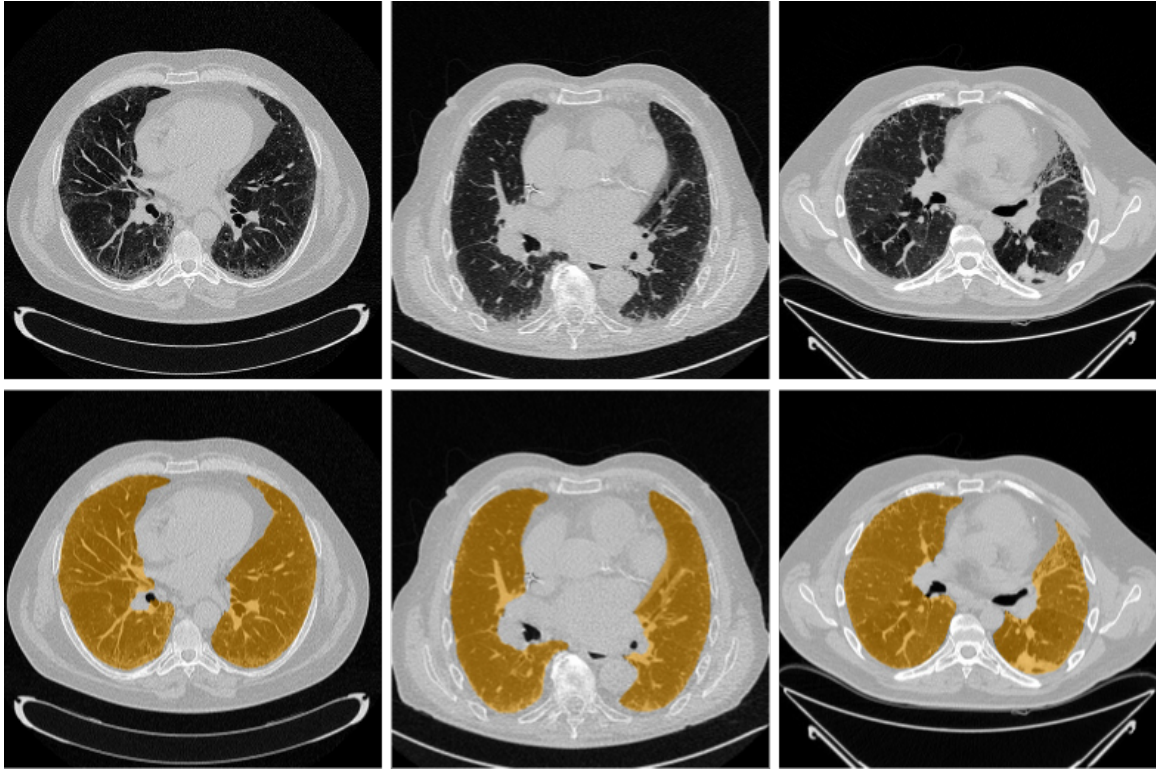


Figure 4: Segmentation results for selected cases from Leuven cohort

The registration process aligns corresponding structures across scans, ensuring the model focuses on disease-related changes. The Learn2Reg challenge, associated with MICCAI 2020 and 2021, provides valuable insights for choosing a suitable registration method for lung CT scans. This challenge compared various approaches on clinically relevant tasks. In the lung CT task, the goal was to register expiration scans to inspiration scans, with corresponding landmarks provided for accuracy evaluation (Hering et al., 2022). Notably, CorrField (Heinrich et al., 2015), a non-rigid registration method, emerged as the top performer among 15 methods, including deep learning and conventional approaches. CorrField achieved a target registration error (the Euclidean distance between corresponding landmarks in the warped fixed and moving scan) of only 1.75mm (Hering et al., 2022).

We use the faster version (implemented in (Hansen and Heinrich, 2021)) of CorrField method (Heinrich et al., 2015), a non-learning-based unsupervised method. CorrField first employs Foerstner operator (Förstner and Gülch, 1987) to extract distinctive keypoints in one 3D volume. Then a dissimilarity distribution over a densely quantized space of displacements is calculated. Finally, a parts-based model is used to infer the smooth motion of connected keypoints and regularize the correspondence field. Specifically, a minimum spanning tree (MST) is generated from the set of sparse keypoints, which enables exact message passing using belief propagation on the graph to regularise the displacement costs.

