
HART: HUMAN ALIGNED RECONSTRUCTION TRANSFORMER

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ABSTRACT

We introduce HART, a unified framework for sparse-view human reconstruction. Given a small set of uncalibrated RGB images of a person as input, it outputs a watertight clothed mesh, the aligned SMPL-X body mesh, and a Gaussian-splat representation for photorealistic novel-view rendering. Prior methods for clothed human reconstruction either optimize parametric templates, which overlook loose garments and human-object interactions, or train implicit functions under simplified camera assumptions, limiting applicability in real scenes. In contrast, HART predicts per-pixel 3D point maps, normals, and body correspondences, and employs an occlusion-aware Poisson reconstruction to recover complete geometry, even in self-occluded regions. These predictions also align with a parametric SMPL-X body model, ensuring that reconstructed geometry remains consistent with human structure while capturing loose clothing and interactions. These human-aligned meshes initialize Gaussian splats to further enable sparse-view rendering. While trained on only 2.3K synthetic scans, HART achieves state-of-the-art results: Chamfer Distance improves by **18–23%** for clothed-mesh reconstruction, PA-V2V drops by **6–27%** for SMPL-X estimation, LPIPS decreases by **15–27%** for novel-view synthesis on a wide range of datasets. These results suggest that feed-forward transformers can serve as a scalable model for robust human reconstruction in real-world settings. Code and models will be released.

1 INTRODUCTION

3D human reconstruction is crucial for applications like virtual try-on, AR/VR, telepresence, and digital content creation. Recent methods based on NeRF (Peng et al., 2021a; Guo et al., 2023; Wang et al., 2022) and 3D Gaussian Splatting (3DGS) (Qian et al., 2024; Guo et al., 2025; Li et al., 2024) excel in both rendering and geometry reconstruction. However, they either require dense-view inputs, accurate camera calibrations, or robust SMPL (Loper et al., 2015) estimations, while training such models for a single person could take minutes to hours. In a more practical scenario, feed-forward inference from a set of unposed sparse-view human images would be preferable due to efficiency and scalability, yet accurately inferring geometry and appearance from such limited inputs remains challenging due to the complexity of human bodies (e.g. articulations and self-occlusions).

Earlier works have tackled the problem of sparse-view human geometry reconstruction by learning generalizable pixel-aligned implicit functions (Saito et al., 2019; 2020; Cao et al., 2023), achieving direct clothed human mesh regression from sparse-view RGB images. However, such methods often assume orthographic projections, which significantly limits their generalization ability to real-world perspective images. Recently, advances in Score Distillation Sampling (SDS) (Poole et al., 2022) have enabled human geometry distillation from pretrained diffusion models, achieving detailed surface reconstruction from uncalibrated images (Xiu et al., 2024; Zeng et al., 2023). However, they optimize human poses in canonical SMPL poses, which often fail to recover complete geometry for loose garments and human-object interactions.

In the broader 3D reconstruction community, general-purpose feed-forward approaches have made rapid progress. Recent works in transformer-based backbones (Wang et al., 2024b; Yang et al., 2025; Zhang et al., 2025; Wang et al., 2025; Tang et al., 2024b) have significantly advanced calibration-free 3D reconstruction from sparse views, enabling a wide range of downstream 3D vision tasks, such as camera pose regression, tracking, and novel view synthesis, with impressive generalization abilities to real-world images. These approaches form the natural backbone for our method. However, they only output raw point clouds that require further meshing, and their predictions remain limited to

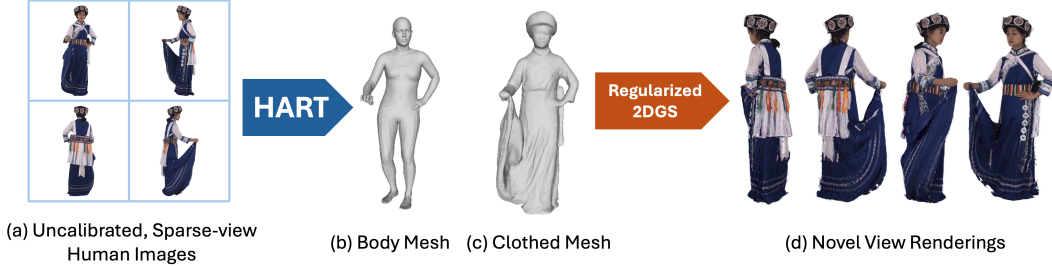


Figure 1: Given (a) uncalibrated, sparse-view human images, our method HART is a unified framework that simultaneously reconstructs (b) the underlying SMPL-X body mesh and (c) the clothed mesh. (d) Our clothed mesh prediction serves as an initialization and regularization to further enable novel view synthesis from sparse views.

pixels visible in the input images. As a result, they fail to capture occluded regions unseen in the input images – especially problematic in human reconstruction with pervasive self-occlusion.

Beyond clothed geometry, estimating a parametric body mesh from multi-view inputs is also of high interest. Existing approaches typically rely on keypoint-based fitting (Pavlakos et al., 2019; eas, 2021; Shuai et al., 2022), which can be brittle under complex poses, self-occlusions, and loose garments. In contrast, our dense point map predictions naturally serve as strong geometric priors. By augmenting our transformer backbone with per-pixel SMPL-X (Pavlakos et al., 2019) tightness (Li et al., 2025) and body-part label heads, we enable prediction of accurate SMPL-X parameters alongside clothed meshes.

We additionally find that our high-quality clothed mesh reconstruction can serve as a good proxy for novel view synthesis. By initializing Gaussian surfels (Huang et al., 2024) from our predicted mesh faces, we could achieve sparse-view human rendering via regularized 2D Gaussian Splatting (Guédon et al., 2025). Our key observation is that *constraining Gaussian Splatting with accurate clothed geometry substantially improves rendering quality while mitigating overfitting*.

In summary, our key contributions lie in unifying feed-forward point map prediction with novel geometry completion modules and parametric body estimation for robust human reconstruction and rendering. Specifically, we introduce Human Aligned Reconstruction Transformer (HART), a unified transformer-based architecture that jointly predicts point maps, surface normals, and SMPL-X tightness vectors with semantic body-part labels. This design enables *simultaneous reconstruction of detailed clothed meshes* and the underlying SMPL-X body meshes in a feed-forward manner. To overcome the limitations of point-map-based frameworks in handling self-occlusions, we introduce a **3D U-Net in the Differentiable Poisson Surface Reconstruction (DPSR)** module. By refining the indicator grid with residual corrections, HART *recovers complete and watertight clothed geometry*. While trained on only 2.3K human scans, our method achieves state-of-the-art performance across multiple benchmarks, including clothed mesh reconstruction, sparse-view SMPL-X estimation, and novel view synthesis. Extensive quantitative and qualitative evaluations further demonstrate that HART generalizes well to real-world human images with loose garments.

2 RELATED WORK

Structure from Motion Structure from Motion (SfM) is a fundamental computer vision problem that involves estimating camera parameters and reconstructing sparse 3D point clouds from multiple images of a static scene (Hartley & Zisserman, 2000; Oliensis, 2000; Özyeşil et al., 2017), with COLMAP (Schönberger & Frahm, 2016) being the most widely adopted framework. Recent years have seen significant advances through deep learning integration, improving keypoint detection (DeTone et al., 2018; Dusmanu et al., 2019; Tyszkiewicz et al., 2020; Yi et al., 2016) and image matching (Chen et al., 2021; Lindenberger et al., 2023; Sun et al., 2021), culminating in end-to-end differentiable SfM approaches (Wang et al., 2024a). A paradigm shift emerged with DUST3R (Wang et al., 2024b) and MAST3R (Leroy et al., 2024), which directly estimate aligned dense point maps from image pairs without requiring camera parameters, and produce these parameters along with 3D reconstructions. Most recently, VGGT (Wang et al., 2025) demonstrates that a standard transformer trained on extensive 3D data can directly predict all 3D attributes (cameras, depth, point maps, tracks) in a single feed-forward pass, achieving state-of-the-art results without post-processing op-

