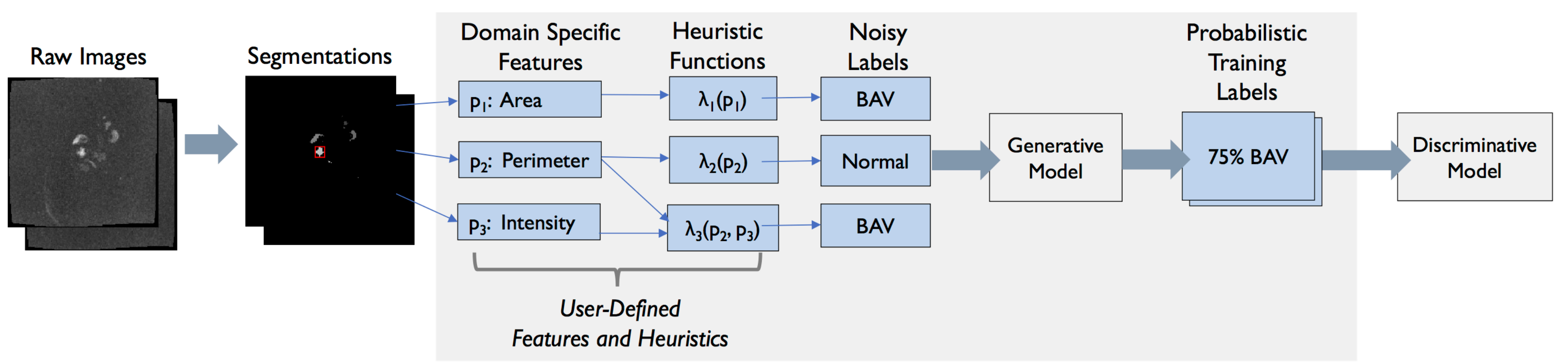


# Automated Training Label Generation for Aortic Valve Classification

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## Weak Supervision Pipeline



## Summary

- **Context:** Bicuspid aortic valve (BAV) is the most prevalent malformation of the heart, affecting 1% of the population
- **Problem:** The lack of labeled data makes developing automated methods challenging
- **Method:** Use weak-supervision to learn a generative model [1] over aortic valve images to produce probabilistic training labels for end models

## Heuristic Functions (HFs)

Create user-defined heuristic functions based on domain knowledge about features

Example HF (area/perimeter ratio):

```
ratio = area / (perimeter**2)
def lambda_ratio(ratio):
    if ratio >= 0.072:
        return 1
    if ratio <= 0.062:
        return -1
    return 0
```

## Weak Supervision Paradigm

- Write user-defined heuristic functions (HFs) over geometric features of images
- Learn relationships between HFs, features, and latent class labels to generate probabilistic labels

## Generative Model

- Learn accuracies and correlations among HFs **using no labeled data**
- Model dependencies as shared / correlated inputs

HF Evaluation Results

HF	Coverage	AUC	Accuracy	F1 score
$\lambda_{\text{area}}$	0.2231	0.6071	0.5064	0.3937
$\lambda_{\text{perimeter}}$	0.1696	N/A	0.1754	0.2985
$\lambda_{\text{ratio}}$ (defined ↑)	0.6339	0.5973	0.6291	0.3525
$\lambda_{\text{intensity}}$	0.1190	0.6379	0.4750	0.4324
$\lambda_{\text{eccentricity}}$	0.7143	0.5873	0.6438	0.3241