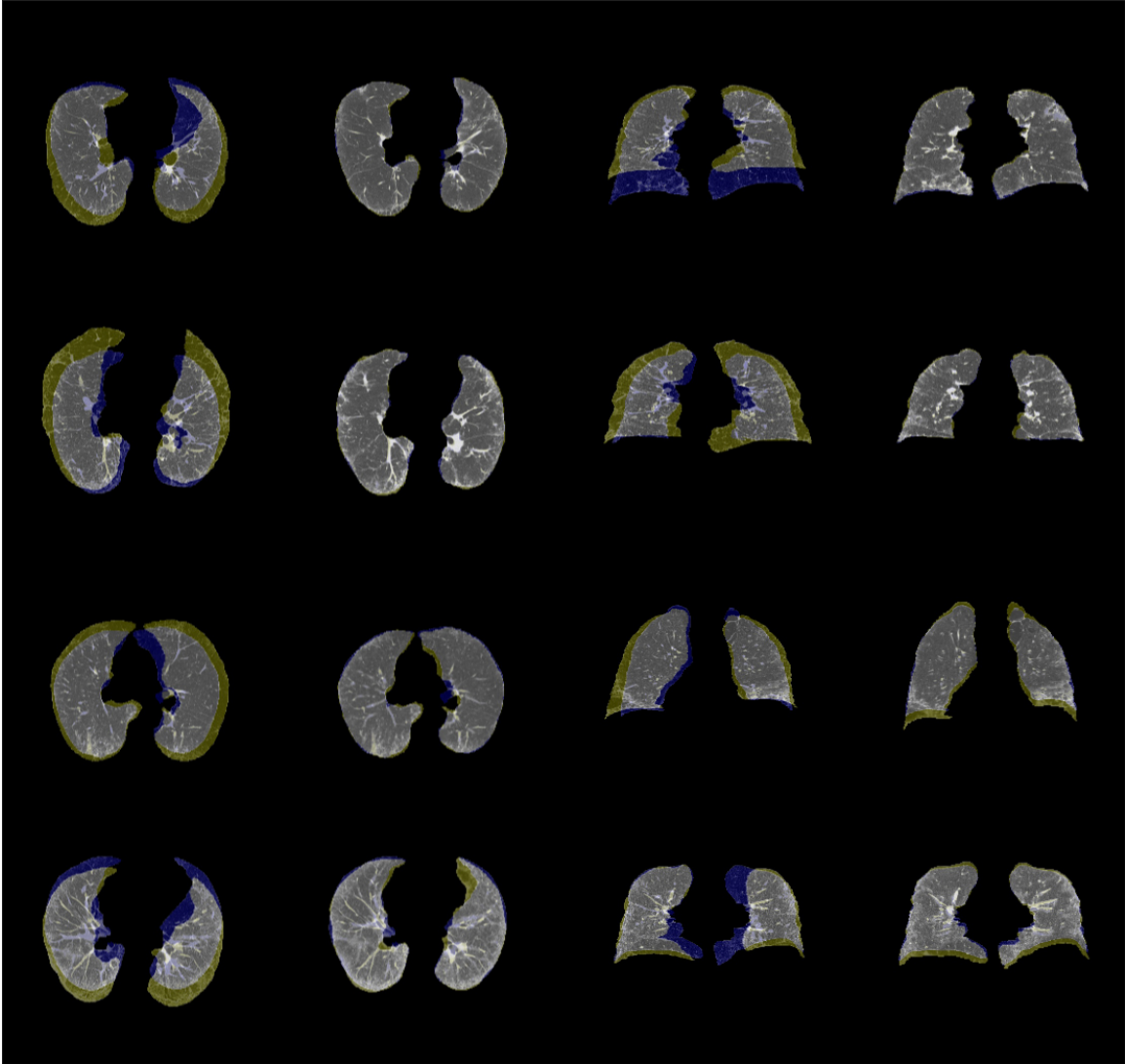


Figure 5: Visualization of four registration outcomes with a focus on lung areas for clarity. The left two columns present axial views before and after registration, while the right two columns showcase coronal views. Baseline scans are denoted in blue, whereas follow-up scans are highlighted in yellow. The merging of colours results in grey or white hues, indicating aligned structures due to RGB amalgamation. Notably, follow-up scans are registered to their corresponding baseline scans. The first two rows illustrate cases with successful registration outcomes, while the subsequent two rows demonstrate instances of varying degrees of misalignment.

To ensure the disease progression model focuses solely on lung tissue, we define keypoints within lung masks for registration. After aligning the longitudinal CT scans to the baseline

CT scan using image registration, we replaced the non-lung region in the registered scans with the corresponding region from the baseline CT scan. This eliminates distractions from surrounding body parts. We leverage the default hyperparameters from the validated implementation (<https://grand-challenge.org/algorithms/corrfield/>) for registration. To verify registration quality, all registered scans undergo visual inspection by me to identify and exclude those with significant errors. However, because of the non-clinical background, there is still risk compared with verification conducted by experienced radiologists.

Appendix D. Additional experiments

In this section, we began by conducting experiments on the initial stage of the model to show the reconstruction performance of 3D-VQ-GAN, both qualitatively and quantitatively. Additionally, we explore the impact of varying hyperparameters on the reconstruction performance. Subsequently, we assess the proposed two-stage model’s effectiveness in disease progression modelling and interpolation tasks, demonstrating its capability to capture the dynamics of disease progression. Finally, we present visualizations of the learned codebook for enhanced interpretability.

Table 3: Reconstruction performance of 3D-VQ-GAN with different hyperparameters.

No.	Vocabulary size	Compression rate	Learning rate	MSE on internal test set	MSE on external test set
1	1024	4	3×10^{-4}	3.76×10^{-3}	6.84×10^{-3}
2	4096	4	3×10^{-4}	3.54×10^{-3}	6.64×10^{-3}
3	256	4	1×10^{-4}	4.88×10^{-3}	8.67×10^{-3}
4	256	4	3×10^{-4}	4.23×10^{-3}	8.10×10^{-3}
5	256	8	3×10^{-4}	6.17×10^{-3}	1.15×10^{-2}

D.1. Reconstruction performance of 3D-VQ-GAN

This experiment investigates the influence of two critical hyperparameters—codebook vocabulary size and compression rate—on the performance of the 3D-VQ-GAN model (Appendix E.2). The codebook vocabulary size specifies the number of discrete latent vectors in the codebook $\mathcal{Z}$, which serve as building blocks for representing input data in the latent space. A larger vocabulary size enables the model to capture finer details in 3D CT scans but increases computational demands. In contrast, the compression rate controls the degree of dimensionality reduction during encoding, reducing the complexity of the latent space representation. While a higher compression rate simplifies the model, it risks losing information and compromising reconstruction quality. To identify the optimal configuration, the model was trained on a training dataset and evaluated on internal and external test sets (Table 3) using quantitative metrics (e.g., reconstruction error) and qualitative visual inspection. A vocabulary size of 256 and a compression rate of 4 were chosen as they offered the best balance between detail preservation, computational efficiency, and reconstruction performance. Figure 6 showcases examples of input 3D CT scans and the corresponding reconstructions generated by VQ-GAN models trained with different hyperparameter settings.