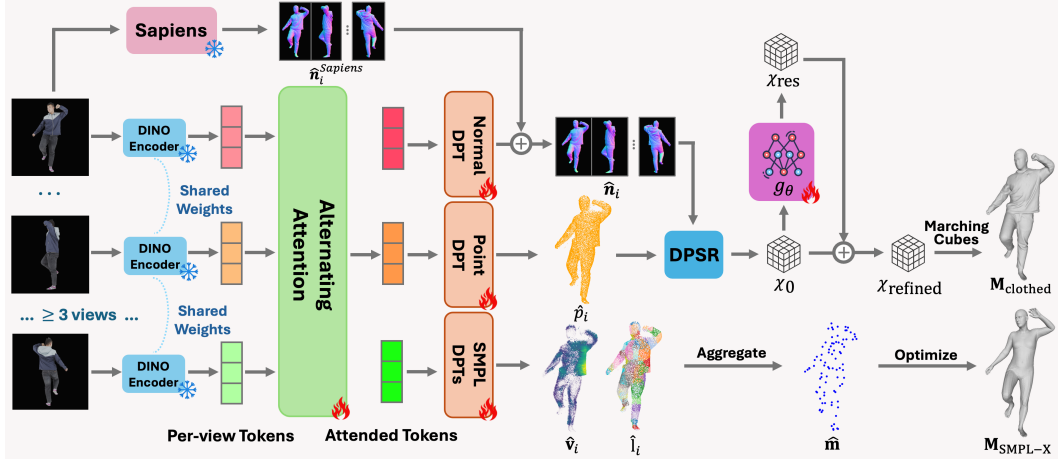


Figure 2: **Overview of our Network Architecture.** Given N uncalibrated human images, our HART transformer first maps input images $\{I_i\}_{i=1}^N$ into per-pixel point maps \hat{p}_i , refined normal maps \hat{n}_i , SMPL-X tightness vectors \hat{v}_i and body part labels \hat{l}_i . The oriented point maps \hat{p}_i , \hat{n}_i for all views are merged and converted to an indicator grid χ_{refined} via Differentiable Poisson Surface Reconstruction (DPSR). A 3D-UNet g_θ is used for grid refinement to account for self-occlusions and a clothed mesh reconstruction M_{clothed} can be obtained by running marching cubes. The SMPL-X tightness vectors and label maps are aggregated into body markers \hat{m} out of which we could optimize a SMPL-X mesh $M_{\text{SMPL-X}}$.

timization. Our work adopts VGGT into the human reconstruction domain and goes beyond point map reconstruction by simultaneously estimating a detailed human mesh and underlying SMPL-X meshes.

Sparse-view 3D Reconstruction Neural Radiance Fields (NeRF) (Mildenhall et al., 2020) have revolutionized novel view synthesis and 3D reconstruction from multi-view images, while 3D Gaussian Splatting (3DGS) (Kerbl et al., 2023) has made radiance field learning and rendering significantly more efficient and scalable. However, the vanilla NeRF/3DGS models require costly per-scene optimization and large numbers of input images (typically 20-100 views) to achieve high-quality. Recent works have explored learning-based approaches that directly reconstruct NeRF or 3DGS from sparse-view images in a feed-forward manner. (Suhail et al., 2022; Lin et al., 2022; Xu et al., 2024; Wu et al., 2024; Hong et al., 2024) proposes to predict radiance fields from sparse-view images using either neural networks trained on large-scale multi-view datasets. (Zhang et al., 2024; Tang et al., 2024a; Chen et al., 2024b; Xu et al., 2025) predicts per-pixel Gaussian splats instead of implicit NeRF, enabling real-time rendering and better scalability to high-resolution images. (Chen et al., 2024a) introduces a latent voxel grid representation to encode 3D Gaussians, achieving better 3D consistency in wide baseline settings. These methods demonstrate promising results on general 3D scenes, but typically require calibrated camera poses as inputs.

Human Reconstruction from Sparse-view Images Earlier works such as (Saito et al., 2019; 2020; Huang et al., 2020) pioneered the use of neural fields for high-fidelity 3D human reconstruction from single RGB images. (Xiu et al., 2022; Zheng et al., 2021) further improved the reconstruction quality by leveraging parametric human models like SMPL (Loper et al., 2015) as guidance. Another line of work (Peng et al., 2021a; Guo et al., 2023; Weng et al., 2022; Wang et al., 2022; Qian et al., 2024) combines NeRF/3DGS and human models for human reconstruction from sparse-view or even monocular videos. These methods usually rely on per-scene optimization over videos. Other works (Cao et al., 2023; Yu et al., 2025; Zhou et al., 2025a; Kwon et al., 2024; Hu et al., 2024) try to directly predict human reconstruction from sparse-view images (typically 3-8 views) in a feed-forward manner. Our work also falls into this category. We distinguish our approach from prior works by leveraging recent point-map-based reconstruction models to process *calibration-free* human images. In contrast, existing methods either rely on accurate camera parameters or assume orthographic projections, an assumption that holds only for synthetic data and fails on real-world images.

3 METHOD

We begin by detailing the architecture of our transformer with per-pixel prediction heads in Sec. 3.1. Sec. 3.2 presents the subsequent occlusion-aware DPSR module for complete human surface reconstruction. Sec. 3.3 outlines our training details, and finally, our geometry-informed novel view synthesis pipeline is described in Sec. 3.4.

3.1 HART: HUMAN ALIGNED RECONSTRUCTION TRANSFORMER

At the core of our method is a human-aligned transformer with downstream heads for per-pixel human attribute predictions. Given a set of N ($N \geq 3$) uncalibrated human images $\{I_i \in \mathbb{R}^{3 \times H \times W}\}_{i=1}^N$ captured in the same body pose, the transformer f is a function that maps the images into a set of per-pixel attributes:

$$f(\{I_i\}_{i=1}^N) = \{\hat{p}_i, \hat{\mathbf{n}}_i, \hat{\mathbf{v}}_i, \hat{l}_i\}_{i=1}^N, \quad (1)$$

where $\hat{p}_i, \hat{\mathbf{n}}_i, \hat{\mathbf{v}}_i \in \mathbb{R}^{3 \times H \times W}$, and $\hat{l}_i \in \mathbb{N}^{H \times W}$ denote the predicted point map, normal map, SMPL-X tightness map, and SMPL-X body-part label map for input image I_i . The oriented point predictions \hat{p}_i and $\hat{\mathbf{n}}_i$ are used to reconstruct the clothed mesh $\mathbf{M}_{\text{clothed}}$, while the SMPL-X tightness and label maps guide the estimation of the parametric body mesh $\mathbf{M}_{\text{SMPL-X}}$. An overview of our network architecture is shown in Fig. 2.

We adopt VGGT (Wang et al., 2025), a recent state-of-the-art feed-forward transformer for general-purpose 3D reconstruction, as the backbone of our framework. Each input image I_i is first patchified into K tokens, denoted as $t^{I_i} \in \mathbb{R}^{K \times C}$, using the DINOv2 encoder (Oquab et al., 2023). These per-view tokens are then fused across images using the alternating attention layers from VGGT, which allows the network to capture both intra-view spatial relationships and cross-view geometric correspondences, forming a powerful representation for subsequent prediction heads.

After the attention layers, the fused tokens t^{I_i} for each image I_i are transformed to dense per-pixel downstream feature maps $F_i \in \mathbb{R}^{C \times H \times W}$ via prediction heads. Following (Wang et al., 2024b; 2025), we adopt DPT head (Ranftl et al., 2021) as our prediction heads.

3.1.1 POINT HEAD AND CAMERA POSE OPTIMIZATION

Similar to (Wang et al., 2024b; 2025), our predicted point maps are *viewpoint-invariant*, meaning that these 3D points are expressed in the coordinate system of the first camera, which we designate as the world reference frame.

Our point map loss follows the formulation of (Wang et al., 2024b) with an aleatoric uncertainty (Kendall & Cipolla, 2016; Novotny et al., 2018) term. Given the ground-truth point map p_i and predicted confidence map \hat{C}_{p_i} , the loss is defined as:

$$\mathcal{L}_{\text{point}} = \sum_{i=1}^N \|\hat{C}_{p_i} \odot (\hat{p}_i - p_i)\|_1 - \alpha \log \hat{C}_{p_i}, \quad (2)$$

It is worth noting that, unlike (Wang et al., 2024b; 2025) and other common SfM frameworks, we do not assume the camera’s principal point at the image center. We observe that this assumption significantly restricts generalization when working with foreground-focused human images, and thus, we explicitly relax it in our formulation. Therefore, we do not adopt VGGT’s pretrained camera head, which assumes centered principal points. Instead, we use RANSAC (Fischler & Bolles, 1981) and PnP (Lepetit et al., 2009) as in (Wang et al., 2024b; Yang et al., 2025) to estimate camera parameters from predicted point maps.

