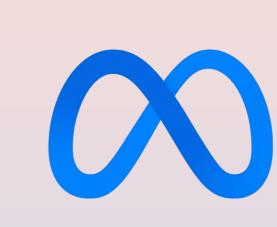
# **Diverse Human Motion Prediction via** Gumbel-Softmax Sampling from an Auxiliary Space







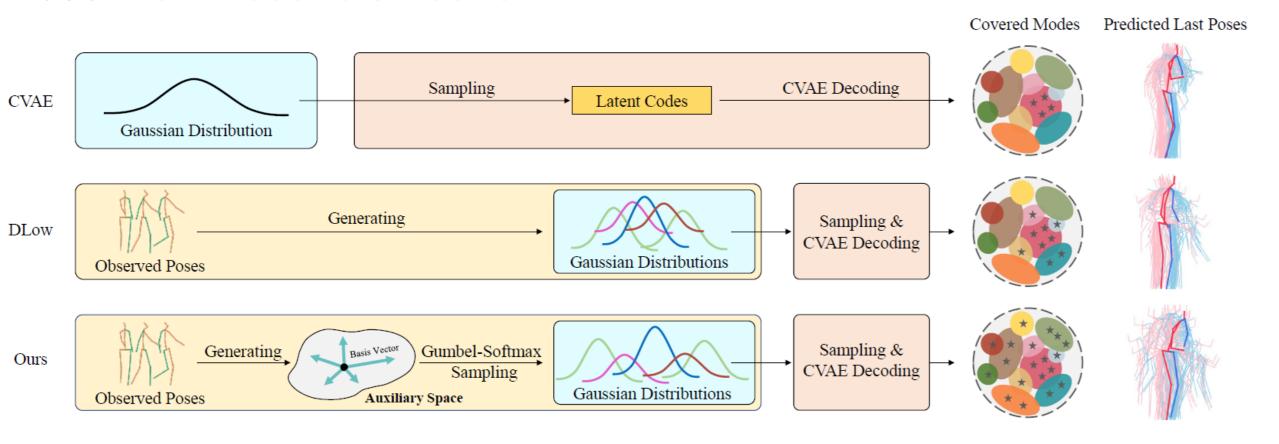


Lingwei Dang <sup>1</sup>, Yongwei Nie <sup>1\*</sup>, Chengjiang Long <sup>2</sup>, Qing Zhang <sup>3</sup>, Guiqing Li <sup>1</sup>