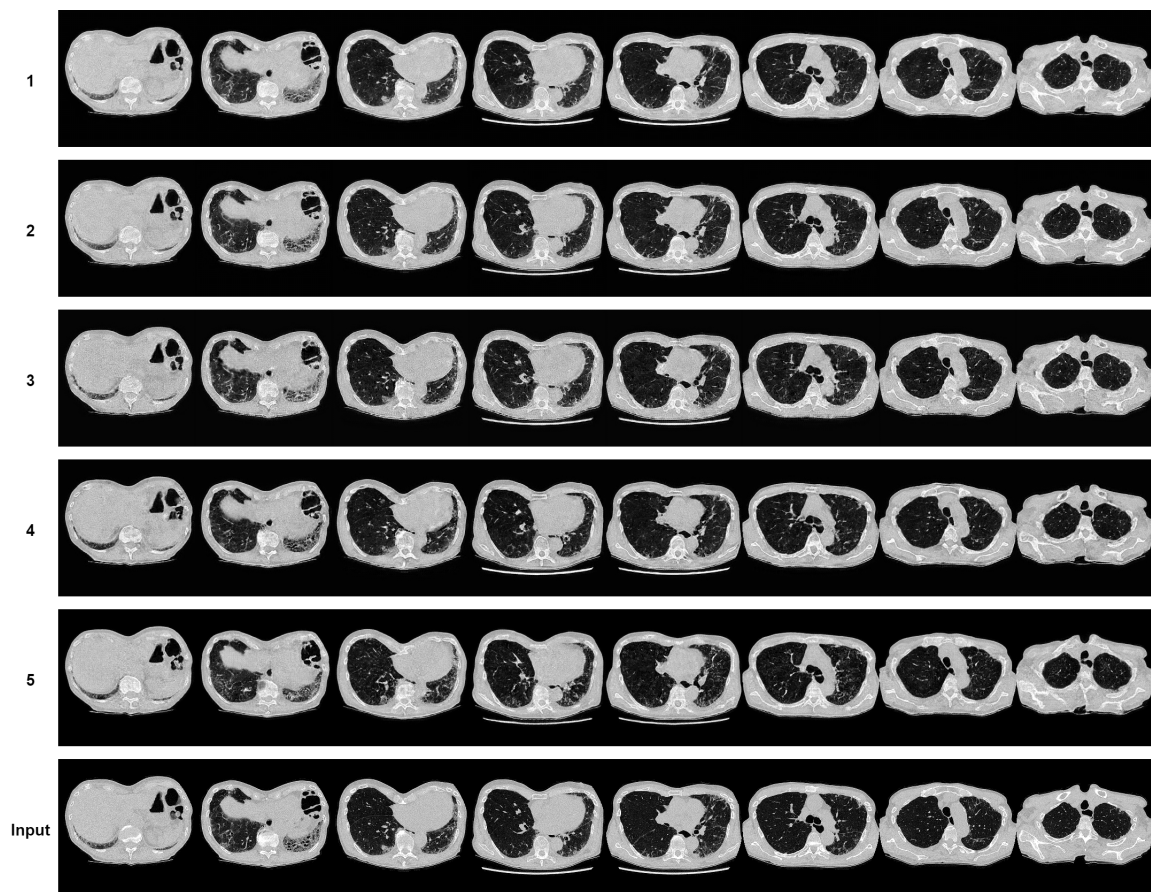


Figure 6: Examples of input 3D CT scans and corresponding CT scans reconstructed by 3D-VQ-GAN with varying hyperparameters, as detailed in Table 3

Appendix E. Details of the Methodology

E.1. Problem formulation

We denote the irregularly sampled longitudinal 3D imaging data of a subject as $\mathcal{X}_{\mathcal{T}} = \{\mathbf{X}_{t_0}, \mathbf{X}_{t_1}, \dots, \mathbf{X}_{t_j}, \dots, \mathbf{X}_{t_T}\}$, where each $\mathbf{X}_{t_j} \in \mathbb{R}^{D \times H \times W \times C}$ (D : depth, H : height, W : width, C : channel) and $\mathcal{T} = \{t_0, t_1, \dots, t_j, \dots, t_T\}$ (t_j : the time of the j^{th} observation of the subject). Each subject can have an arbitrary number of observations. In the context of IPF disease progression modelling, this translates to each patient having an arbitrary number of longitudinal volumetric lung CT scans. The corresponding mask for the region of interest is also segmented. Given $\mathcal{X}_{\mathcal{T}}$, the objective of this work is to build a model capable of generating synthetic 3D imaging data at any time point between t_0 and t_T , illustrating the progression of the disease within a patient over time. In this study, we use 3D volumetric CT scans of IPF patients as an example application.

The proposed method has two stages: In the first stage, a 3D-VQ-GAN is trained to reconstruct CT volumes. In the second stage, a latent (ODE) is trained to model the temporal dynamics from quantised embeddings of longitudinal CT scans generated by the encoder in the first stage, reconstructing continuous trajectories from discrete observations in the latent space (Figure 7).

