
Benchmarking out-of-the-box forecasters of varying scales in biology

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Abstract

Forecasting in biological systems presents different considerations and difficulties from traditional time-series settings, most notably the high-dimensionality associated with modern biological assays. A comprehensive analysis of the performance of modern forecasting methods on biological datasets is currently missing from the literature, in particular one that evaluates potential gains from larger model sizes and their increased complexity. Here, we assess 14 models spanning 4 complexity scales (Baseline, Statistical, Neural, and LLM-based) on 5 time-series datasets. We show that model scale and complexity does not uniformly improve performance across biological datasets, and that in some cases, highly complex models fail to outperform common baselines.

1 Introduction

Time series forecasting has historically been developed and applied by statisticians and econometricians. In recent years, the machine learning community has made strides in developing models that leverage increasing amounts of available longitudinal data. Forecasting problems native to biology however do not take advantage of pre-existing models, opting instead to develop bespoke predictive algorithms [9, 8]. Out-of-the-box forecasting models could reduce time spent creating highly specialized models allowing researchers to focus on understanding biological phenomena. Evaluation of general forecasting models in biological settings has, to our knowledge, not yet been rigorously studied: Of particular interest is the effect model size and complexity has on performance as larger and more elaborate models become available. As such, we evaluate 4 classic baselines, 3 statistical, 6 neural, and one LLM model across 5 domains: The 4 Electric Transformer Temperature (ETT) datasets, 3 selected Chaotic Attractors, 4 Microbiome datasets, 7 single cell Ribonucleic Acid (scRNA) sequencing datasets, and an epidemiological dataset. See table 1 in Appendix A for quantitative descriptions of each.

Non-biological datasets were chosen to give a baseline perspective on model performance, as the ETT and Chaotic Attractor datasets are better understood systems than their biological counterparts. The three biological datasets were selected for their diverse representation of biological scales and high dimensionality. While not a complete view of biology, they provide a sample of contexts in which forecasting models can be applied.

To give a robust assessment of model performance, we use multiple commonly used evaluation metrics, namely: Mean Absolute Error (MAE), Mean Squared Error (MSE), Mean Absolute Percentage Error (MAPE), and symmetric MAPE (sMAPE). While giving a qualitative description of results would help contextualize model performance, what constitutes "good" or "bad" in biology is highly varied and nuanced. For instance, a computational biologist may consider a small error relative to a benchmark model sufficiently good whereas a medical doctor may require that a model be accurate enough to

inform their diagnostic decisions. Consequently, we avoid making any qualitative claims for any specific dataset, instead opting only to discuss models in terms of the evaluation metrics and their performance across different datasets.

Since many datasets are non-standard we select a wide variety of models to generate as thorough an evaluation as possible. We include four classic baselines: the Naive forecast, a Random Walk with Drift (RWD), a Window Average, and the Historic Average. Three well established hyper-parameter optimized statistical models: the Auto Regressive Integrated Moving Average (ARIMA), Error-Trend-Seasonality (ETS), and Theta models. Six modern deep-learning based models: the Autoformer, Informer, N-Beats, N-HiTs, TSMixer, and TimeMixer models [20, 22, 14, 2, 3, 19]. Along with Time-LLM using the Gemma2-2B as the largest model we investigate [11, 18].

2 Methodology

2.1 Data collection & background

Chaotic Attractors have been proposed by Gilpin [10] as a benchmark for forecasting since they are well understood systems which are notoriously difficult to predict. There is also some evidence that chemical kinetics operate as a chaotic system making them a potential surrogate for cell-signalling in lieu of available data [17]. While Gilpin provides dozens of options, we arbitrarily selected 3 (Aizawa, Blasius, and Lorenz) to not remove the biological focus and better evaluate a smaller number of chaotic systems. ETT, the other non-biological dataset, measures the load and oil temperature of two electrical transformers at two stations from a single Chinese province [22].

scRNA seq data was originally collected to infer gene regulatory networks from single-cell transcriptomics [15]. Experimental data included is from human and mouse cell lines, specifically human Embryonic Stem Cells (hESC), human Hepatocyte-like cells (HEPs), mouse Embryonic Stem Cells (mESC), mouse Dendritic Cells (mDC), and mouse Hematopoietic Stem Cells (mHSC-E, mHSC-GM, mHSC-L) from three lineages Erythroid, Granulocyte-Monocyte, and Lymphoid like. While used in cell-fate prediction and gene-regulatory inference, these transcriptional measures do not explicitly include time. Instead a "*pseudotime*" is inferred using an ordering of cells by similarity of gene expression computed using Slingshot [16]. We filter the pseudotime measure to remove duplicates and convert it to date-time for use with general forecasters.

Microbiome data were collected from 4 individuals across two publications [1, 6], both studying the long term dynamics of microbial communities. Here each measurement represents the size of closely related microbial populations called Operational Taxonomic Units (OTUs) and the time-series represents a complex ecology of microorganisms.

Epidemiological data was aggregated across Chinese provinces following China's exit from strict zero-COVID policy for approximately three years by [21]. Measures focus on different respiratory and cardiological ailments aggregated across seven hospitals.

2.2 Model fitting

All data was split with a 70% train, 10% validation, and 20% test ratio. Classic baselines, statistical, and neural models were optimized and fit using the NIXTLA suite of tools [7, 13]. For Time-LLM we used its original implementation. MAE was used as the loss metric for fitting and optimizing deep learning based models except for Time-LLM which used MSE. Each dataset fit models to a short and a long horizon to also investigate sensitivity to prediction size. All models were fit with a maximum compute budget of 5 days on a single Nvidia A6000 GPU, except for Time-LLM which used 6 GPUs in order to fit the Gemma2-2B LLM in memory. Microbiome and scRNA data also frequently exceeded the practical maximum number of dimensions for application of TSMixer, TimeMixer, and Time-LLM models and as such data exceeding 524 dimensions were sub-sampled to include the highest variance 524 features.

3 Results

A total of 2,128 trained model evaluations across each dataset, model, prediction horizon, and evaluation metrics were recorded for both training and test data. To reduce complexity, we will focus

on test set MAE and sMAPE forecast evaluations for the longer time horizon task across all models and datasets (Fig 1). All evaluation metrics are calculated on predictions in the data’s original scale prior to any pre-processing done by the model. If a model predicts a scaled forecast they are un-scaled prior to evaluation which may lead to larger reported metrics than previous publications.

Since MAE summarizes errors directly calculated from observations while sMAPE summarizes relative errors the two metrics can, at times, be discordant. For instance, many OTUs in the microbiome dataset exist at a level difficult to detect (ergo measured as zero) or are introduced to the microbial ecology rather disruptively, leading to long periods of dormancy followed by high levels of activity. This in turn can cause MAE values to accumulate errors from outliers more aggressively than sMAPE, as the latter is bounded by being a proportion, resulting in a more pessimistic MAE assessment of microbiome data for baseline and statistical models. A similar, but less pronounced, phenomenon is visible within the human scRNA sequencing data.

Improved model performance for Chaotic Attractors, ETT, and COVID was associated with an increase in model complexity while Microbiome and scRNA seq data failed to see such gains. This lack of difference in model performance for biological datasets could stem from similar data not being used during model development. Epidemiological data is an exception among biological datasets as its forecasting was very recently a matter of international safety and models perform well on this task. Alternatively the variables, exogenous or otherwise, needed to indicate the observed dynamics may not be available to the models.

