

# Multiclass Domain Adaptation via Iterative Manifold Alignment

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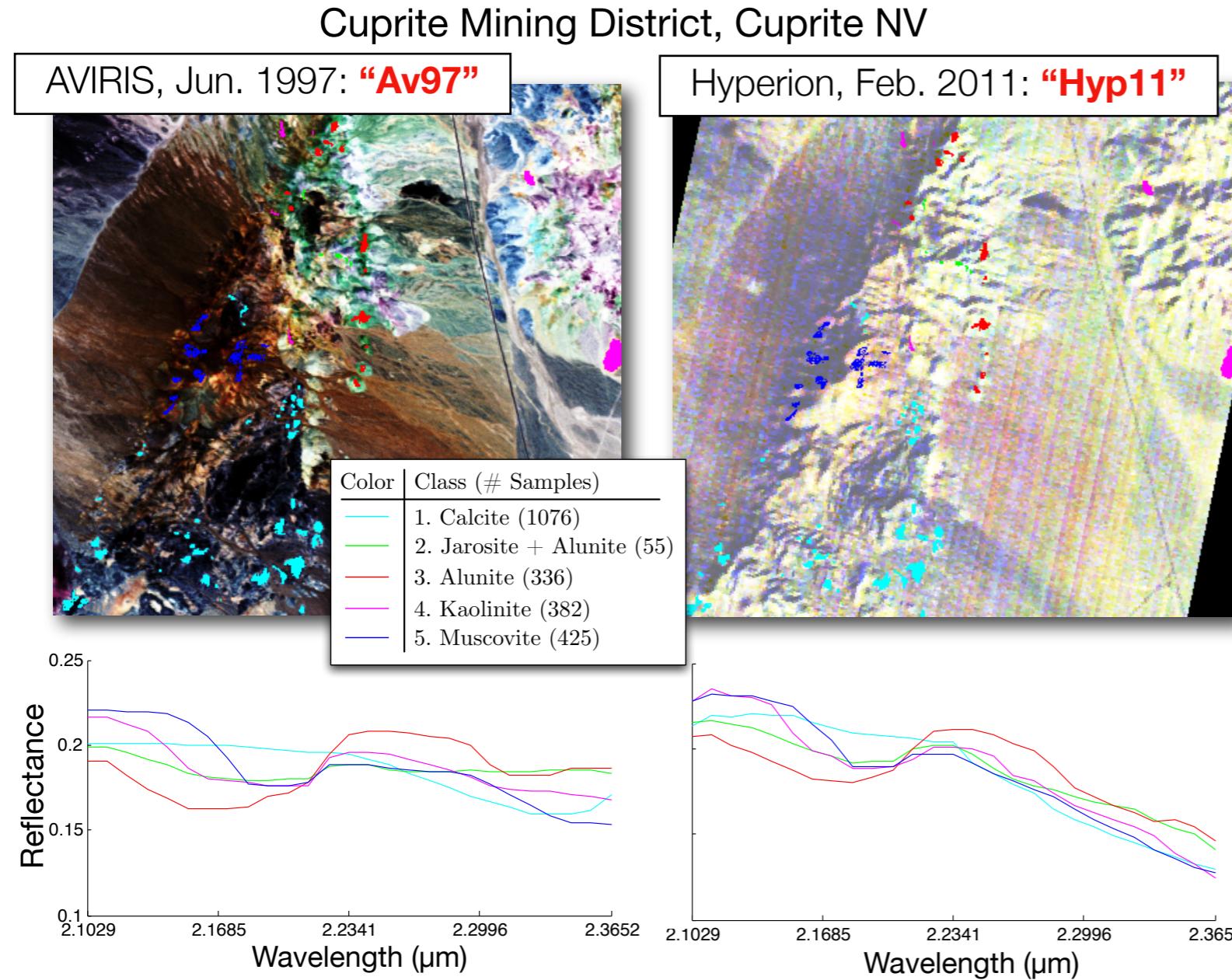
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WHISPERS 2013, Gainesville FL, USA



# Hyperspectral Image Classification Leveraging Multiple Imaging Domains\*

Representative samples for classes of interest often unavailable  
⇒ Can we use spectra captured under **similar** conditions?



**Spectra reflect their capture conditions**

- atmospheric conditions
- seasonal effects
- sensor resolution (spatial + spectral)
- viewing geometry
- different regions
- ...