3.1.2 RESIDUAL NORMAL HEAD

Accurate surface normals are critical for high-fidelity surface reconstruction. We find that directly predicting normals using a DPT head often results in overly smooth or blurry estimates, likely due to the limited capacity of the VGGT backbone for fine-grained local geometry.

To overcome this, we adopt a residual-learning strategy. Instead of learning full normals from scratch, the network predicts *residual normals* $\mathbf{n}_i^{\text{res}} \in \mathbb{R}^{3 \times H \times W}$ with respect to the results of a state-of-the-art human normal estimator (Khrodar et al., 2024), denoted $\mathbf{n}_i^{\text{Sapiens}}$. The final normal map \mathbf{n}_i is computed as:

$$\hat{\mathbf{n}}_i = \text{normalize}(\hat{\mathbf{n}}_i^{\text{Sapiens}} + \hat{\mathbf{n}}_i^{\text{res}}), \quad (3)$$

where $\text{normalize}(\cdot)$ enforces unit length.

This residual formulation leverages the strong prior from $\hat{\mathbf{n}}_i^{\text{Sapiens}}$ while refining high-frequency details and enforcing multi-view consistency; by integrating independently predicted monocular normals across views, our residual normal head yields more coherent and detailed results, which in turn significantly improve subsequent surface reconstruction.

Similar to our point map loss, we define the normal map loss as:

$$\mathcal{L}_{\text{normal}} = \sum_{i=1}^N (\hat{C}_{\mathbf{n}_i} \odot (1 - \hat{\mathbf{n}}_i \cdot \mathbf{n}_i)) - \alpha \log \hat{C}_{\mathbf{n}_i}, \quad (4)$$

Finally, we leverage camera rotation matrices R_{c2w} estimated from our predicted point maps to transform normals to the world reference frame: $\hat{\mathbf{n}}_i^{\text{world}} = R_{c2w} \hat{\mathbf{n}}_i$.

3.1.3 SMPL-X HEADS

We predict two key components that establish correspondence between the clothed surface and the underlying SMPL-X body: **tightness vectors** and **body part labels**. These predictions will enable us to fit SMPL-X meshes to clothed humans.

Tightness Vector Heads. Following ETCH (Li et al., 2025), we predict tightness vectors $\hat{\mathbf{v}}_i$ that point from clothed surface points to their corresponding locations on the underlying body surface. Each tightness vector is decomposed into direction $\hat{\mathbf{d}}_i$ and magnitude \hat{b}_i components, where $\hat{\mathbf{v}}_i = \hat{b}_i \hat{\mathbf{d}}_i$. The direction component captures the geometric relationship between clothing and the body, while the magnitude reflects the looseness of the clothing and varies with the garment type and body region. Contrary to ETCH, which takes sparse point clouds as inputs, we directly predict per-pixel tightness vectors from images using two individual DPT heads for tightness directions and magnitudes. This results in much denser tightness predictions and thus better body fitting results.

Body Part Label Head. We include another DPT head that predicts body part assignment map \hat{l}_i with corresponding confidence map \hat{c}_i , mapping each clothed surface point to one of 86 predefined SMPL-X body markers. This semantic labeling enables us to aggregate tightness-corrected points into sparse body markers, providing anchors for SMPL-X parameter estimation.

Marker Aggregation and SMPL-X Fitting. Given the predicted tightness vectors and part labels, we first compute inner body points as $\hat{\mathbf{y}}_i = \hat{p}_i + \hat{\mathbf{v}}_i$, where \hat{p}_i are the clothed surface points from the Point Head. We then aggregate points with the same part label into sparse body markers:

$$\hat{\mathbf{m}}_k = \frac{\sum_{i:\hat{l}_i=k} (\hat{c}_i)^\alpha \hat{\mathbf{y}}_i}{\sum_{i:\hat{l}_i=k} (\hat{c}_i)^\alpha} \quad (5)$$

where $\hat{\mathbf{m}}_k$ represents the k -th body marker. α is a hyperparameter that controls the influence of confidence weights.

We optimize SMPL-X parameters $(\theta, \beta, \mathbf{t})$ along with a scaling factor s to get the final SMPL-X mesh $\mathbf{M}_{\text{SMPL-X}}$, by minimizing the L2 distance between predicted markers and corresponding SMPL-X surface points:

$$\min_{s, \theta, \beta, \mathbf{t}} \sum_{k=1}^{86} \|\tilde{\mathbf{m}}_k - \hat{\mathbf{m}}_k\|^2 + \lambda_{\text{reg}} \mathcal{L}_{\text{reg}}, \quad (6)$$

where $\tilde{\mathbf{m}}_k$ are markers on the current SMPL-X estimate, and \mathcal{L}_{reg} is an L2 regularization of θ and β . This formulation transforms the challenging clothed human fitting problem into a well-posed sparse marker fitting task, enabling robust and efficient body parameter estimation even under loose clothing. Instead of directly optimizing SMPL-X poses θ , we optimize the pose embedding of VPoser (Pavlakos et al., 2019), which provides a stronger pose regularization.

Following ETCH, the training loss of our SMPL-X branch is a combination of losses on tightness direction, magnitude, label classification, and confidence, defined as:

$$\mathcal{L}_{\text{SMPL}} = \mathcal{L}_d + \mathcal{L}_b + \mathcal{L}_l + \mathcal{L}_c, \\ \mathcal{L}_d = \sum_{i=1}^N (1 - \hat{\mathbf{d}}_i \cdot \mathbf{d}_i), \quad \mathcal{L}_b = \sum_{i=1}^N (\hat{b}_i - b_i)^2, \quad \mathcal{L}_l = -\frac{1}{N} \log(p_{i,k=\hat{l}_i}), \quad \mathcal{L}_c = \sum_{i=1}^N (\hat{c}_i - c_i)^2, \quad (7)$$

where \mathbf{d}_i , b_i , l_i , c_i represent ground-truth tightness vector direction, magnitude, part label, and geodesic distance-based confidence, respectively. For more technical details about our SMPL-X heads, please refer to the appendix.

3.2 CLOTHED MESH RECONSTRUCTION VIA OCCLUSION-AWARE DPSR

With predicted point maps and normal maps, one could apply classical Poisson surface reconstruction methods (Kazhdan & Hoppe, 2013) to obtain a mesh of the human. To this end, our clothed-mesh reconstruction branch builds on the *Differentiable Poisson surface reconstruction* (DPSR) framework of SAP (Peng et al., 2021b) to reconstruct the indicator grid of human shapes, followed by a refinement network to handle occluded regions not seen in input images. This enables our framework to directly produce a watertight mesh $\mathbf{M}_{\text{clothed}}$ via marching cubes (Lorensen & Cline, 1987).

Initial Indicator Grid Generation. Given the predicted human point maps $\mathbf{P} = \{\hat{p}_i[M_i] \in \mathbb{R}^3\}_{i=1}^N$ and world-space normals $\mathbf{N} = \{\hat{\mathbf{n}}_i^{\text{world}}[M_i] \in \mathbb{R}^3\}_{i=1}^N$ (M_i represents foreground human masks), we apply DPSR to generate an initial indicator grid $\chi_0 \in \mathbb{R}^{r \times r \times r}$. The DPSR solves the Poisson equation $\nabla^2 \chi = \nabla \cdot \mathbf{v}$, where \mathbf{v} represents the normal vector field rasterized from the oriented point cloud (\mathbf{P}, \mathbf{N}) . We refer readers to (Peng et al., 2021b) for implementation details.

3D-UNet Refinement. The initial indicator grid χ_0 , while geometrically consistent, often suffers from missing details and gaps in unobserved regions due to the sparse and potentially incomplete nature of the input point maps. This motivates us to learn a 3D-UNet to refine the initial reconstructed indicator grid χ_0 .

Specifically, the 3D-UNet g_θ takes the coarse indicator grid $\chi_0 \in \mathbb{R}^{r \times r \times r}$ as input, and predicts a residual indicator grid χ_{res} with the same resolution. The refined indicator grid is obtained via $\chi_{\text{refined}} = \chi_0 + \chi_{\text{res}}$. For the detailed architecture of this module, please refer to the appendix.

We supervise the final refined indicator grid via χ_{gt} obtained from ground-truth mesh:

$$\mathcal{L}_{\text{DPSR}} = \frac{1}{r^3} \sum_x (\chi_{\text{refined}}(x) - \chi_{\text{gt}}(x))^2. \quad (8)$$

3.3 TRAINING

Training Objective. The total loss of our HART transformer is defined as

$$\mathcal{L} = \mathcal{L}_{\text{point}} + \mathcal{L}_{\text{normal}} + \mathcal{L}_{\text{DPSR}} + \mathcal{L}_{\text{SMPL}}. \quad (9)$$

Similar to VGGT, we observe that our framework converges stably without the need to weight individual loss terms against each other. Please refer to the appendix for implementation details.