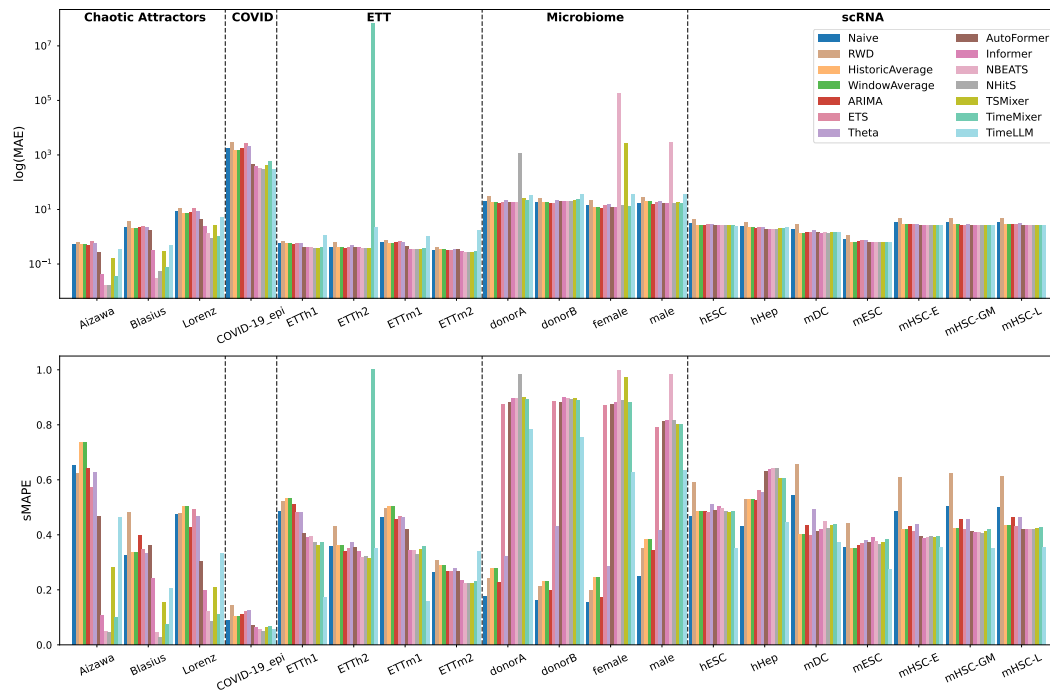


Figure 1: Test set MAE and sMAPE model evaluation on the longest prediction horizon task for each dataset (Lower is better for both).

Inspecting a selection of models on the Lorenz chaotic attractor gives some insights into where these models may be struggling in the biological contexts [12]. Evident from Fig. 2, neural models tend to do well within the basin of each attractor but struggle in the transition between these two modes. Many biological systems of interest exhibit similar structural changes. The microbiome datasets have known non-stationarities, with donorA traveling abroad introducing new microbial communities and donorB experiencing salmonella. Such dynamics can cause rapid but temporary shifts to different modes for each time-series.

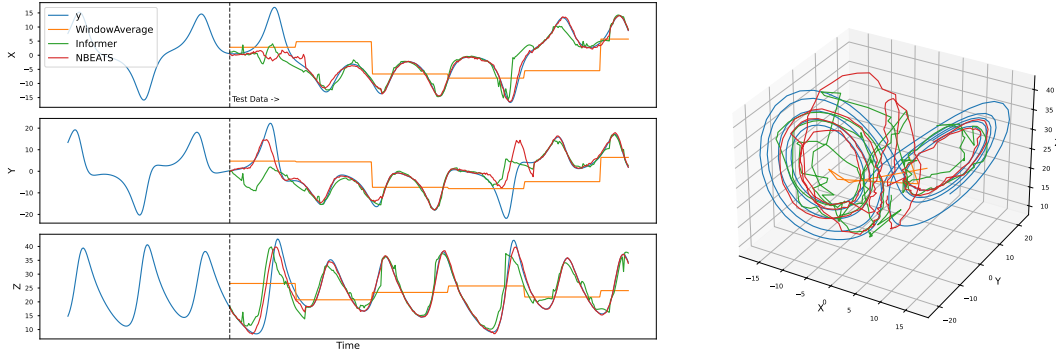


Figure 2: Test set prediction on Lorenz Attractor for a selection of models.

4 Discussion

COVID was the one biological dataset to exhibit performance characteristics similar to non-biological data. Its relatively large MAE is to be expected as respiratory diseases and related ailments measured were during a respiratory disease pandemic in a population of roughly 1.4 billion. More interesting is where model size and complexity failed to provide performance gains, as it could provide insights into future research directions. Forecasting in both microbiome and scRNA data fail to outperform the baseline models in most cases. These biological data offer a new test bed for future models to evaluate performance on what appears to be an out-of-distribution (ood) task compared to more standard datasets like ETT. We believe that the choice of benchmark datasets directly guide model development (ImageNet, CIFAR-100, and Enron Datasets for example). Inclusion of more biologically relevant time series could lead to more powerful general purpose forecasters in biology. Biological data and foundation models also present a novel intersection, both as an ood evaluation of foundation model performance and as diverse data sources. Complimentary to this, quantification of exogenous variables impact on performance in these biological forecasters could lead to novel discoveries of upstream dependencies of the systems' dynamics.

While foundation models offer an exciting research avenue, their potential for inadvertent data leakage given the large amount of training data raises some concern, especially in biological and medical applications. For instance, Time-LLM performance shows an improvement using the Gemma2-2B LLM. However, from these results alone we cannot conclusively attribute this gain to genuine model improvements from the LLama1-7B and GPT2 models as Gemma2-2B may have memorized ETT data (they were published prior to Gemma2-2B's publication). Extending this to biological and healthcare contexts, the potential for data leakage could falsely indicate improved understanding of biological principles or overestimate the performance of clinical predictors.

A noticeable omission from our biological datasets is cell signalling data, a prominent domain of study involving molecular interactions which facilitate cell-to-cell communication and gene regulation. This is due to the way in which cell-signalling data is collected, predominantly by flow or mass cytometry. The latter being a destructive measure of the cell making it difficult to track through time. Regardless of whether cell viability is maintained, measurements are often collected in a non-uniform manner as early dynamics tend to be more relevant to the specific phenomena being studied.

As biological assays continue to improve and decrease in cost, a proactive approach to high-dimensional model development would facilitate rapid application to biological domains with the potential for impactful results in both biology and healthcare. One technique of particular interest is LiveSEQ, it measures single cell transcription of genes while preserving their viability allowing for repeated measurements [5]. Models that can capture the whole genome (approximately 20 thousand genes) to facilitate a systems-level perspective of biology are of particular interest. Many biological systems presented here have classically been studied using extensions of basic dynamical systems, such as the Lotka-Volterra predator prey model applied to microbial ecology. Application of Neural ODEs either as a standalone forecasting model or a component in a foundation time-series model may alleviate some of the issues native to biological data discussed here [4].

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A Appendix

A.1 Data availability

All data and scripts for reproduction of results can be found at <https://figshare.com/s/34a486f130bb8c4aee2b>.