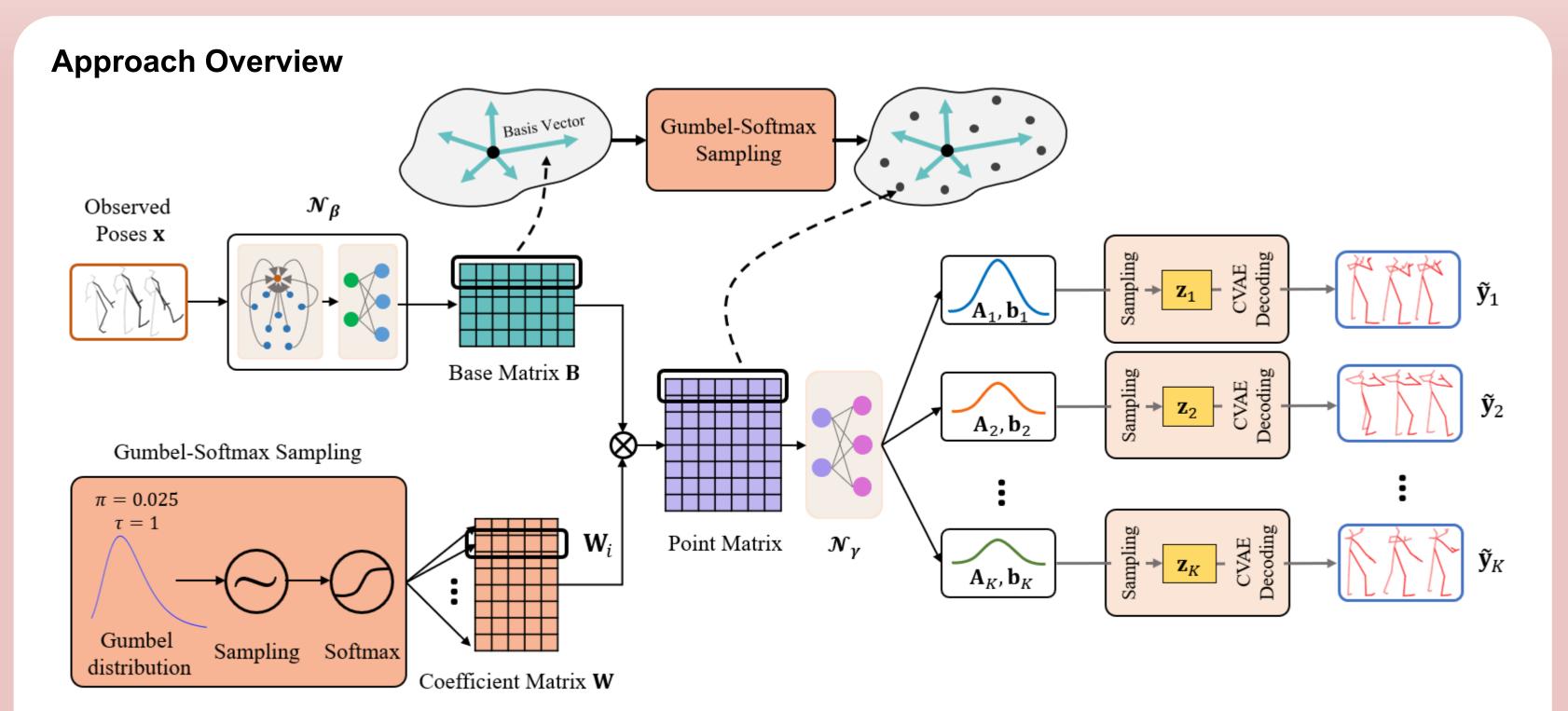
- <sup>1</sup> South China University of Technology, <sup>2</sup> Meta Reality Lab, <sup>3</sup> Sun Yat-sen University
- \*Corresponding author: nieyongwei@scut.edu.cn

# **Background & Motivation**

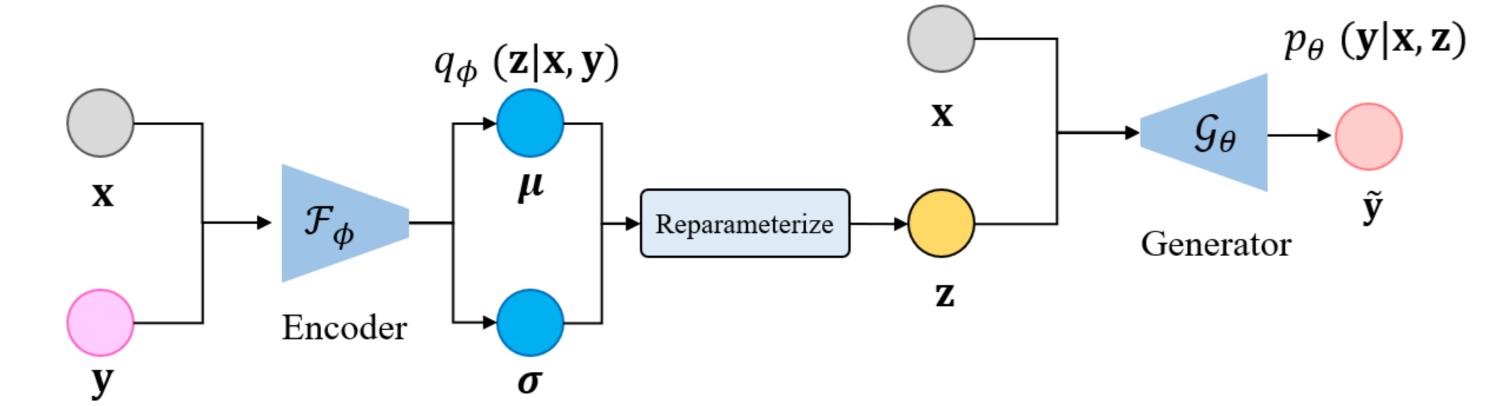
- Diverse human motion prediction aims at predicting multiple possible future sequences from the observed one.
- Poses obtained by previous deep generative networks are not diverse enough.
- Recent work attempted to model the conditional distribution of data but it can only cover a fixed number of modes.
- We propose a novel sampling strategy for sampling very diverse results from an imbalanced multimodal distribution.