Training Data. We train our network with 2,345 subjects from the THuman 2.1 (Yu et al., 2021) dataset with textured scans and ground-truth SMPL-X annotations. We render each subject into 96 views in a 360-degree azimuth trajectory and apply center-cropping around the center of the human masks to only focus on the foreground regions of the human images.

3.4 GEOMETRY-INFORMED NOVEL VIEW SYNTHESIS

Our accurate clothed mesh reconstruction also enables high-quality novel view synthesis (NVS) from sparse-view inputs. Inspired by a recent geometrically-regularized Gaussian splatting method (Guédon et al., 2025), we initialize 2D Gaussian surfels directly on our reconstructed mesh $\mathbf{M}_{\text{clothed}}$ and optimize their attributes to best fit the input images.

Gaussian Surfel Initialization. We instantiate 2D Gaussians at the face centers of our reconstructed mesh, while their orientations are aligned with the local surface normals. Following (Guédon et al., 2025), we parameterize each Gaussian’s covariance matrix to lie tangent to the surface, forming 2D surfels that faithfully respect the underlying geometry.

Optimization. We generally follow (Guédon et al., 2025) but with some modifications: We find it beneficial to disable Gaussian densification and pruning, and fix the number of Gaussians to the number of mesh faces, as they are already sufficiently dense and accurate. We also find it effective to apply a lower learning rate to Gaussian means, scales, and rotations, which further stabilizes training.

We optimize the Gaussian parameters using a combination of losses:

$$\mathcal{L}_{\text{rendering}} = \mathcal{L}_{\text{photo}} + \lambda_d \mathcal{L}_d + \lambda_n \mathcal{L}_n + \lambda_{\text{struct}} \mathcal{L}_{\text{struct}}, \quad (10)$$

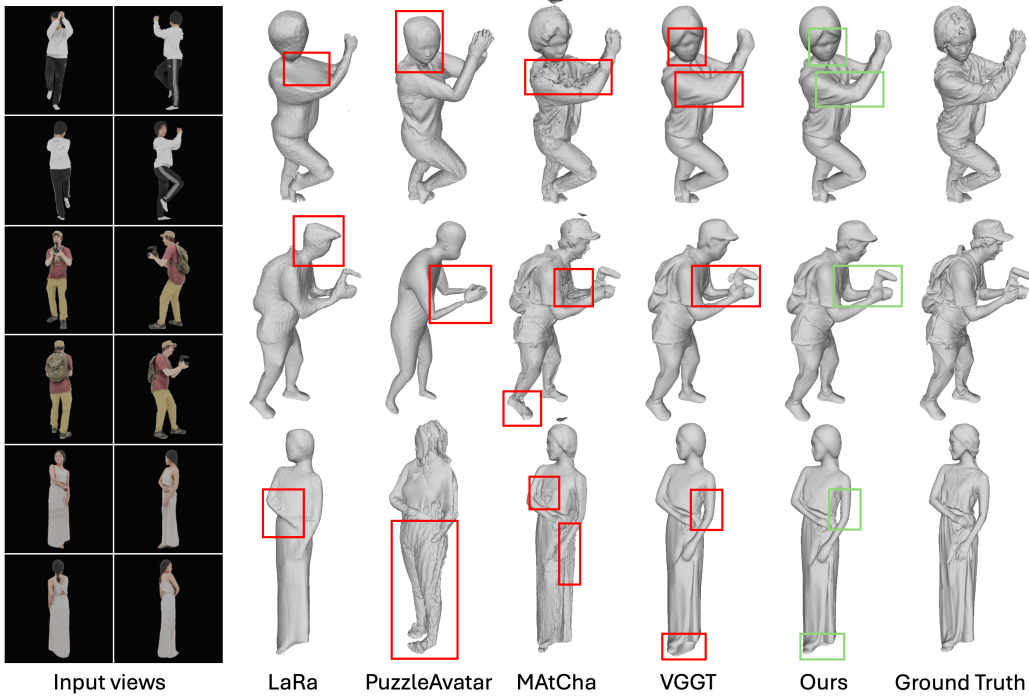


Figure 3: **Clothed Mesh Reconstruction from 4 views.** We show 1 subject from THuman 2.1 (row 1) and 2 from 2K2K test sets (rows 2–3). In contrast to various baselines, our method can recover detailed geometry in both observed and occluded regions.

where $\mathcal{L}_{\text{photo}}$, \mathcal{L}_d , and \mathcal{L}_n denote the photometric loss, the depth distortion, and normal consistency regularization losses adopted from 2DGS (Huang et al., 2024). The structure loss $\mathcal{L}_{\text{struct}}$ follows (Guédon et al., 2025) and regularizes the Gaussian geometry with our reconstructed mesh.

4 EXPERIMENTS

We evaluate our method on clothed mesh reconstruction, SMPL-X estimation, and novel view synthesis. All comparisons with baselines are conducted under a fixed setting of 4 input views. In the appendix, we provide additional results under varying numbers of views as well as baseline details/hyperparameters and ablation studies.

4.1 DATASET

We use three test datasets as our major testbeds: 1) the THuman 2.1 test set with 100 subjects for in-domain evaluation of all three tasks. 2) A subset of 100 subjects from the 2K2K dataset (Han et al., 2023) for cross-domain mesh reconstruction and SMPL-X estimation evaluation. This dataset has more diversity in age, clothing styles, and human–object interactions not present in our training set. 3) The DNA-Rendering dataset (Cheng et al., 2023) for cross-domain novel-view synthesis evaluation; the dataset contains dense-view real-world *raw images* of 41 subjects wearing loose garments and performing intricate human-object interactions.

4.2 CLOTHED MESH RECONSTRUCTION

Baselines. We adopt VGGT (Wang et al., 2025), MAtCha (Guédon et al., 2025), Puzzle Avatar (Xiu et al., 2024), and LaRa (Chen et al., 2024a) as baselines. We finetune VGGT and LaRA on the same training set as our method. For MAtCha, we replace MAST3R-SfM (Leroy et al., 2024) with our estimated camera, while also using Sapiens (Khrodar et al., 2024) for depth estimation, as Sapiens is specialized in the human domain.

Metrics. We evaluate clothed mesh reconstruction quality using Chamfer Distance (CD) ($\times 10^{-3}$), F-Score at a threshold of 0.5%, and Normal Consistency (NC). For Chamfer Distance, we additionally report its two directional components: *Accuracy*, defined as the mean distance from each predicted point to its closest ground-truth point, and *Completeness*, defined as the mean distance

Table 1: **Quantitative Comparison of Clothed Mesh Reconstruction.** Our method achieves the best performance across nearly all metrics, demonstrating both high-fidelity in-domain reconstruction and strong cross-domain generalization.

Methods	THuman 2.1 (In-domain)					2K2K (Cross-domain)				
	Acc.	Comp.	CD	F-Score	NC	Acc.	Comp.	CD	F-Score	NC
VGGT (Wang et al., 2025)	0.0070	0.0140	0.0209	0.9285	/	0.0072	0.0151	0.0222	0.9274	/
MATCha (Guédon et al., 2025)	0.1264	0.0161	0.1425	0.6793	0.6506	0.1175	0.0138	0.1313	0.6938	0.6956
Puzzle Avatar (Xiu et al., 2024)	0.1311	0.1652	0.2963	0.3916	0.7255	0.1374	0.1916	0.3291	0.4095	0.7587
LaRa (Chen et al., 2024a)	0.0334	0.0466	0.0800	0.6466	0.8257	0.0279	0.0409	0.0688	0.6645	0.8705
Ours	0.0067	0.0105	0.0172	0.9354	0.9125	0.0077	0.0093	0.0170	0.9301	0.9479

Table 2: **Quantitative Comparisons of Sparse-view SMPL-X estimation.** Across both in-domain and cross-domain test sets, ours consistently reconstructs more accurate body meshes than others.

Methods	THuman 2.1 (In-domain)		2K2K (Cross-domain)	
	PA-V2V	PA-MPJPE	PA-V2V	PA-MPJPE
MV-SMPLify-X (Zheng et al., 2021; Pavlakos et al., 2019)	21.66	26.11	24.77	29.81
EasyMocap (eas, 2021; Shuai et al., 2022)	25.89	31.22	24.36	26.22
ETCH (Li et al., 2025)	21.49	22.87	27.06	26.22
Ours	15.72	16.18	22.86	24.49

from each ground-truth point to its closest prediction. The total Chamfer Distance is reported as the sum of Accuracy and Completeness.