A.2 Supplemental tables

Dataset	Dimension	Total Trajectory Length	Long Horizon	Short Horizon	Frequency
All Dynamical Systems	3	2000	64	32	Second
ETTh1/ETTh2	7	14400	192	96	Hour
ETTM1/ETTM2	7	57600	192	96	15 Min
COVID	36	955	30	14	Day
Microbiome - donorA	524 (1570)	365	8	4	Day
Microbiome - donorB	524 (1525)	253	8	4	Day
Microbiome - female	524 (552)	185	8	4	Day
Microbiome - male	524 (1254)	443	8	4	Day
scRNA - hESC	524 (17745)	758	16	8	Second
scRNA - hHep	524 (11515)	425	16	8	Second
scRNA - mDC	524 (7371)	383	16	8	Second
scRNA - mESC	524 (18385)	421	16	8	Second
scRNA - mHSC-L	524 (4762)	847	16	8	Second
scRNA -mHSC-E	524 (4762)	1071	16	8	Second
scRNA -mHSC-GM	524 (4762)	889	16	8	Second

Table 1: Summary of datasets used for this work, note that when subsampling was done actual dimensionality is shown in parenthesis.

Dataset (H)	Naive		RWD		Average		Window Average		ARIMA		ETS		THETA		Autoformer		Informer		N-BEATS		N-HITS		TSMixer		Time Mixer		Time-LLM				
	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE			
dyst	Alzwa (32)	0.415	0.394	0.618	1.040	0.574	0.556	0.574	0.556	0.373	0.332	0.365	0.436	0.449	0.546	0.137	0.037	0.037	0.037	0.007	0.000	0.008	0.000	0.036	0.003	0.020	0.001	-	-		
	Alzwa (64)	0.555	0.569	0.656	0.842	0.580	0.594	0.580	0.594	0.519	0.508	0.695	1.117	0.597	0.681	0.269	0.185	0.041	0.004	0.015	0.002	0.016	0.002	0.171	0.071	0.040	0.004	0.330	0.239		
	Blastus (32)	1.542	6.157	13.880	2.243	10.500	2.264	10.500	2.264	1.419	5.461	1.242	5.348	1.460	1.460	1.171	1.627	5.737	0.351	0.412	0.058	0.024	0.066	0.098	0.268	0.208	0.114	0.039	-	-	
	Blastus (64)	2.250	11.346	29.865	1.909	7.498	1.909	7.498	1.909	1.419	5.461	1.242	5.348	1.460	1.460	1.171	1.627	5.737	0.351	0.412	0.058	0.024	0.066	0.098	0.268	0.208	0.114	0.039	0.553	1.130	
ETT	ETTm1 (96)	7.100	88.865	10.454	201.171	7.342	86.320	7.342	86.320	6.189	78.601	7.767	128.536	7.064	90.819	4.372	41.802	1.533	6.653	0.342	0.764	0.395	0.935	3.674	44.981	1.069	3.727	-	-		
	ETTm2 (96)	6.986	85.978	10.222	175.638	7.074	72.860	6.839	90.557	9.251	155.344	9.251	155.344	7.064	90.819	4.372	41.802	1.533	6.653	0.342	0.764	0.395	0.935	3.674	44.981	1.069	3.727	4.795	42.023		
	ETTh1 (96)	0.583	0.725	0.738	1.082	0.541	0.567	0.508	0.518	0.572	0.708	0.572	0.708	0.742	0.471	0.466	0.446	0.446	0.446	0.399	0.442	0.402	0.365	0.411	0.390	0.412	0.390	0.412	0.390	0.412	0.390
	ETTh2 (96)	0.635	0.845	0.809	1.370	0.568	0.620	0.561	0.625	0.626	0.826	0.626	0.826	0.652	0.910	0.509	0.565	0.477	0.498	0.440	0.440	0.434	0.412	0.446	0.453	0.456	0.467	1.311	5.092		
m4	ETTm1 (96)	0.390	0.829	0.768	1.397	0.315	0.381	0.276	0.381	0.387	0.628	0.387	0.628	0.387	0.448	0.377	0.338	0.302	0.233	0.261	0.193	0.256	0.186	0.289	0.228	0.293	0.233	-	-		
	ETTm2 (96)	0.390	0.829	0.768	1.397	0.315	0.381	0.276	0.381	0.387	0.628	0.387	0.628	0.387	0.448	0.377	0.338	0.302	0.233	0.261	0.193	0.256	0.186	0.289	0.228	0.293	0.233	1.161	41.70		
	ETTh1 (96)	0.306	0.252	0.391	0.436	0.314	0.268	0.314	0.268	0.314	0.268	0.314	0.268	0.314	0.268	0.314	0.268	0.314	0.268	0.314	0.268	0.314	0.268	0.314	0.268	0.314	0.268	0.314	0.268	0.314	0.268
	ETTh2 (96)	0.352	0.361	0.434	0.578	0.360	0.373	0.344	0.354	0.352	0.480	0.352	0.480	0.365	0.400	0.336	0.330	0.300	0.291	0.273	0.266	0.275	0.263	0.264	0.204	0.239	0.289	0.264	1.757	9.324	
m5	Female (4)	19.456	1.730e4	32.514	44.79e4	19.947	1.601e4	14.973	1.601e4	14.973	1.601e4	18.931	1.450e4	20.340	1.72e4	19.460	1.56e4	18.713	1.601e4	18.713	1.601e4	18.713	1.601e4	18.713	1.601e4	18.713	1.601e4	18.713	1.601e4	18.713	1.601e4
	Male (4)	21.502	2.010e4	33.508	46.23e4	20.917	1.600e4	17.467	1.600e4	17.467	1.600e4	21.482	1.72e4	23.888	2.077e4	18.710	1.60e4	18.093	1.60e4	18.093	1.60e4	18.093	1.60e4	18.093	1.60e4	18.093	1.60e4	18.093	1.60e4	18.093	1.60e4
	Female (8)	15.146	1.610e4	24.733	44.72e4	14.351	1.25e4	11.694	1.25e4	11.694	9.50e3	15.458	1.580e4	16.349	1.70e4	13.269	1.08e4	13.425	1.230e4	12.464	1.230e4	12.464	1.230e4	12.464	1.230e4	12.464	1.230e4	12.464	1.230e4	12.464	1.230e4