⇒ Poor generalization using a classifier trained with Av97 spectra to Hyp11 spectra (and vice versa)

# Contributions in this Paper

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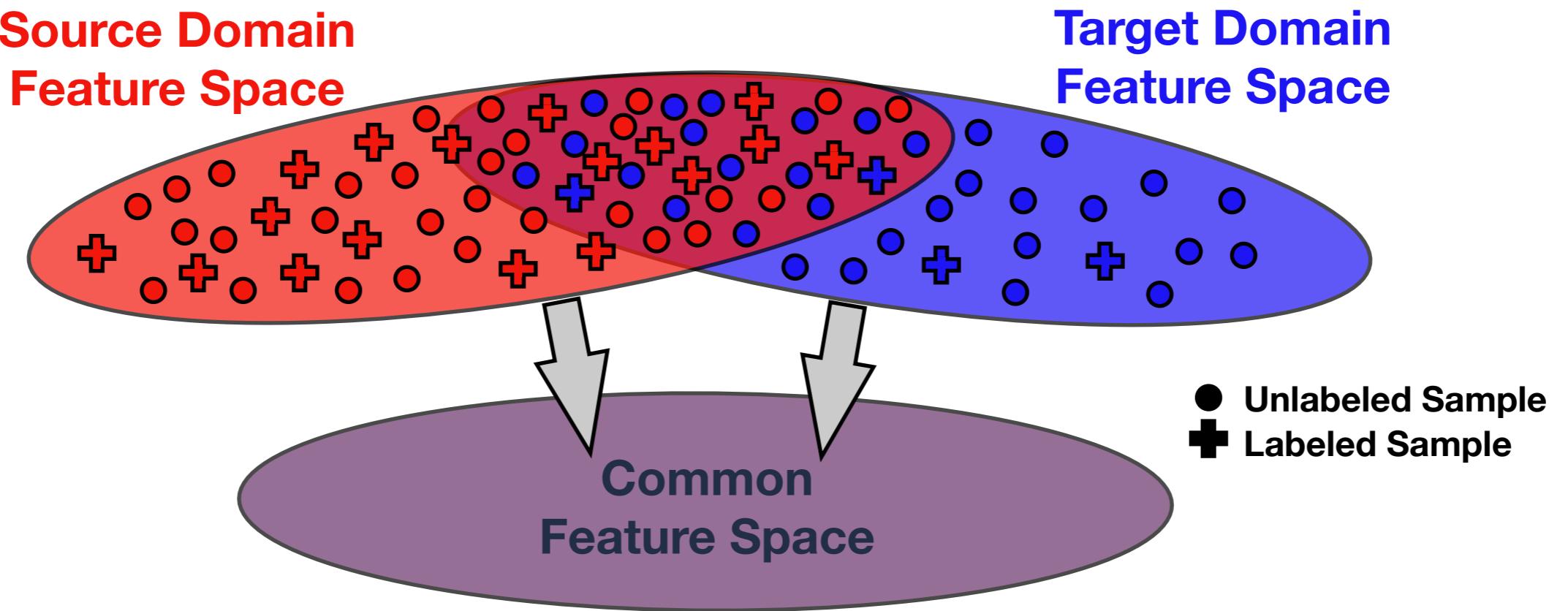
- ▶ Novel methodology for **multiclass, unsupervised** domain adaptation applied to hyperspectral image classification
  - ▶ Extends TRIAL protein alignment algorithm [Venkateswaran et al., 2010] to high-dimensional, multiclass manifold alignment problems
  - ▶ Learns **per-class** linear transformations based on samples representing classes shared between the domains
- ▶ Demonstrate algorithm on real-world AVIRIS and Hyperion images of Cuprite, NV
- ▶ Provide a MATLAB implementation available online at:

<http://tinyurl.com/martial-code>

# Background: Domain Adaptation

**Domain<sup>\*</sup> Adaptation:** improve source to target generalization by reconciling domain-specific differences

\*domain=set of spectra captured under identical conditions



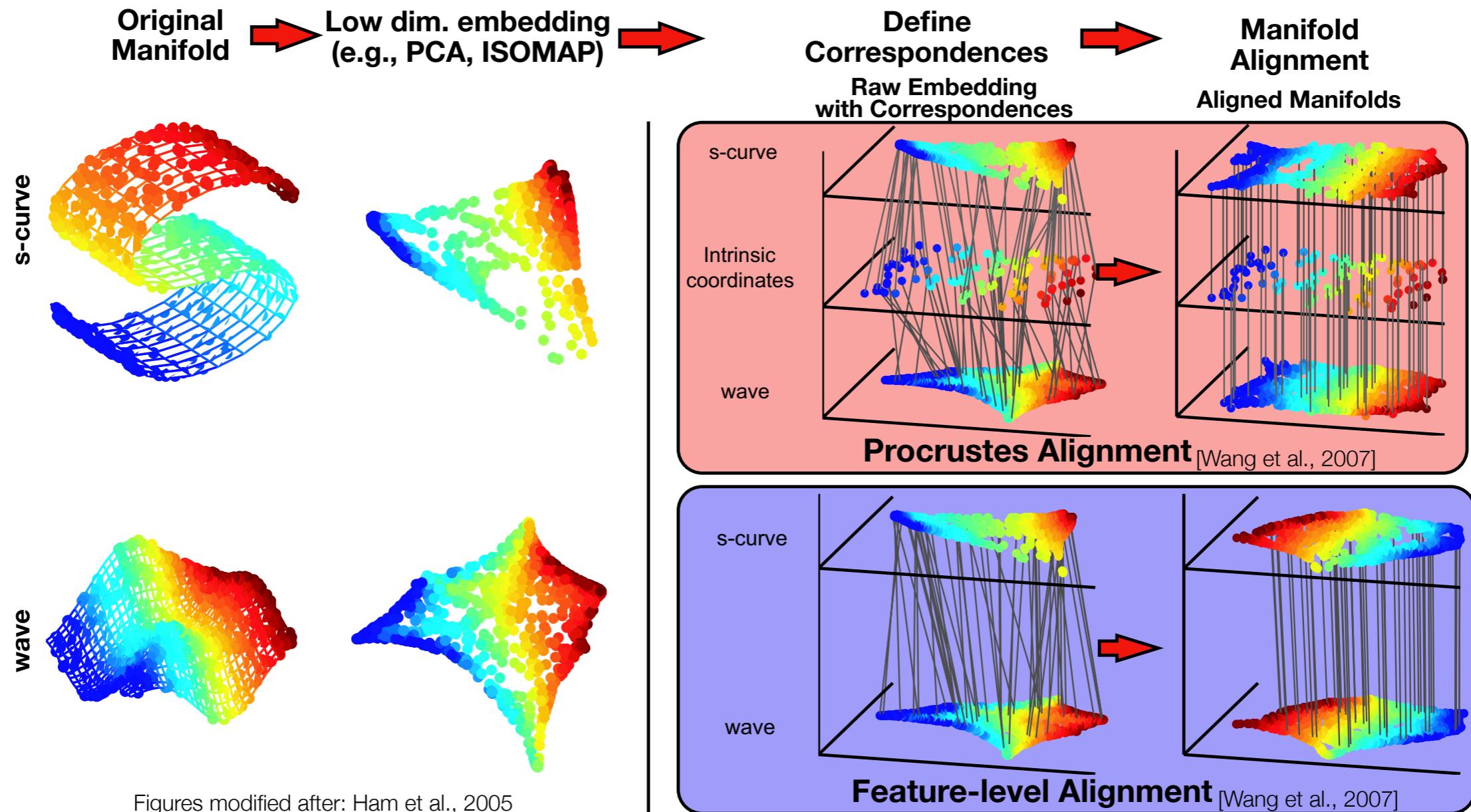
## Contexts:

- I. **Supervised:** small amount of labeled target data available
- II. **Unsupervised:** no labeled target data available ← **this talk**