Discussion. Fig. 3 and Tab. 1 present qualitative and quantitative comparisons for clothed mesh reconstruction. LaRa yields overly smooth surfaces. PuzzleAvatar, constrained by its reliance on parametric body templates, produces inaccurate body shapes and fails to capture loose garments or object interactions. MATCha recovers overall shapes but introduces noisy surfaces. The most competitive baseline, VGGT, produces point maps that could be converted to reasonable meshes with Poisson surface reconstructions. However, it struggles with self-occluded regions. In contrast, our method better captures occluded areas and adds fine details (e.g., facial regions), thanks to our residual 3D-UNet and normal predictions. These advantages are reflected in both qualitative and quantitative metrics, where we significantly outperform VGGT in completeness.

4.3 SMPL-X ESTIMATION

Baselines. We compare our approach against three baselines: EasyMocap (eas, 2021; Shuai et al., 2022), multi-view variants of SMPLify-X (MV-SMPLify-X) (Pavlakos et al., 2019; Zheng et al., 2021), and ETCH (Li et al., 2025). We use (Xu et al., 2022) for 2D keypoint detection required by EasyMocap and MV-SMPLify-X. For ETCH, we finetune the model on clothed meshes reconstructed from the THuman 2.1 training set and evaluate it as a post-processing step on our predicted meshes.

Metrics. We evaluate Mean Vertex-to-Vertex Error (PA-V2V) by comparing all vertices of the SMPL-X mesh, and Mean Per-Joint Position Error (PA-MPJPE) by comparing the body joints. Both metrics are computed after Procrustes Alignment (Gower, 1975) and are reported in millimeters.

Discussion. Fig. 4 and Tab. 2 present qualitative and quantitative comparisons on SMPL-X estimation. EasyMocap and MV-SMPLify-X often yield meshes with inaccurate head poses and body shapes, while ETCH struggles with fine details such as hands and feet as it only allows a small number of input 3D points (around 5000). In contrast, our method produces more reliable SMPL-X

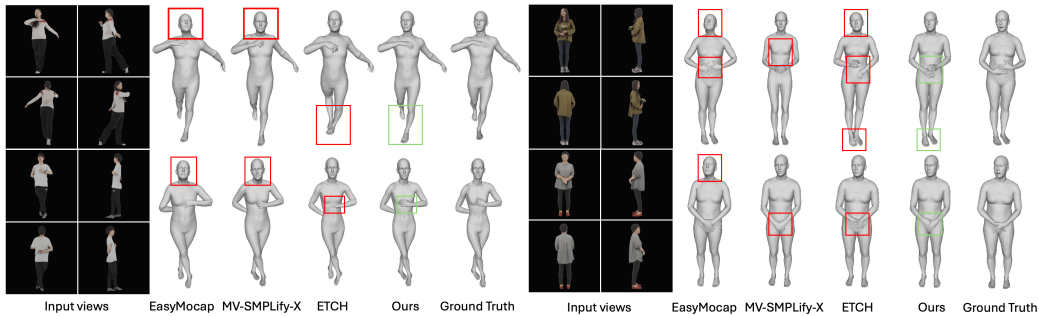


Figure 4: **SMPL-X Mesh Reconstruction from 4 Views:** 2 subjects from THuman (left) and 2 from 2K2K test sets (right). Keypoint-based EasyMocap and MV-SMPLify-X produce inaccurate head poses and body shapes, while ETCH often misstitches reconstructed feet/hands.

Table 3: **Quantitative Comparison of Novel View Synthesis.** Ours consistently outperforms prior arts across synthetic (THuman 2.1) and real-world (DNA Rendering) test sets – with higher fidelity renderings, better perceptual quality (SSIM, LPIPS), and competitive realism (FID).

Methods	THuman 2.1 (Synthetic)				DNA Rendering (Real World)			
	PSNR	SSIM	LPIPS	FID	PSNR	SSIM	LPIPS	FID
LaRa (Chen et al., 2024a)	29.05	0.9464	0.0935	68.12	26.71	0.9209	0.1093	98.09
SEVA (Zhou et al., 2025b)	21.65	0.7843	0.0909	5.03	21.67	0.8029	0.1075	29.68
MAAtCha (Guédon et al., 2025)	30.44	0.9546	0.0537	21.76	26.77	0.9214	0.0708	40.77
Ours	31.70	0.9675	0.0390	14.24	27.54	0.9349	0.0600	36.29



Figure 5: **Novel View Synthesis from 4 Views.** We show qualitative results for novel view synthesis on the DNA-Rendering test set. Benefiting from our accurate reconstruction, we achieve photorealistic rendering while avoiding issues present in baselines, including overly smooth appearance (LaRa), hallucinated textures (SEVA), and floater artifacts (MAAtCha). Please refer to the appendix for more qualitative results.

reconstructions by leveraging much denser body-attribute predictions. These dense cues help the model disambiguate challenging regions under occlusion or loose clothing, while also capturing fine-grained hands/feet poses, leading to more accurate body estimation. Quantitatively, it consistently outperforms all baselines on both in-domain and cross-domain test sets.

4.4 NOVEL VIEW SYNTHESIS

Baselines. We compare our method with LaRa (Chen et al., 2024a), SEVA (Zhou et al., 2025b), and MAAtCha (Guédon et al., 2025). We report direct inference results with pretrained SEVA due to the lack of training code. We provide an additional comparison with GHG (Kwon et al., 2024) for novel view synthesis in the appendix.

Metrics. We evaluate the rendering qualities with four standard metrics: PSNR, SSIM (Wang et al., 2004), LPIPS (Zhang et al., 2018), and FID (Heusel et al., 2017).

Discussion. Fig. 5 and Tab. 3 present qualitative and quantitative comparisons for novel view synthesis. LaRa produces overly blurry renderings due to limited volume resolution, while SEVA generates realistic textures but often over-hallucinates. MAAtCha achieves photorealistic results but suffers from floating artifacts caused by degenerated charts optimization results; constraining Gaussian positions less reduces this issue but leads to overfitting to training views. In contrast, our method produces sharper details and higher visual fidelity by initializing Gaussians from accurate clothed surfaces. This is also reflected by superior quantitative performance on all metrics.

5 CONCLUSION

In this paper, we presented HART, a unified framework for clothed mesh reconstruction, SMPL-X estimation, and novel view synthesis from sparse, uncalibrated human images. It jointly predicts per-pixel point maps, normals, and SMPL-X attributes, enabling recovery of both clothed and body meshes, and facilitating downstream applications such as novel-view synthesis. Extensive experiments demonstrate that HART consistently outperforms state-of-the-art baselines across all tasks.

Limitations & Future Work: While effective, our reconstructions still lack fine-scale details (e.g., fingers, hair) due to limited indicator grid resolutions. Rendering qualities also degrade significantly under very sparse views (e.g., 3 views) or challenging lighting. Future work could explore hierarchical or multi-scale architectures for detail recovery, diffusion priors for improved rendering of occluded regions, and video-based training to enhance temporal consistency and enable animatable reconstructions.

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7 ETHICS STATEMENT

Our work advances human reconstruction, including mesh recovery and novel view synthesis. These contributions hold potential to benefit diverse applications in AR/VR, virtual try-on, and telepresence, fostering progress in both research and real-world use. However, we acknowledge that improving the photorealism and robustness of human reconstruction techniques may also indirectly facilitate misuse, such as the creation of deep fakes or synthetic human content without consent. We emphasize that our models and datasets are intended solely for legitimate academic and industrial research, and we encourage responsible use of the released code and models.

8 REPRODUCIBILITY

To promote openness and ensure reproducibility, we provide comprehensive resources for replicating our results: 1) **Open-source code**. We will release the complete source code used in our experiments, including detailed documentation and preprocessing scripts for constructing the training and test sets, along with step-by-step instructions for reproducing the main results. 2) **Pre-trained models**. To facilitate verification and support downstream research, we will publicly release our trained models.

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A APPENDIX

A.1 MORE DETAILS ABOUT OUR SMPL-X HEADS

As detailed in Sec. 3.1, our transformer contains a total of 3 SMPL-X DPT heads: tightness direction head, tightness magnitude head, and body part label head.