	Donor A (4)	19.112	2.100e4	30.489	5.132e4	18.893	1.917e4	14.508	1.347e4	15.909	1.505e4	19.741	2.683e4	18.501	1.96e4	18.501	1.96e4	18.501	1.96e4	18.501	1.96e4	18.501	1.96e4	18.501	1.96e4	18.501	1.96e4	18.501	1.96e4	18.501	1.96e4
mRNA	Donor A (8)	20.523	2.230e4	29.594	4.349e4	19.893	2.094e4	17.000	1.710e4	18.507	1.840e4	21.635	2.68e4	19.148	2.01e4	19.148	2.01e4	19.148	2.01e4	19.148	2.01e4	19.148	2.01e4	19.148	2.01e4	19.148	2.01e4	19.148	2.01e4	19.148	2.01e4
	Donor B (4)	16.890	1.958e4	26.894	4.792e4	16.744	1.720e4	12.393	1.45e4	12.881	1.162e4	17.385	2.68e4	17.797	1.84e4	17.797	1.84e4	17.797	1.84e4	17.797	1.84e4	17.797	1.84e4	17.797	1.84e4	17.797	1.84e4	17.797	1.84e4	17.797	1.84e4
	Donor B (8)	19.214	2.395e4	28.773	5.462e4	17.377	1.744e4	14.742	1.427e4	15.727	1.605e4	20.461	3.31e4	16.959	1.84e4	16.959	1.84e4	16.959	1.84e4	16.959	1.84e4	16.959	1.84e4	16.959	1.84e4	16.959	1.84e4	16.959	1.84e4	16.959	1.84e4
	Covid (14)	32.247	9.991e5	45.3470	2.112e6	351.586	1.591e6	363.481	1.100e10	364.407	9.736e5	4.05649	1.545e7	475.904	2.255e7	428.269	1.385e7	444.056	1.385e7	444.056	1.385e7	444.056	1.385e7	444.056	1.385e7	444.056	1.385e7	444.056	1.385e7	444.056	1.385e7
p	Covid (30)	350.291	1.744e6	496.837	3.208e6	421.765	1.954e6	492.947	2.284e6	1.496e3	4.091e7	1.229e6	7.115e6	364.569	1.229e6	7.115e6	364.569	1.229e6	7.115e6	364.569	1.229e6	7.115e6	364.569	1.229e6	7.115e6	364.569	1.229e6	7.115e6	364.569	1.229e6	7.115e6
	mESC (8)	2.589	12.593	3.854	27.165	2.107	7.164	2.066	6.931	2.275	7.765	2.457	7.765	2.457	7.765	2.457	7.765	2.457	7.765	2.457	7.765	2.457	7.765	2.457	7.765	2.457	7.765	2.457	7.765	2.457	7.765
	h1HeP (8)	2.655	13.047	3.804	26.137	2.117	7.088	2.104	7.005	2.167	7.063	2.285	8.605	2.140	7.868	2.134	8.007	2.134	8.007	2.134	8.007	2.134	8.007	2.134	8.007	2.134	8.007	2.134	8.007	2.134	8.007
	h1HeP (16)	2.462	11.769	3.651	24.653	2.065	6.903	2.032	6.713	2.108	6.725	2.357	9.489	2.310	7.998	2.310	7.998	2.310	7.998	2.310	7.998	2.310	7.998	2.310	7.998	2.310	7.998	2.310	7.998	2.310	7.998
r	mDC (8)	1.691	5.189	2.679	12.603	1.306	2.759	1.306	2.759	1.306	2.759	1.306	2.759	1.306	2.759	1.306	2.759	1.306	2.759	1.306	2.759	1.306	2.759	1.306	2.759	1.306	2.759	1.306	2.759	1.306	2.759
	mDC (16)	1.767	5.654	2.392	9.983	1.294	2.690	1.324	2.831	1.281	2.853	1.429	3.383	1.282	2.785	1.278	2.873	1.290	2.881	1.290	2.881	1.290	2.881	1.290	2.881	1.290	2.881	1.290	2.881	1.290	2.881
	mESC (8)	0.841	1.397	1.161	2.692	0.625	0.819	0.675	0.819	0.675	0.819	0.675	0.819	0.675	0.819	0.675	0.819	0.675	0.819	0.675	0.819	0.675	0.819	0.675	0.819	0.675	0.819	0.675	0.819	0.675	0.819
	mESC (16)	0.841	1.397	1.161	2.692	0.625	0.819	0.675	0.819	0.675	0.819	0.675	0.819	0.675	0.819	0.675	0.819	0.675	0.819	0.675	0.819	0.675	0.819	0.675	0.819	0.675	0.819	0.675	0.819	0.675	0.819
rRNA	mESC-E (8)	3.413	19.449	5.164	42.423	2.915	11.698	2.915	11.698	2.915	11.698	10.640	33.124	14.702	2.865	11.895	11.936	12.093	12.147	12.093	12.147	12.093	12.147	12.093	12.147	12.093	12.147	12.093	12.147	12.093	12.147
	mESC-E (16)	3.471	19.976	5.108	41.168	3.027	12.069	3.027	12.069	3.027	12.069	9.938	31.224	14.398	2.944	12.271	11.779	12.904	12.147	12.904	12.147	12.904	12.147	12.904	12.147	12.904	12.147	12.904	12.147	12.904	12.147
	mHSC-GM (8)	3.484	19.803	5.216	42.801	2.897	11.372	2.897	11.372	2.897	11.372	10.220	33.224	15.802	2.838	11.994	11.794	12.823	11.752	12.823	11.752	12.823	11.752	12.823	11.752	12.823	11.752	12.823	11.752	12.823	
	mHSC-GM (16)	3.493	20.029	5.015	39.717	2.803	11.021	2.852	12.466	2.850	10.278	13.848	2.841	11.994	11.794	12.823	11.752	12.823	11.752	12.823	11.752	12.823	11.752	12.823	11.752	12.823	11.752	12.823	11.752	12.823	11.752
rRNA	mHSC-L (8)	3.574	20.970	5.371	45.418	2.970	11.768	2.970	11.768	2.874	12.184	2.913	10.580	3.352	12.375	2.906	12.375	2.896	12.375	2.896	12.375	2.896	12.375	2.896	12.375	2.896	12.375	2.896	12.375	2.896	
	mHSC-L (16)	3.566	20.885	5.113	41.130	2.943	11.193	2.9																							