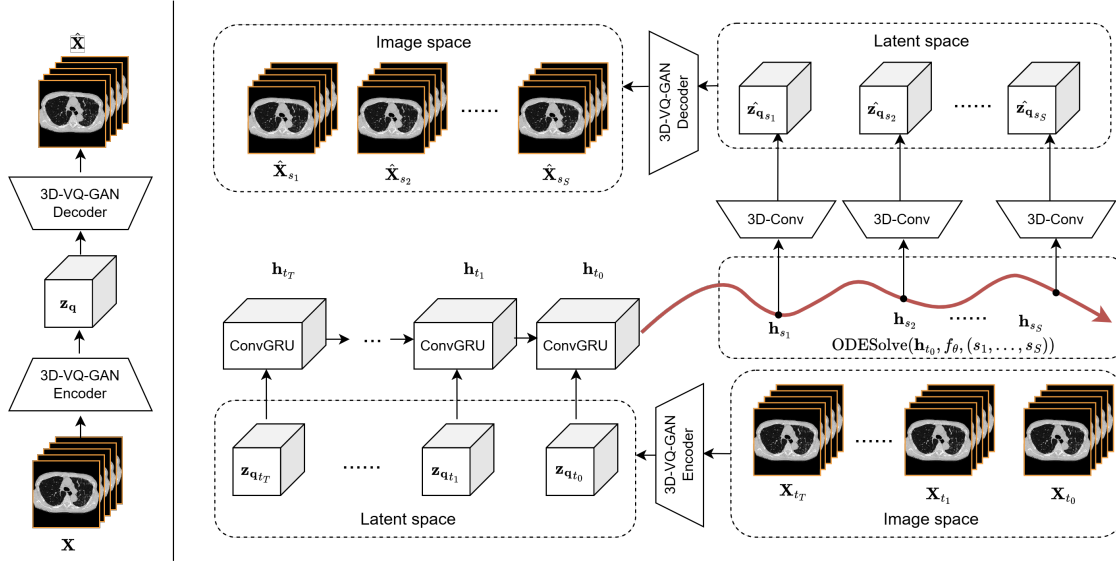


Figure 7: The overview of the proposed two-stage model. The left side is the 3D-VQ-GAN for image reconstruction. The right side is the latent disease ODE for modelling disease progression dynamics from longitudinal 3D imaging data.

E.2. 3D-VQ-GAN for image reconstruction

To capture the dynamics of disease progression in the latent space, which can significantly decrease computational costs, the model needs to first learn an effective and compact latent

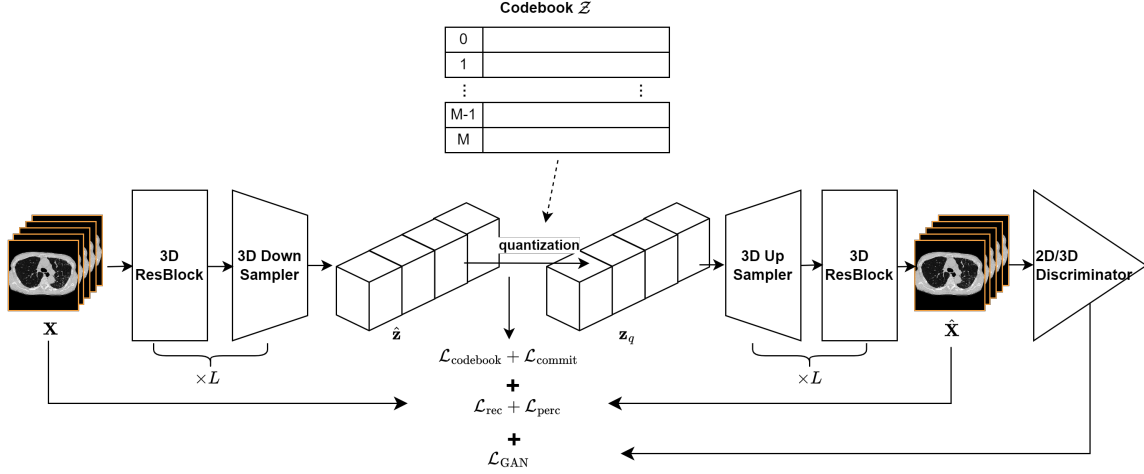


Figure 8: The overview of the 3D-VQ-GAN for image reconstruction.

representation of the input image. In the first stage, we adopt 3D-VQ-GAN (Ge et al., 2022) (Figure 8), which replaces 2D operations of the original VQ-GAN (Esser et al., 2021) with 3D operations. VQ-GAN is a variant of VQ-VAE. VQ-VAE consists of an encoder E and a decoder G and keeps a discrete codebook of learned representations in latent space. Given an input $\mathbf{X}$, the VQ-VAE tries to represent the input image with embeddings from the codebook in the latent space. More specifically, the encoder E projects $\mathbf{X}$ into the embedding $\hat{\mathbf{z}} = E(\mathbf{X}) \in \mathbb{R}^{d \times h \times w \times c}$ in latent space followed by an element-wise quantization operation $\mathbf{q}(\cdot)$ which approximates $\hat{\mathbf{z}}$ by replacing each spatial code $\hat{\mathbf{z}}_{i,j,k} \in \mathbb{R}^c$ with its nearest neighbour in the trainable codebook $\mathcal{Z} = \{\mathbf{z}_m\}_{m=1}^M \in \mathbb{R}^c$. The discrete latent indices and embeddings after quantization are denoted as $\mathbf{c} \in \mathbb{Z}^{d \times h \times w}$ and $\mathbf{z}_\mathbf{q} \in \mathbb{R}^{d \times h \times w \times c}$ respectively. $\mathbf{z}_\mathbf{q}$ then goes through the decoder to reconstruct the input $\hat{\mathbf{X}} = G(\mathbf{z}_\mathbf{q})$, using: $\mathbf{z}_\mathbf{q} = \mathbf{q}(\hat{\mathbf{z}}) = \arg \min_{\mathbf{z}_m \in \mathcal{Z}} \|\hat{\mathbf{z}}_{i,j,k} - \mathbf{z}_m\|$.