A.1.1 TIGHTNESS DIRECTION AND MAGNITUDE HEADS

For the tightness direction head, we predict a 3D vector field $\hat{\mathbf{d}}_i \in \mathbb{R}^{3 \times H \times W}$, where each vector points from the per-pixel point map \hat{p}_i toward the nearest surface point of the underlying SMPL-X body mesh. The tightness magnitude head predicts a scalar field $\hat{b}_i \in \mathbb{R}^{H \times W}$, representing the lengths of these vectors. Together, they form the full tightness vectors $\hat{\mathbf{v}}_i = \hat{b}_i \hat{\mathbf{d}}_i$, which we use to compute inner body points $\hat{\mathbf{y}}_i = \hat{p}_i + \hat{\mathbf{v}}_i$ for marker aggregation and SMPL-X fitting.

Unlike ETCH (Li et al., 2025), which enforces SE(3) equivariance with a fixed SO(3) anchor array to improve generalization, we directly predict the 3D directions. Since our formulation relies on 2D features from ViT encoders rather than per-point 3D features, enforcing strict equivariance provides limited benefit in our setting.

A.1.2 BODY PART LABEL HEAD

Another key attribute for marker-based SMPL-X fitting is provided by our body part label head, which assigns each clothed surface point to one of 86 predefined SMPL-X body markers.

The label head predicts two sets of logits using a DPT decoder: 1) an 86-dimensional classification vector $\mathbf{z}_i \in \mathbb{R}^{86}$, and 2) an 86-dimensional confidence vector $\mathbf{c}_i \in \mathbb{R}^{86}$.

The classification logits are normalized via softmax to produce a per-pixel probability distribution:

$$p_{i,k} = \frac{\exp(\mathbf{z}_{i,k})}{\sum_{k'=1}^{86} \exp(\mathbf{z}_{i,k'})}. \quad (11)$$

In parallel, the confidence scores \mathbf{c}_i provide uncertainty estimates. Following (Li et al., 2025; Bhatnagar et al., 2020), we compute the aggregated confidence \hat{c}_i as:

$$\hat{c}_i = \sum_{k=1}^{86} p_{i,k} \cdot \mathbf{c}_{i,k}. \quad (12)$$

The final body part label assignment is obtained as the most probable class:

$$\hat{l}_i = \arg \max_{k \in \{1, \dots, 86\}} p_{i,k}. \quad (13)$$

Thus, the body part label head produces a feature map of shape $\mathbb{R}^{172 \times H \times W}$, which encodes both classification probabilities and per-label confidences. These are aggregated into per-pixel label and confidence maps, $\hat{l}_i \in \mathbb{N}^{H \times W}$ and $\hat{c}_i \in \mathbb{R}^{H \times W}$, enabling reliable body part assignment and uncertainty-aware aggregation for the subsequent marker-based SMPL-X fitting.

A.2 ARCHITECTURE OF OUR INDICATOR GRID REFINEMENT MODULE

As discussed in 3.2, we integrate a 3D U-Net into the Differentiable Poisson Surface Reconstruction (DPSR) module to refine the indicator grid and address self-occlusions. The architecture of this refinement module is detailed in Tab. 4. Because our indicator grid χ_0 has a high resolution ($512 \times 512 \times 512$), directly applying a 3D U-Net leads to out-of-memory issues. To overcome this, we first downsample the grid by a factor of 4 using convolutional layers with nonlinear activations. The downsampled grid is then processed with a 3D U-Net, and the output is upsampled back to the original resolution to form the residual grid prediction χ_{res} . We further observe that using deconvolutional layers in the upsampling module introduces checkerboard artifacts, resulting in noisy surfaces in occluded regions. To avoid this, we adopt convolutional and trilinear interpolation-based upsampling layers, which yield smoother and more accurate surface reconstructions.

Table 4: **Architecture of our Indicator Grid Refinement module.** The module consists of a down-sampling block, a 3D U-Net (Çiçek et al., 2016) backbone, and an upsampling block. Starting from the initial indicator grid χ_0 , obtained by applying DPSR to the predicted per-pixel oriented point maps (\mathbf{P} , \mathbf{N}), we first downsample the grid by a factor of 4. The downsampled grid is processed by the 3D U-Net, and then upsampled back to the original resolution to produce the residual indicator grid χ_{res} .

#	Layer Description	Output Dim.
Input		
–	Initial indicator grid χ_0	$D \times H \times W \times 1$
Downsample		
1	$(4 \times 4 \times 4 \text{ conv}, 16 \text{ features, stride } 2), \text{ReLU}$	$\frac{1}{2} D \times \frac{1}{2} H \times \frac{1}{2} W \times 16$
2	$(4 \times 4 \times 4 \text{ conv}, 32 \text{ features, stride } 2), \text{ReLU}$	$\frac{1}{4} D \times \frac{1}{4} H \times \frac{1}{4} W \times 32$
3D U-Net		
3	Encoder: $(3 \times 3 \times 3 \text{ conv}, 32 \text{ features, stride } 1) \times 2$	$\frac{1}{4} D \times \frac{1}{4} H \times \frac{1}{4} W \times 32$
4	Encoder: $(3 \times 3 \times 3 \text{ conv}, 64 \text{ features, stride } 2)$	$\frac{1}{8} D \times \frac{1}{8} H \times \frac{1}{8} W \times 64$
5	Encoder: $(3 \times 3 \times 3 \text{ conv}, 128 \text{ features, stride } 2)$	$\frac{1}{16} D \times \frac{1}{16} H \times \frac{1}{16} W \times 128$
6	Decoder: Upsample $\times 2 + (3 \times 3 \times 3 \text{ conv}, 64 \text{ features, stride } 1) \times 2$	$\frac{1}{8} D \times \frac{1}{8} H \times \frac{1}{8} W \times 64$
7	Decoder: Upsample $\times 2 + (3 \times 3 \times 3 \text{ conv}, 32 \text{ features, stride } 1) \times 2$	$\frac{1}{4} D \times \frac{1}{4} H \times \frac{1}{4} W \times 32$
8	Final $(1 \times 1 \times 1 \text{ conv}, 32 \text{ features, stride } 1)$	$\frac{1}{4} D \times \frac{1}{4} H \times \frac{1}{4} W \times 32$
Upsample		
9	$(3 \times 3 \times 3 \text{ conv}, 16 \text{ features, stride } 1), \text{ReLU}$	$\frac{1}{4} D \times \frac{1}{4} H \times \frac{1}{4} W \times 16$
10	Trilinear Upsample $\times 2$	$\frac{1}{2} D \times \frac{1}{2} H \times \frac{1}{2} W \times 16$
11	$(3 \times 3 \times 3 \text{ conv}, 8 \text{ features, stride } 1), \text{ReLU}$	$\frac{1}{2} D \times \frac{1}{2} H \times \frac{1}{2} W \times 8$
12	Trilinear Upsample $\times 2$	$D \times H \times W \times 8$
13	$(3 \times 3 \times 3 \text{ conv}, 1 \text{ feature, stride } 1)$	$D \times H \times W \times 1$
Output		
–	Residual indicator grid χ_{res}	$D \times H \times W \times 1$



Figure 6: **Qualitative Results on Clothed Mesh Reconstruction from the DNA-Rendering Test Set.** We show one of the 4 input images in row 1 and our reconstructed meshes in row 2. Although trained only on synthetic human scans, our method generalizes effectively to real-world images, producing accurate clothed meshes even under challenging conditions with complex garments and human-object interactions.

Table 5: **Effect of the number of input views.** Performance consistently improves as the number of input views increases across all three tasks. With only 3 views, the reconstructions and renderings already achieve decent scores, but increasing to 4 or more views yields notable gains in geometry completeness, SMPL-X robustness, and novel view fidelity. The best results are obtained with 8 input views, where reconstructions are most complete and renderings most photorealistic.

Number of input views	Clothed Mesh Reconstruction					SMPL-X Estimation		Novel View Synthesis			
	Acc.	Comp.	CD	F-Score	NC	PA-V2V	PA-MPJPE	PSNR	SSIM	LPIPS	FID
3 views	0.0088	0.0130	0.0218	0.9041	0.9057	17.66	18.13	30.46	0.9585	0.0481	22.02
4 views	0.0067	0.0105	0.0172	0.9354	0.9125	16.96	17.67	31.70	0.9675	0.0390	14.24
6 views	0.0049	0.0083	0.0132	0.9611	0.9200	16.87	17.53	34.06	0.9799	0.0244	5.42
8 views	0.0044	0.0077	0.0121	0.9675	0.9229	16.56	17.31	35.11	0.9833	0.0199	4.04

A.3 QUALITATIVE RESULTS FOR CLOTHED MESH RECONSTRUCTION ON DNA-RENDERING

As shown in Fig. 6, our method successfully reconstructs clothed meshes with accurate geometry even in challenging scenarios involving complex garments and human-object interactions, highlighting its robustness across domains.