Dataset (H)	Naive		RWD		Average		Window Average		ARIMA		ETS		THETA		Autoreformer		Informr		N-BEATS		N-HTS		TSMixer		Time Mixer		TimeLLM							
	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE						
Alzora (32)	0.438	0.419	0.686	1.213	0.695	0.693	0.395	0.350	0.481	0.481	0.379	0.481	0.389	0.611	0.128	0.028	0.040	0.003	0.009	0.000	0.009	0.000	0.039	0.026	0.002	0.026	0.002	0.026	0.002	0.026				
	0.555	0.555	0.855	1.713	0.855	0.855	0.481	0.481	0.481	0.481	0.481	0.481	0.481	0.481	0.481	0.481	0.481	0.481	0.481	0.481	0.481	0.481	0.481	0.481	0.481	0.481	0.481	0.481	0.481	0.481				
	1.609	6.387	2.347	14.284	2.492	11.705	1.478	5.638	1.299	5.253	1.299	5.253	1.299	5.253	1.949	1.078	0.653	0.331	0.282	0.037	0.003	0.127	0.003	0.245	0.126	0.036	0.126	0.036	0.126	0.036				
	2.291	11.748	3.689	31.630	2.016	7.897	1.192	11.109	2.531	16.173	2.531	16.173	2.531	16.173	1.707	1.778	0.790	0.326	0.034	0.004	0.054	0.009	0.248	0.076	0.012	0.076	0.012	0.076	0.012	0.076	0.012			
Blastus (64)	0.299	0.299	0.441	0.882	0.441	0.441	0.299	0.299	0.441	0.441	0.299	0.441	0.299	0.441	0.299	0.299	0.299	0.299	0.299	0.299	0.299	0.299	0.299	0.299	0.299	0.299	0.299	0.299	0.299	0.299	0.299			
	1.609	6.387	2.347	14.284	2.492	11.705	1.478	5.638	1.299	5.253	1.299	5.253	1.299	5.253	1.949	1.078	0.653	0.331	0.282	0.037	0.003	0.127	0.003	0.245	0.126	0.036	0.126	0.036	0.126	0.036	0.126	0.036		
	2.291	11.748	3.689	31.630	2.016	7.897	1.192	11.109	2.531	16.173	2.531	16.173	2.531	16.173	1.707	1.778	0.790	0.326	0.034	0.004	0.054	0.009	0.248	0.076	0.012	0.076	0.012	0.076	0.012	0.076	0.012	0.076	0.012	
	8.457	125.261	12.100	264.859	8.537	104.481	6.852	90.750	8.774	159.925	8.302	120.661	8.302	120.661	4.429	58.674	1.905	9.546	0.328	0.014	0.368	0.390	4.085	20.857	1.354	5.416	1.354	5.416	1.354	5.416	1.354	5.416		
Lorenz (64)	0.607	0.963	0.683	1.109	0.556	0.693	0.541	0.697	0.592	0.838	0.592	0.838	0.603	0.925	0.420	0.410	0.410	0.442	0.369	0.337	0.377	0.350	0.362	0.338	0.375	0.348	0.348	0.348	0.348	0.348	0.348	0.348		
	0.602	0.895	0.711	1.182	0.571	0.701	0.557	0.715	0.592	0.883	0.592	0.883	0.608	0.925	0.421	0.408	0.410	0.442	0.369	0.337	0.377	0.350	0.362	0.338	0.375	0.348	0.348	0.348	0.348	0.348	0.348	0.348		
	0.375	0.325	0.681	0.353	0.281	0.353	0.342	0.258	0.368	0.304	0.414	0.394	0.414	0.394	0.375	0.375	0.375	0.292	0.309	0.234	0.311	0.241	0.320	0.247	0.314	0.236	0.314	0.236	0.314	0.236	0.314	0.236		
	0.437	0.433	0.648	0.945	0.404	0.354	0.342	0.310	0.422	0.400	0.422	0.400	0.422	0.400	0.422	0.422	0.422	0.408	0.375	0.331	0.393	0.367	0.381	0.343	0.343	0.343	0.343	0.343	0.343	0.343	0.343	0.343	0.343	
ETT	0.596	1.005	0.677	1.223	0.551	0.687	0.574	0.973	0.624	1.089	0.624	1.089	0.631	0.917	0.423	0.468	0.337	0.312	0.319	0.287	0.318	0.290	0.307	0.281	0.319	0.287	0.319	0.287	0.319	0.287	0.319	0.287		
	0.596	1.005	0.677	1.223	0.551	0.687	0.574	0.973	0.624	1.089	0.624	1.089	0.631	0.917	0.423	0.468	0.337	0.312	0.319	0.287	0.318	0.290	0.307	0.281	0.319	0.287	0.319	0.287	0.319	0.287	0.319	0.287		
	0.596	1.005	0.677	1.223	0.551	0.687	0.574	0.973	0.624	1.089	0.624	1.089	0.631	0.917	0.423	0.468	0.337	0.312	0.319	0.287	0.318	0.290	0.307	0.281	0.319	0.287	0.319	0.287	0.319	0.287	0.319	0.287		
	0.596	1.005	0.677	1.223	0.551	0.687	0.574	0.973	0.624	1.089	0.624	1.089	0.631	0.917	0.423	0.468	0.337	0.312	0.319	0.287	0.318	0.290	0.307	0.281	0.319	0.287	0.319	0.287	0.319	0.287	0.319	0.287		
ETTm1 (192)	0.560	0.913	0.641	1.133	0.567	0.728	0.517	1.067	0.578	0.928	0.578	0.928	0.583	0.925	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	
	0.560	0.913	0.641	1.133	0.567	0.728	0.517	1.067	0.578	0.928	0.578	0.928	0.583	0.925	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	
	0.560	0.913	0.641	1.133	0.567	0.728	0.517	1.067	0.578	0.928	0.578	0.928	0.583	0.925	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346
	0.560	0.913	0.641	1.133	0.567	0.728	0.517	1.067	0.578	0.928	0.578	0.928	0.583	0.925	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346	0.346
ETTm2 (192)	0.322	0.268	0.432	0.482	0.341	0.273	0.317	0.250	0.324	0.268	0.341	0.273	0.317	0.250	0.347	0.306	0.292	0.231	0.278	0.217	0.277	0.215	0.274	0.204	0.291	0.226	0.291	0.226	0.291	0.226	0.291	0.226		
	0.322	0.268	0.432	0.482	0.341	0.273	0.317	0.250	0.324	0.268	0.341	0.273	0.317	0.250	0.347	0.306	0.292	0.231	0.278	0.217	0.277	0.215	0.274	0.204	0.291	0.226	0.291	0.226	0.291	0.226	0.291	0.226		
	0.322	0.268	0.432	0.482	0.341	0.273	0.317	0.250	0.324	0.268	0.341	0.273	0.317	0.250	0.347	0.306	0.292	0.231	0.278	0.217	0.277	0.215	0.274	0.204	0.291	0.226	0.291	0.226	0.291	0.226	0.291	0.226		
	0.322	0.268	0.432	0.482	0.341	0.273	0.317	0.250	0.324	0.268	0.341	0.273	0.317	0.250	0.347	0.306	0.292	0.231	0.278	0.217	0.277	0.215	0.274	0.204	0.291	0.226	0.291	0.226	0.291	0.226	0.291	0.226		
Male (4)	1.282	1.282	3.024	3.024	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282		
	1.282	1.282	3.024	3.024	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282		
	1.282	1.282	3.024	3.024	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	
	1.282	1.282	3.024	3.024	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	1.282	
Female (4)	1.405	1.405	3.103	3.103	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405		
	1.405	1.405	3.103	3.103	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405		
	1.405	1.405	3.103	3.103	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	
	1.405	1.405	3.103	3.103	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	1.405	
Donor A (8)	20.633	2.454	33.762	6.267	18.968	1.977	15.124	1.461	16.635	1.599	15.124	1.461	16.635	1.599	15.124	1.461	16.635	1.599	15.124	1.461	16.635	1.599												