For the non-differentiable quantization operation, VQ-VAE uses a straight-through estimator (Bengio et al., 2013) which copies gradients from decoder input $\mathbf{z}_\mathbf{q}$ to encoder output $\hat{\mathbf{z}}$ (Van Den Oord et al., 2017).

$$\mathbf{z}_\mathbf{q} = \mathbf{q}(\hat{\mathbf{z}}) = \arg \min_{\mathbf{z}_m \in \mathcal{Z}} \|\hat{\mathbf{z}}_{i,j,k} - \mathbf{z}_m\| \quad (1)$$

The VQ-VAE loss $\mathcal{L}_{\text{vqvae}}$ consists of three terms: reconstruction loss $\mathcal{L}_{\text{rec}}$, codebook loss $\mathcal{L}_{\text{codebook}}$ and commitment loss $\mathcal{L}_{\text{commit}}$. $\mathcal{L}_{\text{rec}}$ is used for optimizing both encoder and decoder. $\mathcal{L}_{\text{codebook}}$ is used only for optimizing the codebook by pushing embeddings in the codebook to be close to the output of the encoder. $\mathcal{L}_{\text{commit}}$ is employed to enforce the encoder commits to an embedding in the codebook (Van Den Oord et al., 2017).

$$\mathcal{L}_{\text{vqvae}} = \underbrace{\|\mathbf{X} - \hat{\mathbf{X}}\|_1}_{\mathcal{L}_{\text{rec}}} + \underbrace{\|\text{sg}[E(\mathbf{X})] - \mathbf{z}_\mathbf{q}\|_2^2}_{\mathcal{L}_{\text{codebook}}} + \underbrace{\beta \|\text{sg}[\mathbf{z}_\mathbf{q}] - E(\mathbf{X})\|_2^2}_{\mathcal{L}_{\text{commit}}} \quad (2)$$

$\text{sg}[\cdot]$ is the stop-gradient operator here.

In addition to the VQ-VAE loss, VQ-GAN also uses GAN loss $\mathcal{L}_{\text{GAN}}$ and perceptual loss $\mathcal{L}_{\text{perc}}$ to improve the reconstruction quality as well as increase the compression rate. Similar to 3D-VQ-GAN (Ge et al., 2022), we use two discriminators D_{2d} and D_{3d} . D_{2d} is used to distinguish the real slice and the reconstructed slice of 2D plane. D_{3d} is used to distinguish real 3D input $\mathbf{X}$ and reconstruction $\hat{\mathbf{X}}$ to encourage the consistency between slices:

$$\mathcal{L}_{\text{GAN}} = \log D_{2d/3d}(\mathbf{X}) + \log(1 - D_{2d/3d}(\hat{\mathbf{X}})) \quad (3)$$

Perceptual loss (Zhang et al., 2018) measures the distance of the true input and reconstruction in the feature space of a VGG network (Simonyan and Zisserman, 2014).

$$\mathcal{L}_{\text{perc}} = \sum_l w_l ||\text{VGG}^{(l)}(\hat{\mathbf{X}}) - \text{VGG}^{(l)}(\mathbf{X})||_1 \quad (4)$$

$\text{VGG}^{(l)}(\cdot)$ extracted the features of l^{th} layer of VGG. w_l is a learned weight for scaling. The overall loss of 3D-VQ-GAN $\mathcal{L}_{3D-VQ-GAN}$ would be

$$\begin{aligned} & \min_{E,G,Z} \left(\max_{D_{2d}, D_{3d}} (\lambda_{\text{GAN}} \mathcal{L}_{\text{GAN}}) + \right. \\ & \left. \min_{E,G,Z} (\lambda_{\text{perc}} \mathcal{L}_{\text{perc}} + \lambda_{\text{rec}} \mathcal{L}_{\text{rec}} + \mathcal{L}_{\text{codebook}} + \beta \mathcal{L}_{\text{commit}}) \right) \end{aligned} \quad (5)$$

E.3. Disease ODE: modelling latent disease progression dynamics

E.3.1. OVERVIEW

As shown in Figure 7, given the trained encoder of 3D-VQ-GAN, longitudinal input 3D imaging data $\mathbf{X}_{t_0}, \mathbf{X}_{t_1}, \dots, \mathbf{X}_{t_T}$ for each patient can be projected to a series of quantized embeddings $\mathbf{z}_{\mathbf{q}_{t_0}}, \mathbf{z}_{\mathbf{q}_{t_1}}, \dots, \mathbf{z}_{\mathbf{q}_{t_T}}$. This sequence of embeddings can be considered as samples from the continuous disease trajectory of that subject in the embedding space. To reconstruct the continuous trajectory from discrete observations, we adapt the common latent ODE structure, an encoder-decoder-based latent-variable time series model. In this application, the primary focus lies on capturing changes within specific Regions of Interest (ROIs), i.e. lung area. To isolate and emphasize these areas in the analysis, we apply a masking technique that excludes regions outside of the ROI in the latent embedding series. The overview of the latent disease ODE is shown in Figure 7. Firstly, we use convolution-based gated recurrent unit (3D-ConvGRU) neural network (Ballas et al., 2015) as an encoder to embed the input sequence $\mathbf{z}_{\mathbf{q}_{t_0}}, \mathbf{z}_{\mathbf{q}_{t_1}}, \dots, \mathbf{z}_{\mathbf{q}_{t_T}}$ into a latent initial state $\mathbf{h}_{t_0}$. Then, the continuous latent trajectory can be generated by using an ODE solver given $\mathbf{h}_{t_0}$. Finally, the latent trajectory is projected back to the embedding space of 3D-VQ-GAN to get embeddings $\hat{\mathbf{z}}_{\mathbf{q}_{s_1}}, \hat{\mathbf{z}}_{\mathbf{q}_{s_2}}, \dots, \hat{\mathbf{z}}_{\mathbf{q}_{s_S}}$ at any target timesteps $\mathcal{S} = \{s_1, s_2, \dots, s_S\}$. Feeding this sequence to the trained decoder G of 3D-VQ-GAN can reconstruct the 3D imaging data at target timesteps $\hat{\mathbf{X}}_{s_1}, \hat{\mathbf{X}}_{s_2}, \dots, \hat{\mathbf{X}}_{s_S}$.

E.3.2. LATENT ENCODER: 3D-CONVGRU

ConvGRU (Ballas et al., 2015) leverages convolutions within the GRU framework, enabling it to simultaneously process both spatial and temporal information in sequential data.