# **Proposed Approach**



## **Architecture of the pretrained CVAE**



## Pseudocode for the overall approach and the Gumbel-Softmax sampling strategy

Algorithm 1 Diverse sampling from a complex distribution by random Gumbel-Softmax sampling from an auxiliary space

**Input:** Observed pose sequence  $\mathbf{x}$ , number of samples K, auxiliary space generation network  $\mathcal{N}_{\beta}$ , Gaussian distribution generation network  $\mathcal{N}_{\mathcal{V}}$ , CVAE decoder network  $\mathcal{G}_{\theta}$  that models the target complex distribution

#### **Output:** A set of samples $\{\tilde{y}_k\}_{k=1}^K$

- 1:  $B = N_{\beta}(x) // generate$  an auxiliary space given input poses 2:  $\mathbf{W} \leftarrow \text{Gumbel-Softmax sampling} // generate a coefficient ma$ *trix by* Algorithm 2
- 3: P = WB // Multiply W and B to obtain a point matrix P 4:  $\{A_k, b_k\}_{k=1}^K = \mathcal{N}_{\gamma}(P)$  // convert points into means and variances
- 5:  $\epsilon \sim \mathcal{N}(0,1)$  // sampling an  $\epsilon$  from the normal distribution
- variance  $A_k$  and mean  $b_k$  by reparameterization trick
- $\mathbf{z}_k = \mathbf{A}_k \boldsymbol{\epsilon} + \mathbf{b}_k$  // sample  $\mathbf{z}_k$  from Gaussian distribution of 8:  $\tilde{\mathbf{y}}_k = \mathcal{G}_{\theta}(\mathbf{x}, \mathbf{z}_k)$  // decode  $\mathbf{z}_k$  and  $\mathbf{x}$  into a result  $\tilde{\mathbf{y}}_k$

## Algorithm 2 Gumbel-Softmax coefficient matrix generation

**Input:** Number of coefficient vectors K, dimension size M of a coefficient vector, Gumbel distribution parameters  $\pi$  and  $\tau$ **Output:** A coefficient matrix  $\mathbf{W} \in \mathbb{R}^{K \times M}$ 

- 1: Declare a matrix  $\mathbf{W} \in \mathbb{R}^{K \times M}$
- 2: **for** i = 1 to K **do**
- for j = 1 to M do
- $u \sim U(0,1)$  // sample a value from uniform distribution  $g = -\log(-\log(u))$
- end for
- $\mathbf{W}_i = \text{Softmax}(\mathbf{W}_i) / \text{normalize the } i^{th} \text{ row of } \mathbf{W}$ 9: end for

## 9: end for

# **Loss functions**

6: **for** k = 1 to K **do** 

 $\mathcal{L}_{hdiv} = rac{1}{K(K-1)} \sum_{i=1}^K \sum_{j=1}^K \max\left(0, \eta - \left\| ilde{\mathbf{y}}_i - ilde{\mathbf{y}}_j
ight\|_2
ight) \quad \mathcal{L}_{acc} = \min_k \left\|\mathbf{y} - ilde{\mathbf{y}}_k
ight\|_2, k \in [1, K] \quad \mathcal{L}_{KL}' = \mathcal{KL}(r_{eta, \gamma}(\mathbf{z}_k \mid \mathbf{x}) \|p(\mathbf{z})), k \in [1, K]$ 

# Contributions

- A novel sampling method converts the sampling of the distribution into randomly sampling of points from an auxiliary space for diverse and accurate sampling.
- A Gumbel-Softmax sampling method and a hinge-diversity loss both improve the performance of our method.
- Extensive experimental results demonstrate the effectiveness of our approach.