Dataset (H)	Naive		Average		Window Average		ARIMA		ETS		THETA		Autoforecaster		Informant		N-BEATS		N-HITS		TSMixer		Time Mixer		Time-LLM				
	MAPE	sMAPE	MAPE	sMAPE	MAPE	sMAPE	MAPE	sMAPE	MAPE	sMAPE	MAPE	sMAPE	MAPE	sMAPE	MAPE	sMAPE	MAPE	sMAPE	MAPE	sMAPE	MAPE	sMAPE	MAPE	sMAPE	MAPE	sMAPE			
dsf	Alzawa (32)	15.053	0.547	13.272	0.755	24.663	0.755	14.159	0.511	5.951	0.384	13.264	0.492	8.701	0.271	1.094	0.103	0.137	0.020	0.088	0.022	1.237	0.097	0.097	0.051	-	-		
	Alzawa (64)	16.441	0.650	20.731	0.627	23.815	0.754	15.442	0.538	9.006	0.566	18.772	0.617	11.052	0.410	2.148	0.092	0.193	0.038	0.214	0.041	2.003	0.285	1.604	0.096	17.673	0.448		
	Bilsius (32)	0.994	0.217	2.482	0.371	2.024	0.338	2.024	0.338	0.897	0.194	0.956	0.218	11.876	0.359	0.465	0.176	0.082	0.047	0.052	0.027	0.340	0.142	0.481	0.149	0.750	0.249		
	Bilsius (64)	1.000	0.220	2.500	0.375	2.025	0.338	2.025	0.338	0.897	0.194	0.956	0.218	11.876	0.359	0.465	0.176	0.082	0.047	0.052	0.027	0.340	0.142	0.481	0.149	0.750	0.249		
ETT	Lorenz (32)	3.248	0.378	5.288	0.475	3.555	0.425	3.306	0.319	4.636	0.380	3.322	0.374	3.086	0.287	1.086	0.143	0.298	0.045	0.527	0.043	1.506	0.254	0.734	0.113	-	-		
	Lorenz (64)	2.265	0.402	3.550	0.485	3.056	0.481	3.056	0.481	3.260	0.470	2.271	0.397	3.046	0.314	1.046	0.130	0.368	0.057	0.584	0.039	1.962	0.162	0.467	0.062	0.896	0.275		
	ETTh1 (96)	4.306	0.492	5.611	0.538	3.598	0.513	3.622	0.484	4.771	0.484	4.445	0.490	3.517	0.443	3.180	0.424	2.737	0.397	2.753	0.397	2.907	0.400	2.908	0.401	-	-		
	ETTh1 (92)	4.747	0.516	6.379	0.553	3.529	0.524	4.091	0.504	4.701	0.510	5.044	0.515	3.342	0.462	3.251	0.443	2.812	0.331	2.783	0.426	3.006	0.421	3.138	0.426	2.83464	0.216		
ETT	ETTh2 (96)	2.982	0.369	3.702	0.413	2.129	0.380	2.245	0.361	2.556	0.361	2.939	0.374	2.115	0.380	2.164	0.363	1.789	0.310	1.917	0.318	1.641	0.300	1.956	0.325	-	-		
	ETTh2 (92)	2.732	0.400	3.735	0.433	2.540	0.410	2.416	0.389	2.720	0.396	3.095	0.407	2.818	0.411	1.267	0.235	2.204	0.358	2.159	0.360	2.142	0.363	5.57568	1.000	8.67284	0.126		
	ETTh1 (96)	3.808	0.455	5.313	0.494	2.692	0.482	3.803	0.445	4.238	0.460	3.780	0.447	2.229	0.391	1.724	0.320	1.501	0.284	1.514	0.281	1.681	0.305	1.732	0.308	-	-		
	ETTh1 (92)	4.130	0.493	5.231	0.522	2.736	0.500	4.121	0.483	4.578	0.498	4.033	0.486	2.490	0.428	2.090	0.377	1.925	0.352	2.075	0.356	1.865	0.342	1.633	0.310	100.24091	0.195		
mHSC	ETTh2 (96)	2.770	0.359	3.469	0.411	2.770	0.359	3.469	0.411	2.770	0.359	3.469	0.411	2.770	0.359	3.469	0.411	2.770	0.359	3.469	0.411	2.770	0.359	3.469	0.411	2.770	0.359	3.469	0.411
	ETTh2 (92)	2.338	0.365	2.913	0.395	2.184	0.379	2.239	0.359	2.309	0.364	2.388	0.370	1.936	0.344	1.731	0.325	1.574	0.302	1.575	0.305	1.545	0.305	1.668	0.318	2.92865	0.184		
	Male (4)	1.675	0.243	3.375	0.338	1.891	0.315	1.193	0.268	2.155	0.802	2.222	0.334	1.714	0.811	1.248	0.844	1.144	0.830	1.147	0.833	0.971	0.789	1.056	0.793	-	-		
	Female (4)	1.248	0.195	2.660	0.160	1.371	0.160	0.915	0.121	1.427	0.871	1.435	0.172	2.435	0.947	1.026	0.886	1.85566	1.000	1.010	0.886	0.725	0.860	0.803	0.862	4.16466	0.658		
mHSC	Donor A (4)	1.561	0.134	2.633	0.185	1.651	0.207	1.651	0.207	1.651	0.207	1.651	0.207	1.651	0.207	1.651	0.207	1.651	0.207	1.651	0.207	1.651	0.207	1.651	0.207	1.651	0.207	1.651	0.207
	Donor A (8)	1.836	0.160	3.293	0.221	1.979	0.215	1.182	0.173	1.760	0.879	2.005	0.248	1.664	0.898	1.000	1.000	1.232	0.902	2.242	0.886	0.988	0.838	0.888	0.870	2.99526	0.641		
	Donor B (4)	1.984	0.166	3.286	0.222	2.183	0.267	1.431	0.215	1.910	0.882	2.319	0.304	1.880	0.890	1.383	0.900	1.277	0.898	1.69700	0.981	0.973	0.877	0.935	0.876	2.14466	0.794		
	Donor B (8)	1.688	0.197	3.384	0.272	1.743	0.250	1.095	0.206	1.300	0.826	1.710	0.295	1.564	0.839	1.158	0.866	1.236	0.863	1.125	0.870	1.219	0.856	1.162	0.837	-	-		
epl	Donor B (16)	1.786	0.212	2.793	0.292	1.743	0.308	1.272	0.261	1.498	0.838	1.809	0.351	1.305	0.853	1.145	0.870	1.122	0.875	1.142	0.871	1.154	0.869	0.869	0.836	2.03866	0.702		
	Covid (14)	0.109	0.050	0.154	0.073	0.129	0.058	0.107	0.054	7.902	0.111	0.127	0.059	0.105	0.074	0.094	0.070	0.103	0.075	0.106	0.076	0.108	0.075	0.066	0.055	-	-		
	Covid (30)	0.115	0.054	0.158	0.073	0.129	0.058	0.132	0.072	0.592	0.115	0.125	0.057	0.154	0.095	0.072	0.061	0.004	0.026	0.026	0.110	0.080	0.154	0.092	0.078	0.134	0.062		
	mHSC (8)	0.788	0.398	1.172	0.497	0.599	0.394	0.582	0.393	0.635	0.428	0.706	0.431	0.603	0.447	0.631	0.447	0.624	0.451	0.629	0.451	0.612	0.441	0.441	0.387	0.440	-	-	
mRNA	mHSC (16)	0.800	0.406	1.147	0.500	0.592	0.403	0.582	0.381	0.606	0.419	0.650	0.425	0.625	0.440	0.618	0.451	0.608	0.441	0.625	0.438	0.584	0.432	0.395	0.438	1.07066	0.316		
	mHSC (32)	1.600	0.424	2.257	0.519	1.417	0.453	1.387	0.458	1.538	0.514	1.518	0.494	1.342	0.512	1.393	0.506	1.386	0.507	1.379	0.505	1.343	0.505	1.032	0.477	-	-		
	mHSC (64)	1.405611	0.427	1.756611	0.516	1.195611	0.355	1.195611	0.361	1.614611	0.344	1.722611	0.403	1.077611	0.351	1.132611	0.353	1.092611	0.351	1.190611	0.354	1.062611	0.290	1.188610	0.327	1.74266	0.368		
	mHSC (16)	1.302611	0.463	1.419611	0.513	1.326611	0.356	1.315611	0.371	1.586611	0.378	1.8086610	0.378	1.185611	0.330	1.278611	0.332	1.208611	0.330	1.319611	0.360	1.696610	0.299	2.471610	0.338	4.93665	0.297		
mHSC	mHSC (8)	6.60585	0.335	9.86665	0.428	7.82465	0.314	7.27385	0.319	6.71865	0.333	9.17465	0.350	7.54265	0.332	7.10465	0.339	7.21865	0.336	7.12665	0.341	7.07165	0.319	7.77565	0.335	-	-		
	mHSC (16)	6.54585	0.339	1.05266	0.425	8.16165	0.319	7.79385	0.330	7.94585	0.326	9.63065	0.341	7.54265	0.332	6.75865	0.347	7.16265	0.335	7.69065	0.329	8.09765	0.333	6.56865	0.327	6.08365	0.254		
	mHSC-E (8)	1.254	0.480	1.949	0.611	1.059	0.417	0.934	0.421	1.007	0.412	1.121	0.449	0.928	0.452	0.869	0.429	0.872	0.434	0.930	0.428	0.958	0.436	0.979	0.434	-	-		
	mHSC-E (16)	1.281	0.481	1.916	0.609	1.087	0.423	0.929	0.453	1.053	0.417	1.140	0.445	0.908	0.459	0.924	0.431	0.912	0.434	0.895	0.438	0.946	0.422	0.947	0.426	7.28365	0.367		
mHSC-GM	mHSC-GM (8)	1.273	0.525	1.999	0.637	1.010	0.444	0.827	0.479	0.992	0.440	1.109	0.473	0.831	0.464	0.813	0.460	0.833	0.459	0.884	0.455	0.823	0.445	0.871	0.469	7.14465	0.367		
	mHSC-L (8)	1.273	0.525	1.997	0.653	1.010	0.459	0.859	0.477	0.972	0.451	1.178	0.473	0.831	0.479	0.787	0.477	0.747	0.480	0.781	0.477	0.881	0.445	0.804	0.479	-	-		
	mHSC-L (16)	1.280	0.524	1.916	0.645	0.999	0.454	0.819	0.494	0.981	0.451	1.105	0.485	0.812	0.474	0.766	0.477	0.768	0.477	0.786	0.472	0.821	0.466	0.833	0.467	8.99765	0.375		
	mHSC-L (16)	1.280	0.524	1.916	0.645	0.999	0.454	0.819	0.494	0.981	0.451	1.105	0.485	0.812	0.474	0.766	0.477	0.768	0.477	0.786	0.472	0.821	0.466	0.833	0.467	8.99765	0.375		