Building on the concept of ConvGRU from (Ballas et al., 2015), which employs 2D convolutions, this application utilizes 3D convolutions instead. This modified unit is referred to as 3D-ConvGRU and the corresponding update function is named 3D-ConvGRUCell. Given the sequence of quantized embeddings $\mathbf{z}_{\mathbf{q}_{t_0}}, \mathbf{z}_{\mathbf{q}_{t_1}}, \dots, \mathbf{z}_{\mathbf{q}_{t_T}}$, 3D-ConvGRU models the time series by making next-step prediction based on previous hidden state in an autoregressive way. The 3D-ConvGRU is run backwards as suggested by (Chen et al., 2018) and can be formulated as: $\mathbf{h}_{t_{i-1}} = \text{3D-ConvGRUCell}(\mathbf{h}_{t_i}, \mathbf{z}_{\mathbf{q}_{t_{i-1}}})$, where $\mathbf{h}_{t_i}$ is the hidden state on t_i .

E.3.3. LATENT DECODER

The latent decoder comprises three components: a neural ODE, a 3D convolution layer, and a linear composition layer. This decoder architecture is adapted from (Park et al., 2021).

The neural ODE defines a continuous hidden state $\mathbf{h}(t)$ which is the solution of an ODE initial-value problem (IVP) as follows (Chen et al., 2018; Rubanova et al., 2019). Here the initial status is $\mathbf{h}_{t_0}$ produced by the above 3D-ConvGRU.

$$\frac{d\mathbf{h}(t)}{dt} = f_{\theta}(\mathbf{h}(t), t), \quad \mathbf{h}(t_0) = \mathbf{h}_{t_0} \quad (6)$$

f_{θ} is a neural network parameterized by θ and f_{θ} defines the dynamics of $\mathbf{h}(t)$. By employing a numerical ODE solver, the hidden states $s_1, s_2, \dots, s_S$ at any target timesteps can be obtained based on the initial status $\mathbf{h}_{t_0}$. This method excels by accommodating more complex dynamics within the latent state, as opposed to relying on restrictive assumptions like linearity (Sauty and Durrleman, 2022; Kim et al., 2021). This enables more flexible disease progression modelling by using neural networks to directly parameterize the changes in the hidden state. Subsequently, a single 3D convolution layer takes two hidden states $\mathbf{h}_{s_i}, \mathbf{h}_{s_{i-1}}$ and outputs the difference map $\mathbf{D}_{s_i}$, approximating the difference $\Delta\mathbf{z}_{\mathbf{q}_{s_i}}$ between the current $\mathbf{z}_{\mathbf{q}_{s_i}}$ and the previous $\mathbf{z}_{\mathbf{q}_{s_{i-1}}}$.

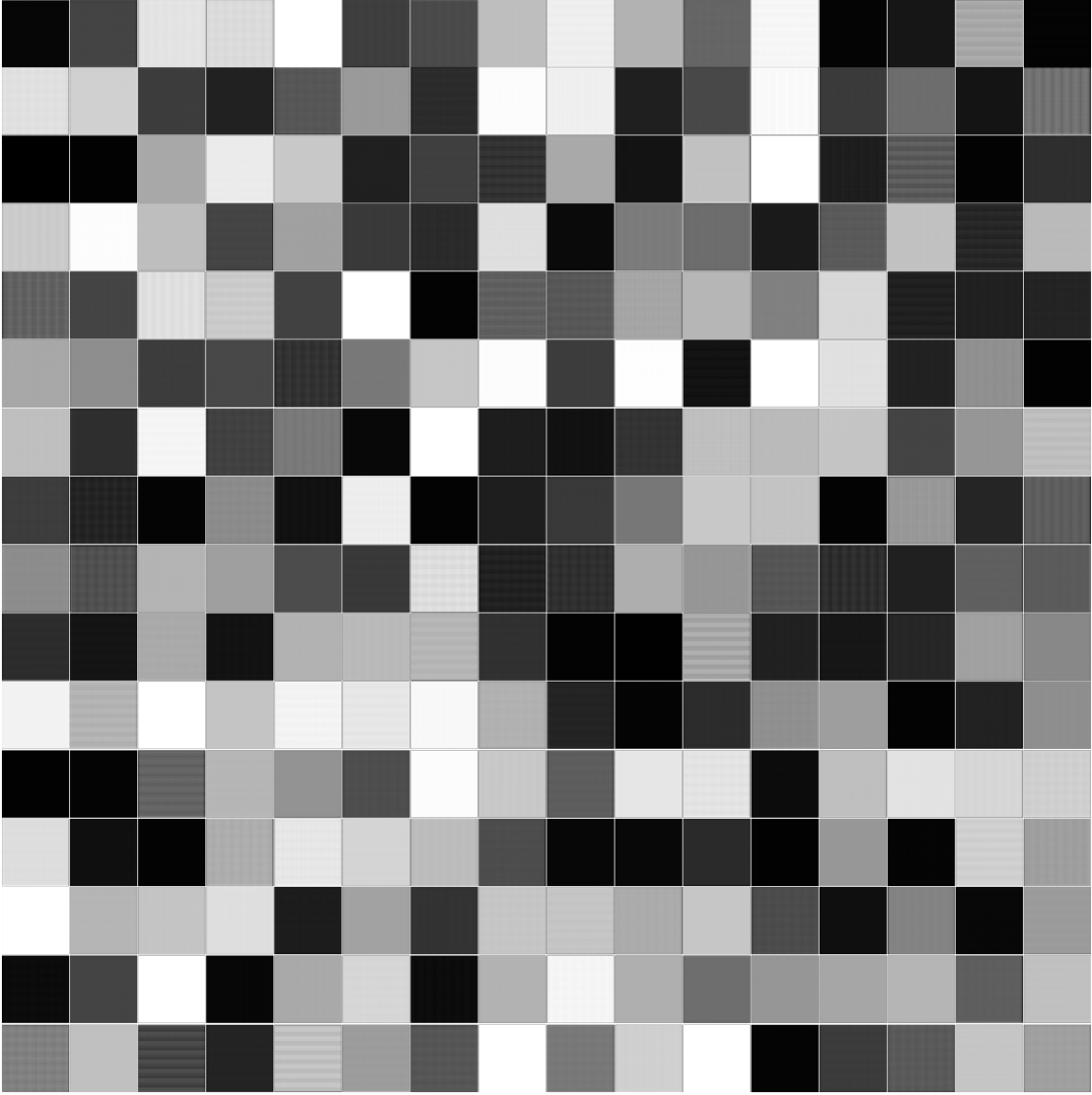
The final output of the latent decoder $\hat{\mathbf{z}}_{\mathbf{q}_{s_i}}$ is generated by combining previous generated output $\hat{\mathbf{z}}_{\mathbf{q}_{s_{i-1}}}$ with the difference map. The loss for training the latent disease ODE comprises the sum of two components. The reconstruction loss, denoted as $\mathcal{L}_{\text{recon}}$, is defined as $\|\hat{\mathbf{z}}_{\mathbf{q}} - \mathbf{z}_{\mathbf{q}}\|_2^2$, and the difference loss, denoted as $\mathcal{L}_{\text{diff}}$, is calculated as $\|\mathbf{D}_{s_i} - \Delta\mathbf{z}_{\mathbf{q}_{s_i}}\|_2^2$.