#### **Quantitative Results**

#### **Comparisons with baselines**

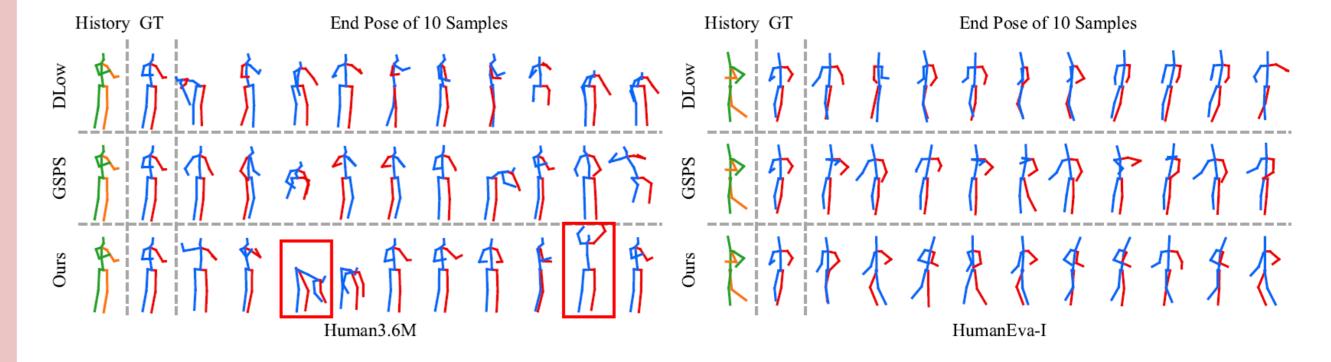
	Method		]	Human3.	6M [18]		HumanEva-I [36]						
	Method	APD↑	ADE ↓	FDE ↓	MMADE ↓	MMFDE ↓	APD↑	ADE ↓	FDE ↓	MMADE↓	MMFDE ,		
deterministic	LTD [31]	0.000	0.516	0.756	0.627	0.795	0.000	0.415	0.555	0.509	0.613		
deterministic	MSR [13]	0.000	0.508	0.742	0.621	0.791	0.000	0.371	0.493	0.472	0.548		
stochastic	Pose-Knows [41]	6.723	0.461	0.560	0.522	0.569	2.308	0.269	0.296	0.384	0.375		
	MT-VAE [42]	0.403	0.457	0.595	0.716	0.883	0.021	0.345	0.403	0.518	0.577		
	HP-GAN [6]	7.214	0.858	0.867	0.847	0.858	1.139	0.772	0.749	0.776	0.769		
	BoM [7]	6.265	0.448	0.533	0.514	0.544	2.846	0.271	0.279	0.373	0.351		
	GMVAE [14]	6.769	0.461	0.555	0.524	0.566	2.443	0.305	0.345	0.408	0.410		
	DeLiGAN [17]	6.509	0.483	0.534	0.520	0.545	2.177	0.306	0.322	0.385	0.371		
	DSF [43]	9.330	0.493	0.592	0.550	0.599	4.538	0.273	0.290	0.364	0.340		
	DLow [44]	11.741	0.425	0.518	0.495	0.531	4.855	0.251	0.268	0.362	0.339		
	GSPS [30]	14.757	0.389	0.496	0.476	0.525	5.825	0.233	0.244	0.343	0.331		
	Ours	15.310	0.370	0.485	0.475	0.516	6.109	0.220	0.234	0.342	0.316		