Table 4: Train set MAPE and sMAPE evaluations

Dataset (H)	Naive		RWD		Average		Window Average		ARIMA		ETS		THETA		Autoreformer		Informer		N-BEATS		N-HITS		TSMixer		Time Mixer		Time-LLM				
	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE	MAE	MSE			
dyst	3.931	0.573	7.657	0.555	5.433	0.766	5.433	0.766	3.646	0.539	5.542	0.381	5.137	0.518	1.848	0.270	0.557	0.126	0.088	0.028	0.106	0.027	0.581	0.106	0.210	0.061	11.872	0.465			
	4.884	0.654	7.201	0.624	5.259	0.757	5.259	0.757	4.527	0.642	8.902	0.574	4.855	0.626	9.628	0.357	0.466	0.382	0.107	0.062	0.047	0.150	0.046	1.070	0.282	0.394	0.099	-			
	1.215	0.242	2.981	0.405	2.212	0.371	2.212	0.371	1.072	0.340	1.108	0.220	1.178	0.248	4.301	0.361	0.361	0.349	0.241	0.069	0.044	0.046	0.025	0.313	0.156	0.148	0.074	0.690	0.207		
	2.190	0.326	3.811	0.483	1.750	0.355	1.750	0.355	1.392	0.400	7.200	0.403	2.203	0.334	4.301	0.361	0.361	0.349	0.241	0.069	0.044	0.046	0.025	0.313	0.156	0.148	0.074	-	-		
	30.601	0.439	39.277	0.305	58.978	0.308	58.978	0.308	9.444	0.360	7.200	0.403	30.822	0.424	1.162	0.332	0.621	0.164	0.158	0.052	0.120	0.043	1.066	0.266	0.341	0.108	-	-	-		
	9.462	0.474	4.379	0.476	23.110	0.304	23.110	0.304	12.382	0.429	11.901	0.492	9.569	0.468	0.824	0.304	0.251	0.197	0.263	0.122	0.154	0.085	0.317	0.209	0.234	0.111	1.387	0.333	-	-	
ETT	3.973	0.476	4.442	0.508	3.005	0.511	3.005	0.511	3.211	0.487	3.829	0.470	3.947	0.462	2.530	0.390	2.286	0.384	2.014	0.359	1.988	0.368	1.940	0.346	2.163	0.349	-	-	-		
	4.025	0.486	4.829	0.522	3.026	0.534	3.026	0.534	2.990	0.511	3.897	0.483	3.987	0.482	2.079	0.405	2.624	0.392	2.243	0.393	2.295	0.374	2.449	0.362	2.381	0.372	0.321	0.173	-	-	
	2.176	0.333	3.105	0.387	1.960	0.332	1.960	0.332	2.004	0.324	2.203	0.332	2.461	0.348	1.478	0.310	1.346	0.301	1.069	0.270	1.129	0.268	1.164	0.277	1.074	0.269	-	-	-	-	
	3.226	0.357	4.363	0.430	3.054	0.363	3.116	0.340	3.174	0.351	3.448	0.373	3.448	0.373	3.466	0.355	1.565	0.341	1.270	0.318	1.391	0.322	1.266	0.316	3.41668	1.000	1.852e-5	0.351	-	-	
	3.610	0.442	4.130	0.471	2.769	0.492	3.388	0.435	3.835	0.447	3.078	0.435	2.363	0.395	1.983	0.332	3.395	1.983	0.332	1.857	0.319	1.901	0.316	1.897	0.308	2.012	0.313	-	-	-	-
	3.827	0.463	4.367	0.497	2.774	0.505	3.598	0.457	4.070	0.469	3.645	0.464	2.356	0.418	2.062	0.345	2.103	0.345	2.239	0.345	2.239	0.345	2.239	0.345	2.141	0.347	2.411	0.357	1.778e-3	0.160	-
ETTh2 (192)	1.524	0.244	1.896	0.279	1.314	0.266	1.314	0.266	1.404	0.246	1.516	0.242	1.463	0.253	1.303	0.249	1.187	0.223	1.153	0.210	1.142	0.208	1.084	0.206	1.052	0.210	-	-	-	-	
ETTh2 (96)	1.665	0.265	2.155	0.309	1.414	0.288	1.414	0.288	1.562	0.268	1.626	0.266	1.718	0.279	1.450	0.266	1.237	0.236	1.155	0.224	1.217	0.224	1.120	0.222	1.136	0.232	4.320e-5	0.341	-	-	
micro	1.141	0.224	2.422	0.326	1.445	0.306	1.445	0.306	0.891	0.265	1.781	0.280	1.631	0.332	1.304	0.787	0.999	0.816	0.858	0.801	0.865	0.803	0.798	0.802	0.802	0.802	0.802	0.802	0.802	0.802	
	1.245	0.248	2.221	0.350	1.645	0.382	1.645	0.382	1.067	0.345	1.668	0.292	1.983	0.417	0.954	0.813	0.915	0.818	0.858	0.801	0.865	0.803	0.798	0.802	0.802	0.802	0.802	0.802	0.802	0.802	
	1.363	0.149	2.324	0.203	1.314	0.201	1.314	0.201	0.974	0.146	1.621	0.864	1.860	0.229	3.201	0.944	1.025	0.878	1.707e6	1.000	1.015	0.879	0.879	0.939	1.442	0.877	2.239e7	0.636	-	-	
	1.545	0.154	2.710	0.199	1.263	0.247	1.263	0.247	1.124	0.172	1.477	0.869	1.944	0.286	1.421	0.874	1.092	0.880	1.540e4	0.999	1.610	0.885	0.885	2.075	0.974	1.354	0.880	3.018e6	0.626	-	-
	1.741	0.164	3.281	0.234	1.927	0.223	1.927	0.223	1.268	0.183	1.519	0.873	1.962	0.265	1.487	0.895	1.000	1.000	1.886	0.899	2.214	0.889	0.899	2.075	0.891	2.175	0.899	-	-	-	-