Feeding $\hat{\mathbf{z}}_{\mathbf{q}_{s_i}}$ to the trained decoder G of 3D-VQ-GAN can reconstruct the corresponding 3D image $\hat{\mathbf{X}}_{s_i}$. The generative process of the decoder can be formulated as follows.

$$\begin{aligned} \mathbf{h}_{s_1}, \mathbf{h}_{s_2}, \dots, \mathbf{h}_{s_S} &= \text{ODESolve}(\mathbf{h}_{t_0}, f_{\theta}, (s_1, \dots, s_S)), \\ \mathbf{D}_{s_i} &= \text{3DConv}(\mathbf{h}_{s_i}, \mathbf{h}_{s_{i-1}}), \\ \hat{\mathbf{z}}_{\mathbf{q}_{s_i}} &= \mathbf{D}_{s_i} + \hat{\mathbf{z}}_{\mathbf{q}_{s_{i-1}}}, \\ \hat{\mathbf{X}}_{s_i} &= G(\hat{\mathbf{z}}_{\mathbf{q}_{s_i}}) \end{aligned} \quad (7)$$

E.4. Visualization of codebook

Every entry in the codebook corresponds to a distinctive representation or code assigned to a specific region or pattern within the input space. Utilizing the techniques outlined in (Irie et al., 2023), we visually represent each code in the learned codebook by creating a latent representation $\mathbf{z}_{\mathbf{q}}$ using only that specific code. The resulting latent representation is then

Figure 9: A visualization of the codebook ($M = 256$)

projected back into the 3D image space (see Figure 9). These visualizations exhibit varying grayscale intensities and textures, highlighting the diverse characteristics associated with different codes. This diversity within the codebook suggests that the model has effectively captured a broad array of features, enabling it to generate samples with varied and realistic qualities.

Appendix F. More Related Work

F.1. Synthetic medical image generation

Synthetic medical image generation proves particularly useful in various applications, classified into two types: unconditional and conditional, depending on whether constraints (e.g., images, a specific disease state, imaging modality, etc.) are applied respectively. The most common generative models used for image generation include Generative Adversarial Network (GAN) (Creswell et al., 2018), VAE (Kingma and Welling, 2013), and diffusion models (Ho et al., 2020). These models have demonstrated success in natural image generation and have shown their potential in the context of medical images. However, 3D imaging data (e.g., CT, MRI) is widely used in the medical field and generating realistic 3D images poses more significant challenges compared to 2D natural images due to the inherent complexity of three-dimensional space and the additional considerations required for realism. More specifically, unlike a 2D image with a single viewpoint, generating 3D images requires modelling the whole 3D structure which involves capturing depth information, spatial relationships, and fine details - essentially the "world behind the image". This requires not only higher computational resources but also more advanced techniques to model these detailed 3D structures with fidelity. The challenge is further amplified in the medical domain, where accurate representation of anatomical structures and simulation of physiological processes add significant layers of complexity.

Methods employing 3D-GANs have been proposed for the synthesis of 3D imaging data (Ferreira et al., 2022; Singh and Raza, 2021). However, training these models poses a considerable challenge due to increased computational and memory demands. In response to this issue, several memory-efficient 3D-GANs have been introduced (Sun et al., 2022; Uzunova et al., 2019). GAN-based models are widely used in generating volumetric medical imaging data (Ferreira et al., 2024). However, these models face additional challenges including mode collapse, non-convergence, and lack of interpretability. Mode collapse occurs when GANs fail to capture the full diversity of training data distribution and get stuck producing a limited set of outputs (Bau et al., 2019). Training GANs can also be difficult due to the need to balance and synchronize discriminator and generator. This often requires careful hyperparameter tuning and network architecture design to ensure convergence. Additionally, GANs typically lack interpretability, as it is challenging to understand what GANs have learned in the latent representation (Shen et al., 2020). In contrast, VAE (Kingma and Welling, 2013) has gained popularity for its explicit latent space representation and stable training process.

The Vector Quantized Variational Autoencoder (VQ-VAE) (Van Den Oord et al., 2017), a variant of VAE, was introduced to learn a discrete latent space, where continuous latent representations in the traditional VAE are quantized to discrete codes using a codebook. While the discrete latent space enhances efficiency and compactness, it also limits the model's ability to capture the full complexity of the input data, leading to blurry generated images. To address this limitation, VQ-VAE-2 (Razavi et al., 2019) utilized hierarchical multi-scale latent maps for large-scale image generation. VQ-GAN (Esser et al., 2021), a variant of VQ-VAE, incorporated a discriminator and perceptual loss, combining the strengths of both VQ-VAE and GAN to generate high-resolution images. Ge et al. (Ge et al., 2022) extended VQ-GAN for image modelling to 3D-VQ-GAN for video modelling.