A.4 ADDITIONAL DETAILS FOR BASELINE SETUPS

We provide additional details for baseline setups for our 3 downstream tasks.

Clothed Mesh Reconstruction. For our method and VGGT (Wang et al., 2025), the predicted geometries are aligned with the ground truth via the Umeyama (Umeyama, 1991) algorithm at the point map level. To ensure fairness under uncalibrated settings, we use the camera parameters estimated by our method rather than ground-truth for LaRa (Chen et al., 2024a) and MATCha (Guédon et al., 2025), and apply the same Umeyama solution to align their predicted meshes with the ground truth. For Puzzle Avatar (Xiu et al., 2024), since the human mesh is optimized in SMPL-X A-pose, we use ground-truth SMPL-X parameters to perform nearest-neighbor SMPL skinning to warp the canonical mesh into posed space, which also roughly aligns the warped clothed mesh with the ground-truth clothed mesh.

SMPL-X Estimation. Both EasyMocap (eas, 2021; Shuai et al., 2022) and MV-SMPLify-X (Pavlakos et al., 2019; Zheng et al., 2021) rely on keypoint fitting. For fair comparisons under uncalibrated settings, we also use the camera parameters estimated by our method for keypoint triangulation and projection.

Note that ETCH (Li et al., 2025) originally does not use shape or pose regularizations during marker fitting. For fair comparison, we also use the same regularizations as in our method.

As with our method, we assume that the global scale of the scene is unknown. Consequently, we also optimize the SMPL-X scale for the baselines. For EasyMocap and Multi-view SMPLify-X, the scale is jointly optimized with the other SMPL-X parameters. In contrast, for ETCH, we observed that optimizing the scale in the same manner fails to converge, likely due to the sparsity of the sampled points it can process. To address this, we first normalize the height of all input meshes to 1.7 m and then optimize the remaining SMPL-X parameters.

Novel View Synthesis. We construct the DNA-Rendering (Cheng et al., 2023) test set using one frame from each of the 47 subjects in parts 0 and 1, excluding 6 subjects interacting with thin-structured objects, thus having unreliable foreground masks. For each subject, we use the 16 horizontal views and use either 4/6/8 views as inputs to our model, while the rest is held out for evaluation. Following (Jin et al., 2025), we re-estimate color correction matrices and obtain improved segmentation masks by voting with multiple segmentation models (Lin et al., 2021; Zheng et al., 2024).

To align our predicted clothed meshes with the ground-truth cameras for the evaluation purpose, we train 2DGS (Huang et al., 2024) on all 16 views and render depths from all these views from the optimized Gaussians. These depth maps serve as pseudo ground-truth for aligning our predicted geometry via Umeyama alignment.

Table 6: **Quantitative results on 6-view and 8-view Novel View Synthesis.** Under higher number of input views, our method still consistently outperform MAtCha on both synthetic and real-world test sets.

Methods	THuman 2.1 (Synthetic)				DNA Rendering (Real World)			
	PSNR	SSIM	LPIPS	FID	PSNR	SSIM	LPIPS	FID
6 input views								
MAtCha (Guédon et al., 2025)	33.08	0.9750	0.0317	7.05	27.44	0.9332	0.0593	29.71
Ours	34.06	0.9799	0.0244	5.42	28.44	0.9449	0.0522	30.42
8 input views								
MAtCha (Guédon et al., 2025)	34.34	0.9810	0.0237	4.50	27.75	0.9389	0.0520	25.04
Ours	35.11	0.9833	0.0199	4.04	28.86	0.9502	0.0455	24.56

Table 7: **Quantitative results on 3-view Novel View Synthesis.** Compared to GHG (Kwon et al., 2024), our method achieves higher PSNR, SSIM, and lower LPIPS, indicating more faithful and perceptually realistic renderings, while GHG attains a slightly lower FID due to its use of a diffusion-based inpainting model.

Methods	THuman 2.1 (Synthetic)			
	PSNR	SSIM	LPIPS	FID
GHG (Kwon et al., 2024)	23.46	0.9181	0.0740	19.04
Ours	27.10	0.9480	0.0574	22.19

A.5 EFFECT OF NUMBER OF INPUT VIEWS

Tab. 5 shows the effect of the number of input views on our method across all 3 downstream tasks. We observe consistent performance gains as the number of input views increases. Even with only 3 views, our method already produces competitive quantitative scores, and adding more views steadily improves the metrics across all tasks. Moving from 3 to 4 views yields clear improvements across all metrics, showing the benefit of increasing viewpoint coverage. With 6 and 8 views, reconstruction errors drop further, SMPL-X estimation becomes more accurate, and novel view synthesis achieves higher fidelity with fewer artifacts. Using 8 views achieves the best overall performance, as denser inputs help resolve occlusions and capture finer details.

For qualitative results on novel view synthesis with different numbers of input views, please refer to Sec. A.6.

A.6 ADDITIONAL RESULTS FOR NOVEL VIEW SYNTHESIS (NVS)

A.6.1 ADDITIONAL COMPARISONS ON DIFFERENT NUMBER OF INPUT VIEWS

As shown in the top part of Fig. 7, we provide additional 4-view NVS results comparing with LaRa (Chen et al., 2024a), SEVA (Zhou et al., 2025b), and MAtCha (Guédon et al., 2025). To further demonstrate robustness under varying numbers of input views, we compare against MAtCha—the most competitive baseline for NVS—under 6- and 8-view settings. The bottom part of Fig. 7 and Tab. 6 show that our method achieves consistent improvements across most metrics on both synthetic and real-world test sets. While MAtCha’s results improve with more views, its quality remains limited by inaccurate geometry initialization from its aligned charts, and its strategy of allowing Gaussians to move more freely (with densification and pruning)¹ makes it more prone to overfitting training views. In contrast, our method leverages accurate clothed-mesh constraints, producing higher-quality and more faithful novel view renderings.

A.6.2 COMPARISON WITH GHG ON 3 INPUT VIEWS

We provide an additional comparison with GHG (Kwon et al., 2024) for novel view synthesis under the 3-view setting. GHG tends to overfit to the training camera distributions and produces misaligned renderings on real-world inputs. For this reason, we restrict the comparison to the THuman test set, using its official test set. Since GHG was trained on only a subset of THuman 2.1 subjects, we train our model on the same reduced set for fairness and evaluate against the released GHG pretrained

¹Although MAtCha paper claims Gaussian positions and covariances are fixed, their official code still optimizes them, and we find that learning all gaussian attributes and enabling gaussian densification/pruning consistently improves their performance.