#### **Ablation study results**

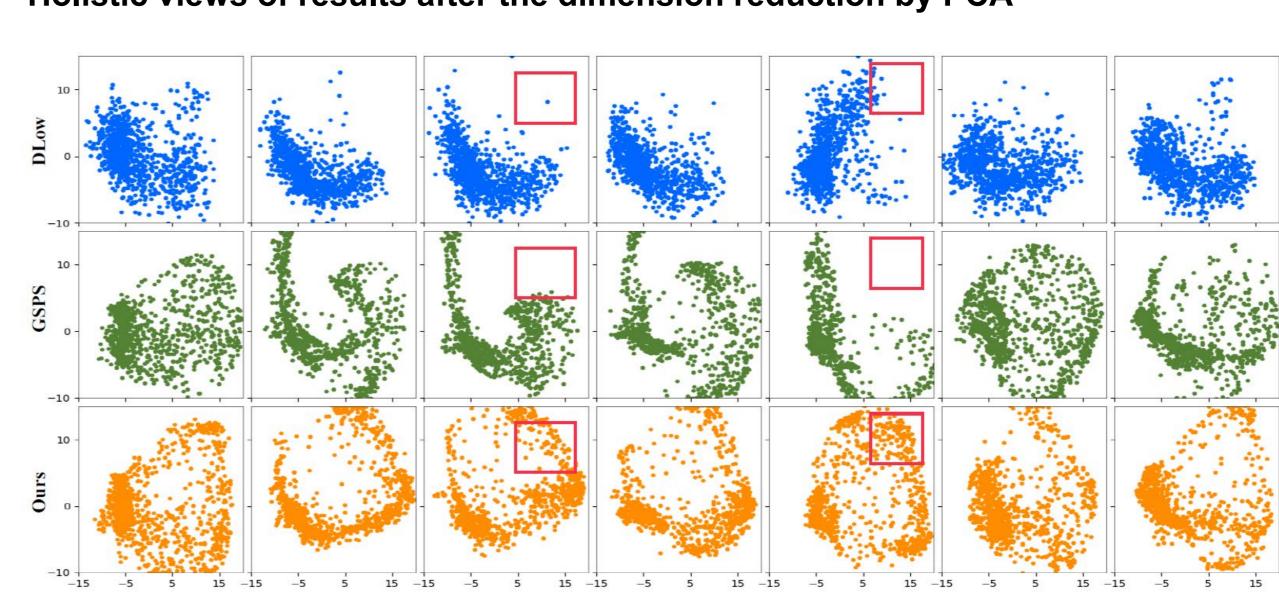
	① Number of basis vectors					② Dimension of auxiliary space				③ Sampling method			$\textcircled{4} N_{\gamma}$		$\bigcirc$ $\mathcal{L}_{hdiv}$ v.s. $\mathcal{L}_{div}$			
	20	30	40*	50	60	32	64	128*	256	512	Gumbel*	Gaussian	Uniform	$w/N_{\gamma}^*$	w/o N <sub>γ</sub>	$\mathcal{L}_{hdiv}(25)^*$	$\mathcal{L}_{div}$ (25)	$\mathcal{L}_{div}$ (1300)
APD↑	5.929	5.946	5.993	5.969	5.951	5.885	5.931	5.993	5.963	5.957	5.993	5.847	5.730	5.993	5.182	5.993	3.843	5.993
$ADE \downarrow$	0.234	0.234	0.231	0.229	0.233	0.236	0.233	0.231	0.233	0.236	0.231	0.240	0.233	0.231	0.229	0.231	0.211	0.235
FDE ↓	0.240	0.243	0.240	0.239	0.241	0.245	0.243	0.240	0.241	0.243	0.240	0.246	0.241	0.240	0.236	0.240	0.218	0.242
MMADE ↓	0.345	0.345	0.340	0.339	0.338	0.337	0.342	0.340	0.336	0.342	0.340	0.343	0.344	0.340	0.322	0.340	0.309	0.343
MMFDE ↓	0.321	0.319	0.313	0.315	0.312	0.312	0.318	0.313	0.310	0.316	0.313	0.320	0.323	0.313	0.298	0.313	0.287	0.321

## **Qualitative Results**

# **Comparisons with baselines**



## Holistic views of results after the dimension reduction by PCA



# Datasets & Metric & Project

- Datasets: Human3.6M, HumanEva-I Dataset
- Metrics: APD, ADE, FDE, MMADE, MMFDE
- Link: <a href="https://github.com/Droliven/diverse">https://github.com/Droliven/diverse</a> sampling



[MSRGCN] Dang L, Nie Y, Long C, et al. MSR-GCN: Multi-Scale Residual Graph Convolution Networks for Human Motion Prediction. ICCV, 2021. [DLow] Yuan Y, Kitani K. Dlow: Diversifying latent flows for diverse1 human motion prediction. ECCV, 2020.

[GSPS] Mao W, Liu M, Salzmann M. Generating smooth pose sequences for diverse human motion prediction. ICCV, 2021.

Key References

Acknowledgement •

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