## Limited Labeled Dataset

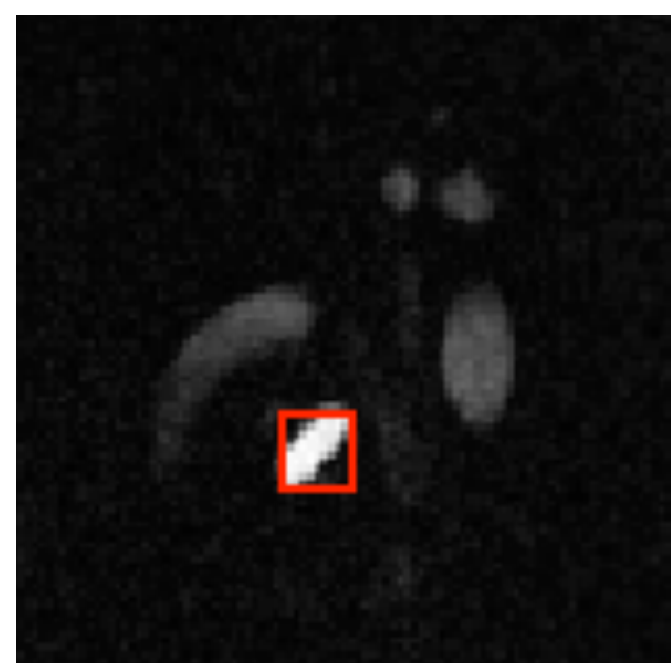
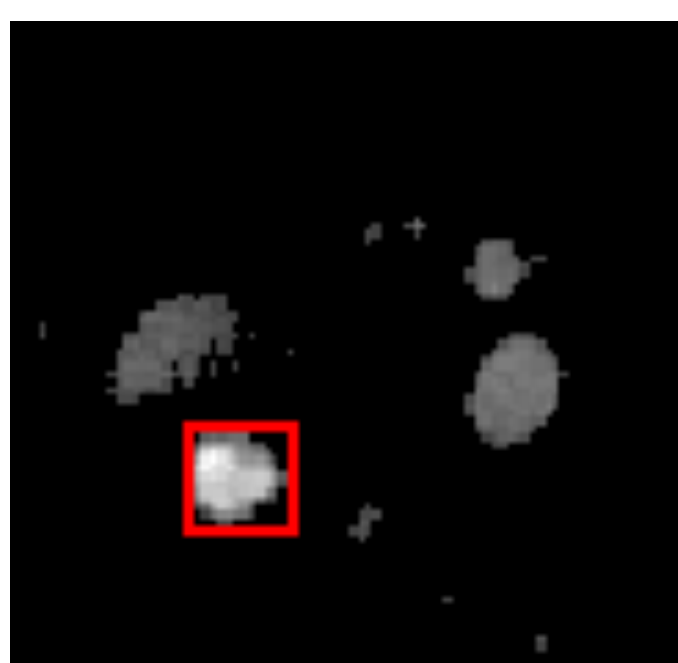
- **Phase-contrast MRI** targets the aortic valve, showing areas of higher flow with greater intensity
- **UK Biobank (UKBB)** released a dataset of 100,000 adult cardiac MRI sequences
- In collaboration with cardiologists, we **hand-labeled 112 samples** (10.7% BAV)

## Feature Extraction

- Preprocess images to isolate regions of interest
- Extract **geometric features** (e.g. area, intensity, eccentricity) from labeled regions

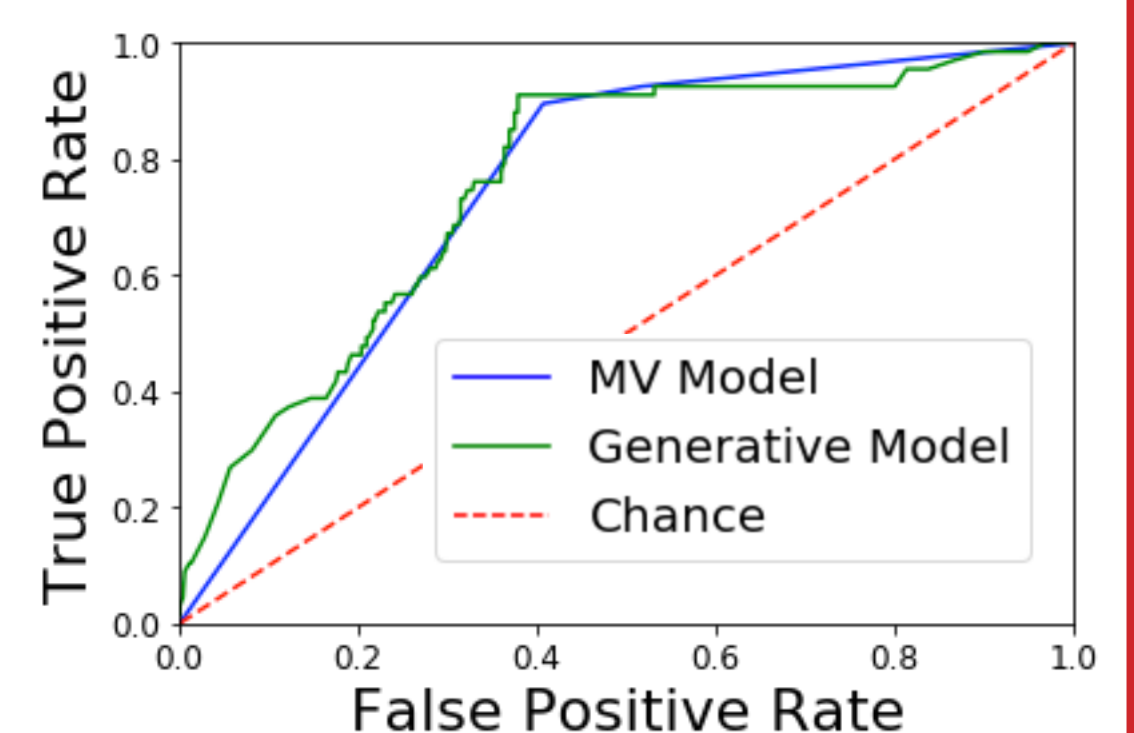
Normal

BAV



## Results

Our generative model sees improvements over majority vote (MV):  
+ 1.33 AUC  
+ 17.24% accuracy



## Future Work

- Fine-tune weak supervision in conjunction with CNN for full classification pipeline
- Perform genome-wide association studies (GWAS) based on BAV classification labels