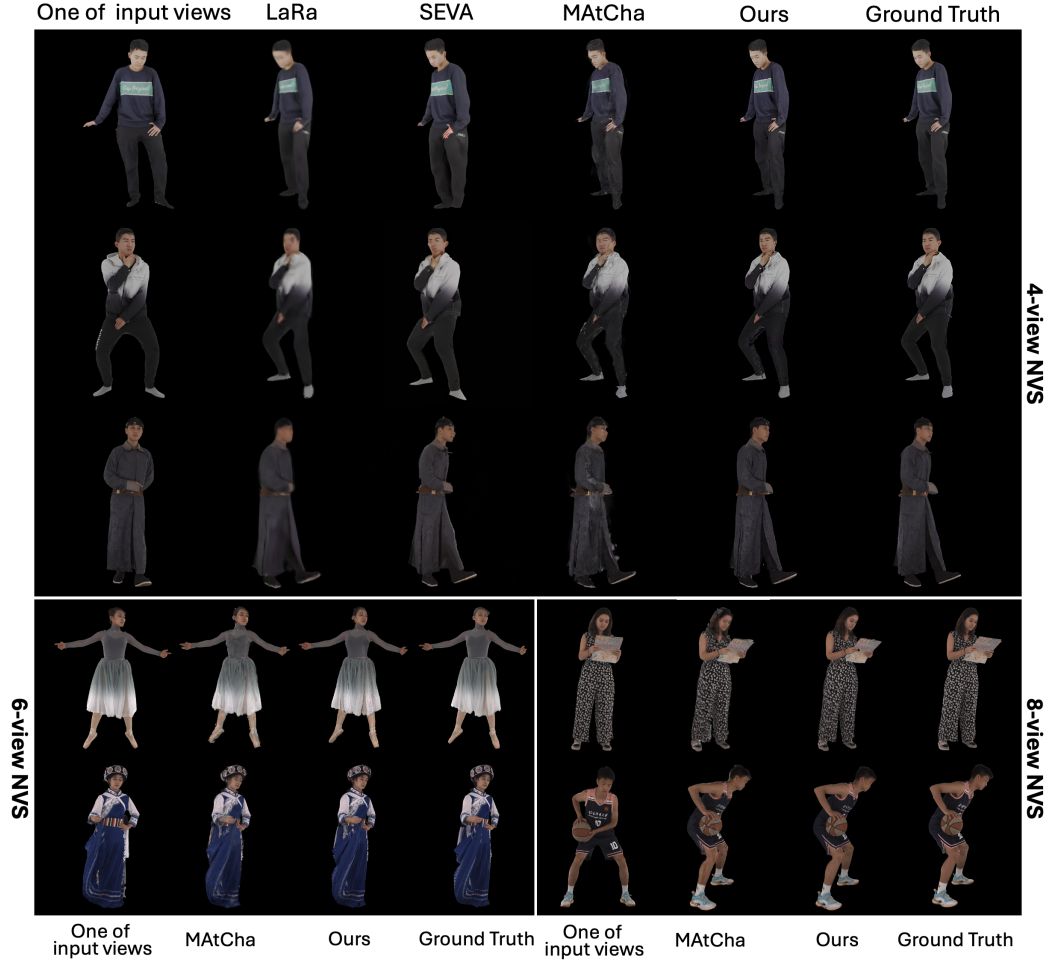


Figure 7: Additional Qualitative Results on 4-view, 6-view and 8-view Novel View Synthesis. We present results on two THuman subjects and one DNA-Rendering subject for 4-view NVS, comparing against LaRa (Chen et al., 2024a), SEVA(Zhou et al., 2025b), and MAtCha(Guédon et al., 2025). As discussed in Fig. 5, our method consistently produces higher-quality renderings than all baselines. We further compare with MAtCha under 6-view and 8-view settings on DNA-Rendering subjects. While MAtCha’s results improve with more input views and achieve photorealistic renderings, it continues to suffer from floating artifacts due to less reliable Gaussian initialization from charts. In contrast, our method delivers renderings that more closely align with the ground truth.

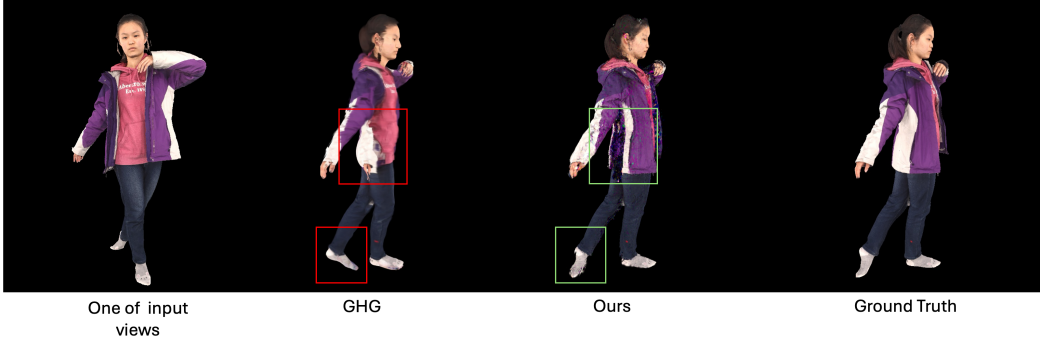


Figure 8: **Qualitative Results on 3-view Novel View Synthesis.** Although GHG produces photo-realistic novel views, it fails to recover the correct body shape in loose garments due to its reliance on SMPL mesh, and it occasionally produces incorrect poses due to errors in SMPL estimation. Our method, on the other hand, recovers the body shape better due to the initialization from more accurate clothed geometry.

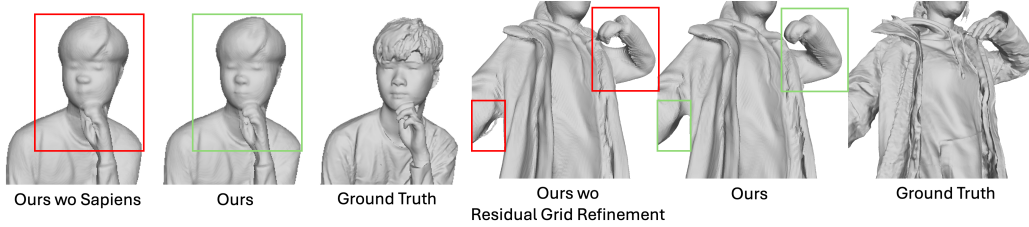


Figure 9: **Ablation Studies.** Removing Sapiens (Khrodkar et al., 2024) normals results in blurrier surfaces, while removing the indicator grid refinement leads to incomplete and less accurate geometry in self-occluded regions. Our full method produces the most detailed, accurate, and complete meshes.

model. As GHG performs best when using ground-truth camera parameters, we adopt the same setup for our method during the novel view synthesis part in this comparison.

As shown in Fig. 8 and Tab. 7, GHG relies on a SMPL body mesh as the template, which struggles to recover accurate body shapes under loose garments, and leads to inaccurate body poses due to errors in SMPL estimations. In contrast, our method renders more faithful body shapes by leveraging a more accurate clothed-mesh initialization.

A.7 ABLATION STUDIES

We ablate our method on two critical design choices. First, we remove the use of the Sapiens model (Khrodkar et al., 2024) for base normal prediction and instead train the network to regress full normal maps from scratch. This variant is denoted as *Ours w/o Sapiens Normals*. Second, we disable the indicator grid refinement and directly reconstruct the mesh from the initial indicator grid χ_0 , obtained from per-pixel oriented point maps. This variant is denoted as *Ours w/o Indicator Grid Refinement*.

As shown in Tab. 8 and Fig. 9, predicting normals entirely from scratch, rather than as residuals to Sapiens normals, results in blurrier surfaces and a clear drop across all metrics. Similarly, removing

Table 8: **Ablation Studies on Clothed Geometry.** Removing either the Sapiens normals or the indicator grid refinement degrades reconstruction accuracy, highlighting their importance.

Methods	Acc.	Comp.	CD	F-Score	NC
Ours w/o Sapiens Normals	0.0074	0.0114	0.0188	0.9253	0.9066
Ours w/o Indicator Grid Refinement	0.0089	0.0138	0.0227	0.9150	0.9012
Ours	0.0067	0.0105	0.0172	0.9354	0.9125

the residual grid refinement reduces the pipeline to standard Poisson-based reconstruction on VGGT (Wang et al., 2025) point maps, which leads to even more significant performance degradation and inaccurate geometry in occluded regions.

A.8 IMPLEMENTATION DETAILS

Our network operates at an input image resolution of 518×518 and an indicator grid resolution of $512 \times 512 \times 512$. We finetune the model from the pretrained VGGT-1B checkpoint, using an initial learning rate of $1e-4$ for the SMPL-X branch (trained from scratch) and $1e-5$ for the remaining modules, with cosine decay down to a minimum of $1e-6$. To stabilize training, we apply gradient norm clipping at 0.5. For efficiency, we use bfloat16 precision and gradient checkpointing to reduce GPU memory usage. Unlike VGGT, we additionally freeze the DINO encoder to further save memory. To improve the generalization on different numbers of input views, we randomly alternate between 3 to 8 views during training. We train the network for 20 epochs with 10,000 steps per epoch, which takes approximately 50 hours with 8 NVIDIA L40S GPUs.

Our SMPL-X marker fitting uses a Gauss–Newton optimizer similar to (Li et al., 2025), implemented with the Levenberg–Marquardt algorithm (Roweis, 1996). The optimization is performed in two stages: in the first stage, we optimize the poses along with the first two shape coefficients, and in the second stage, we additionally optimize the remaining shape coefficients. Thanks to the lightweight marker formulation, the entire fitting procedure converges within only a few seconds.

Following (Guédon et al., 2025), our geometry-informed novel view synthesis optimizes the 2D gaussians for 7,000 steps, which takes approximately 5 minutes on a single L40S GPU.

A.9 LLM USAGE DISCLOSURE

In this manuscript, we use LLMs for grammar polishing and sentence-level structure refinement.