While pure GAN-based models dominate 3D medical image generation, VAE and VQ-VAE architectures are gaining traction. Existing applications focus primarily on brain and heart MRI scans (Liu et al., 2024; Tudosi et al., 2020). Khader et al. (Khader et al., 2023) demonstrated the potential of 3D-VQ-GAN for lung CT scans by combining it with transformers to generate realistic 3D CT scans based on a set of 2D radiographs. This highlights the capability of 3D-VQ-GAN for compressing volumetric lung CT scans.

Diffusion models (Ho et al., 2020; Croitoru et al., 2023) represent another emerging area in generative modelling. Diffusion models are a powerful class of probabilistic generative models that can learn complex distributions. These models initiate with a forward diffusion stage, where the input data is iteratively perturbed by adding noise, ultimately resulting in purely Gaussian noise. Subsequently, the models learn to reverse this diffusion process, aiming to reconstruct the original noise-free data from the noisy data samples (Kazerouni et al., 2023). While diffusion models can generate diverse and high-quality images, their application in 3D imaging data synthesis remains underexplored due to their high computational cost and low sampling efficiency compared to VAE and GAN families. Khader et al. (Khader et al., 2022) employed a diffusion model in the lower-dimensional latent space of VQ-GAN rather than the image space to reduce computational costs and increase sampling efficiency.

F.2. Temporal synthesis

Temporal synthesis can be viewed as a challenge that involves combining static image synthesis with temporal dynamics modelling. Recurrent Neural Networks (RNNs), Long Short-Term Memory (LSTM), and Gated Recurrent Unit (GRU) are frequently employed in temporal analysis. In addition, the recent success of transformer-based models in sequential data processing has sparked considerable interest due to their potential in modelling longitudinal data (Li et al., 2022).

Previous research on temporal synthesis often concentrated on video generation, with GAN-based models being the predominant methods inspired by the success of GANs in image generation. However, GAN-based approaches may face challenges in capturing long-term dependencies. Additionally, generating high-resolution frames or long video sequences presents difficulties due to prohibitively high memory and time costs during both training and inference (Ge et al., 2022). Some methods explore non-GAN-based generative models for video generation. Models presented in (Yan et al., 2021; Ge et al., 2022; Le Moing et al., 2021) employ VQ-VAE-based models and transformers for video generation, while (Ho et al., 2022; Voleti et al., 2022) utilize the diffusion model for video generation. Computational complexity, extended inference times, and temporal consistency remain open questions for these models. Other works, such as (Kanaa et al., 2021; Park et al., 2021; Xia et al., 2022), combine a typical encoder-decoder architecture with latent neural ODEs to capture temporal dynamics in the latent space for continuous-time video generation.

Prior research in temporal synthesis for 3D imaging data has primarily focused on modelling two areas: normal brain ageing and disease progression in AD. This is often achieved by generating synthetic longitudinal brain MRIs. Normal ageing of the brain is characterized by a gradual loss of grey matter, particularly in the frontal, temporal, and parietal regions (Lorenzi et al., 2015). In contrast, the brain morphology observed in AD patients reflects

a combination of both normal ageing and pathological matter loss specific to the disease (Lorenzi et al., 2015). These two processes can be modelled independently or jointly using temporal synthesis techniques (Sivera et al., 2019). Ravi et al. (Ravi et al., 2022) introduced the 4D-Degenerative Adversarial NeuroImage Net (4D-DANI-Net), a model crafted to generate high-resolution longitudinal MRI scans that replicate subject-specific neurodegeneration within the contexts of ageing and dementia. TR-GAN (Fan et al., 2022) was conceived to predict multi-session future MRIs based on prior observations, utilizing a single generator. Sauty et al. (Sauty and Durrleman, 2022) proposed a model that amalgamates a VAE with a latent linear mixed-effect model to estimate linear individual trajectories in latent space, enabling the sampling of patients’ trajectories at any given time point. While this model transforms observations at discrete time points into continuous disease progression trajectories, it relies on a strong assumption about linear trajectories in latent space. This linear assumption provides a simplified depiction of disease progression, but it falls short in capturing the inherent complexity observed in real-world disease dynamics. More flexible and adaptive approaches are needed to characterize disease progression trajectories effectively (Kim et al., 2021). To address this limitation, Martí-Juan et al. (Martí-Juan et al., 2023) employed a recurrent VAE where the latent space is parametrized with an RNN, defining more flexible disease evolution dynamics.

These temporal synthesis models for 3D imaging data offer substantial potential for clinical applications. These applications include: 1) Data Imputation: Longitudinal datasets are quite useful for the study of progressive diseases. However, longitudinal datasets often contain missing or incomplete data due to various reasons, such as missed appointments, dropout from the study, etc. (Fan et al., 2022) and (Fan et al., 2024) complement missing sessions for longitudinal MRI dataset expansion based on these models. 2) Assessing Treatment Efficacy: These models can create simulated longitudinal data that closely mimics the natural disease progression. This allows researchers to compare longitudinal imaging biomarkers between treated and untreated individuals at any point in time. By observing how the simulated disease course is altered by treatment, researchers can gain valuable insights into the treatment’s effectiveness in slowing or even halting the disease process. This information can be crucial for designing future clinical trials and making informed treatment decisions. 3) Discovery of Temporal Biomarkers: Temporal synthesis models offer the ability to generate rich longitudinal imaging features. Analyzing the relationships between these features over time and how they connect to clinical outcomes can provide valuable insights. Researchers can leverage this approach to unlock the underlying mechanisms of disease progression and potentially discover novel temporal biomarkers.