	1.944	0.175	3.311	0.241	2.037	0.278	2.037	0.278	1.451	0.227	1.767	0.876	2.154	0.321	1.652	0.884	1.263	0.896	1.289	0.897	1.61310	0.982	0.982	2.639	0.900	1.552	0.892	2.281e6	0.782	-	-
Donor B (4)	1.206	0.139	1.960	0.190	1.127	0.183	1.127	0.183	0.996	0.161	1.029	0.872	1.292	0.373	0.949	0.852	0.811	0.878	0.836	0.873	0.795	0.882	1.086	0.883	1.148	0.876	-	-	-	-	
Donor B (8)	1.464	0.161	2.404	0.213	1.289	0.229	1.289	0.229	1.283	0.198	1.326	0.885	1.734	0.429	1.230	0.880	1.021	0.899	0.941	0.895	0.948	0.894	1.112	0.896	1.395	0.887	5.037e6	0.755	-	-	
epi	0.150	0.079	0.277	0.142	0.191	0.080	0.191	0.080	0.161	0.081	0.334	0.100	0.176	0.095	0.100	0.049	0.077	0.038	0.081	0.041	0.084	0.042	0.086	0.042	0.096	0.047	0.111	0.055	-	-	
	0.248	0.089	0.487	0.142	0.289	0.103	0.289	0.103	0.261	0.111	0.704	0.123	0.353	0.125	0.141	0.069	0.124	0.065	0.118	0.058	0.098	0.050	0.132	0.062	0.177	0.068	0.111	0.055	-	-	
rRNA	hESC (16)	0.906	0.458	1.356	0.569	0.712	0.476	0.712	0.476	0.690	0.472	0.752	0.486	0.825	0.511	0.668	0.497	0.698	0.499	0.696	0.699	0.508	0.679	0.489	0.506	0.679	0.489	0.678	0.491	-	-
	hESC (8)	0.904	0.467	1.330	0.591	0.717	0.484	0.717	0.484	0.700	0.484	0.733	0.481	0.764	0.509	0.683	0.489	0.669	0.505	0.679	0.498	0.685	0.485	0.654	0.482	0.644	0.484	1447129.000	0.351	-	-
	hHep (8)	2.188	0.410	2.801	0.501	1.815	0.485	1.815	0.485	1.748	0.481	1.692	0.563	1.779	0.535	2.376	0.629	2.450	0.630	2.543	0.627	2.477	0.624	2.252	0.612	2.207	0.610	-	-	-	-
	hHep (16)	2.217	0.431	3.049	0.531	1.658	0.529	1.658	0.529	1.694	0.526	1.777	0.563	1.757	0.555	2.495	0.630	2.545	0.637	2.499	0.642	2.310	0.642	2.257	0.606	2.262	0.606	1975036.000	0.444	-	-
	mDC (8)	3.299e9	0.510	3.529e9	0.585	1.997e9	0.426	1.997e9	0.426	1.982e9	0.425	3.310e9	0.406	2.931e9	0.481	3.793e9	0.423	3.923e9	0.429	4.892e9	0.434	3.617e9	0.427	3.896e9	0.454	4.207e9	0.462	-	-	-	-
	mDC (16)	3.530e9	0.545	4.480e9	0.657	2.408e9	0.402	2.408e9	0.402	2.385e9	0.436	3.305e9	0.396	2.590e9	0.494	4.012e9	0.412	4.243e9	0.419	3.564e9	0.450	4.777e9	0.424	2.907e9	0.453	4.143e9	0.437	5.775e5	0.374	-	-
	mESC (8)	2.975e5	0.354	4.840e5	0.444	3.818e5	0.349	3.818e5	0.349	3.664e5	0.352	5.847e5	0.396	4.805e5	0.391	3.871e5	0.370	3.778e5	0.383	3.964e5	0.376	3.704e5	0.384	4.001e5	0.375	4.157e5	0.376	-	-	-	-
	mESC (16)	5.912e5	0.354	8.742e5	0.441	4.170e5	0.352	4.170e5	0.352	3.775e5	0.363	5.212e5	0.369	5.389e5	0.380	2.883e5	0.372	1.631e5	0.391	2.551e5	0.375	2.977e5	0.367	3.025e5	0.371	2.898e5	0.383	7.421e5	0.274	-	-
	mHSC-E (8)	1.248	0.474	1.953	0.599	1.016	0.411	1.016	0.411	0.905	0.414	1.039	0.406	1.119	0.443	0.870	0.391	0.824	0.387	0.814	0.388	0.879	0.384	0.887	0.394	0.905	0.392	-	-	-	-
	mHSC-E (16)	1.286	0.486	1.915	0.608	1.062	0.421	1.062	0.421	0.896	0.431	1.059	0.412	1.071	0.439	0.857	0.394	0.894	0.389	0.873	0.391	0.850	0.394	0.914	0.391	0.946	0.395	5.578e5	0.356	-	-
	mHSC-GM (8)	1.328	0.498	2.071	0.630	1.089	0.426	1.089	0.426	0.904	0.440	1.066	0.421	1.232	0.471	0.847	0.412	0.873	0.406	0.800	0.409	0.830	0.412	0.937	0.415	0.920	0.414	-	-	-	-
	mHSC-GM (16)	1.308	0.502	1.959	0.625	1.074	0.424	1.074	0.424	0.850	0.446	1.061	0.421	1.169	0.458	0.848	0.413	0.836	0.410	0.865	0.408	0.890	0.407	0.883	0.413	0.881	0.420	4.820e5	0.349	-	-
mHSC-L (8)	1.276	0.508	1.965	0.631	1.012	0.439	1.012	0.439	0.860	0.453	0.991	0.433	1.210	0.479	0.805	0.424	0.778	0.422	0.774	0.423	0.774	0.420	0.856	0.431	0.881	0.428	-	-	-	-	
mHSC-L (16)	1.294	0.499	1.885	0.613	0.997	0.434	0.997	0.434	0.815	0.464	0.991	0.431	1.133	0.464	0.801	0.421	0.755	0.421	0.763	0.421	0.788	0.418	0.834	0.423	0.801	0.428	6.198e5	0.356	-	-	

Table 5: Test set MAPE and sMAPE evaluations