# Background: Manifold Alignment

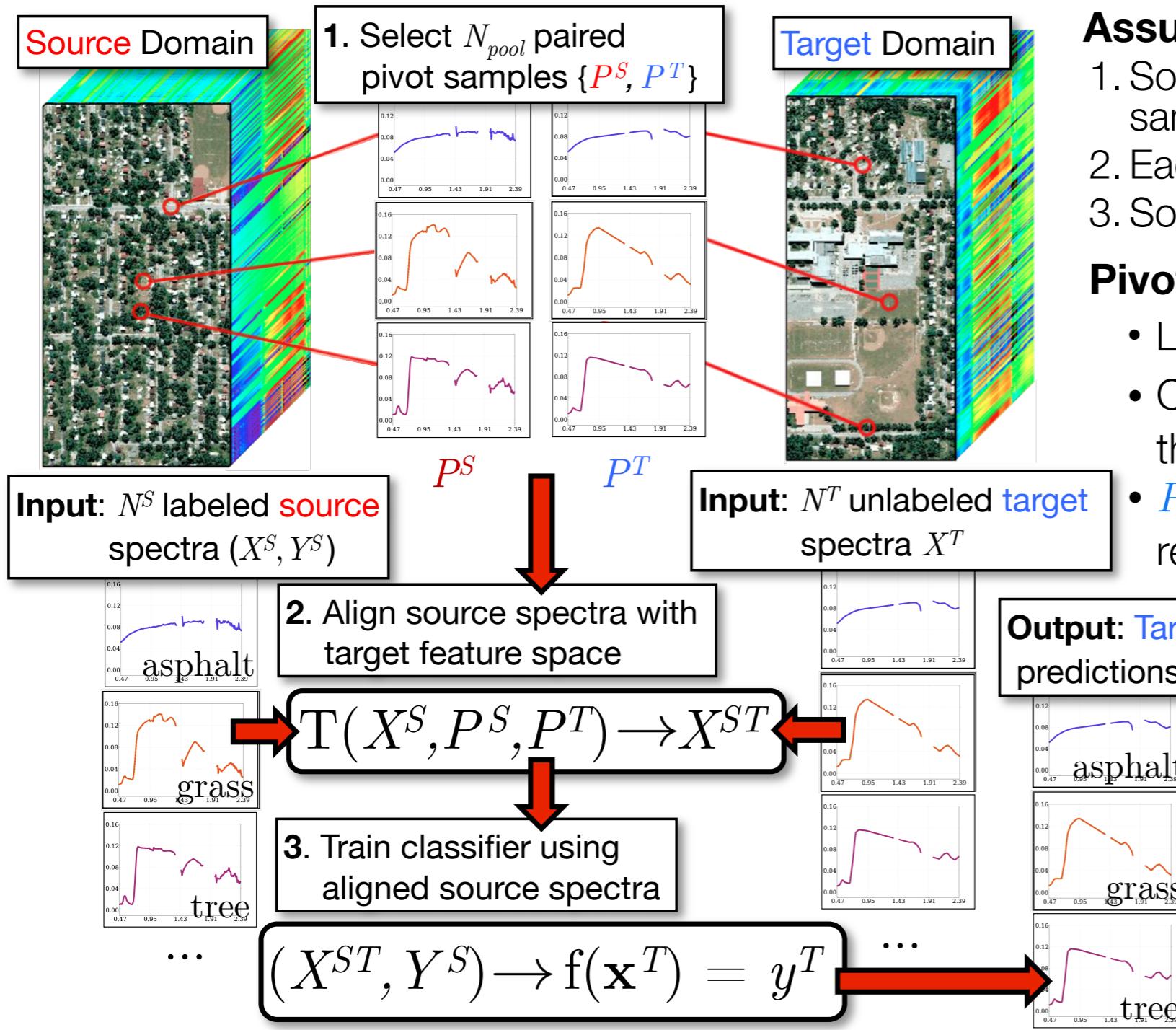
[Ham et. al, 2005, Wang et al., 2007]

**Manifold Alignment:** computes mapping(s) to align source and target feature spaces



- Successfully applied to hyperspectral image classification problems [Yang et al., WHISPERS 2011]
- Existing approaches: **supervised** and learn a **single** transform between manifolds

# MAnifold Reconciliation Through Iterative ALignment (MARTIAL) Framework



## Assumptions:

1. Source / target spectra convolved to same wavelengths
2. Each spectrum scaled by its  $L^2$  norm
3. Source and target domains “similar”\*

## Pivot Samples:

- Labeled pairs of the form:  $(\mathbf{p}^S, \mathbf{p}^T, y^P)$
- Choose (e.g., from labels)  $P^S \subset X^S$  that characterize source classes
- $P^T \subset X^T$  automatically selected to reflect structure of  $P^S$

\* “similar”  $\Rightarrow$  better than random error on target domain with source-trained classifier

# Automatic Pivot Selection Relational (“R-space”) Transformation

[Bue et al., WHISPERS 2010-2011]

For sample  $\mathbf{x}^D$  and pivot set  $P^D$  from domain  $D \in \{S, T\}$ ,  
map  $\mathbf{x}^D$  from  $\mathcal{R}^n \rightarrow \mathcal{R}^Q$  according to

$$R(\mathbf{x}^D, P^D) = \left( \frac{d(\mathbf{x}^D, \mathbf{p}_1^D)}{\sum_{\ell=1}^Q d(\mathbf{x}^D, \mathbf{p}_\ell^D)}, \dots, \frac{d(\mathbf{x}^D, \mathbf{p}_Q^D)}{\sum_{\ell=1}^Q d(\mathbf{x}^D, \mathbf{p}_\ell^D)} \right)$$

where

$$d(\mathbf{x}^D, \mathbf{p}^D) = \|\mathbf{x}^D - \mathbf{p}^D\|_2^*$$

$$Q = \sum_{k=1}^K Q_k$$

$Q_k$  = # of pivots for class  $k$

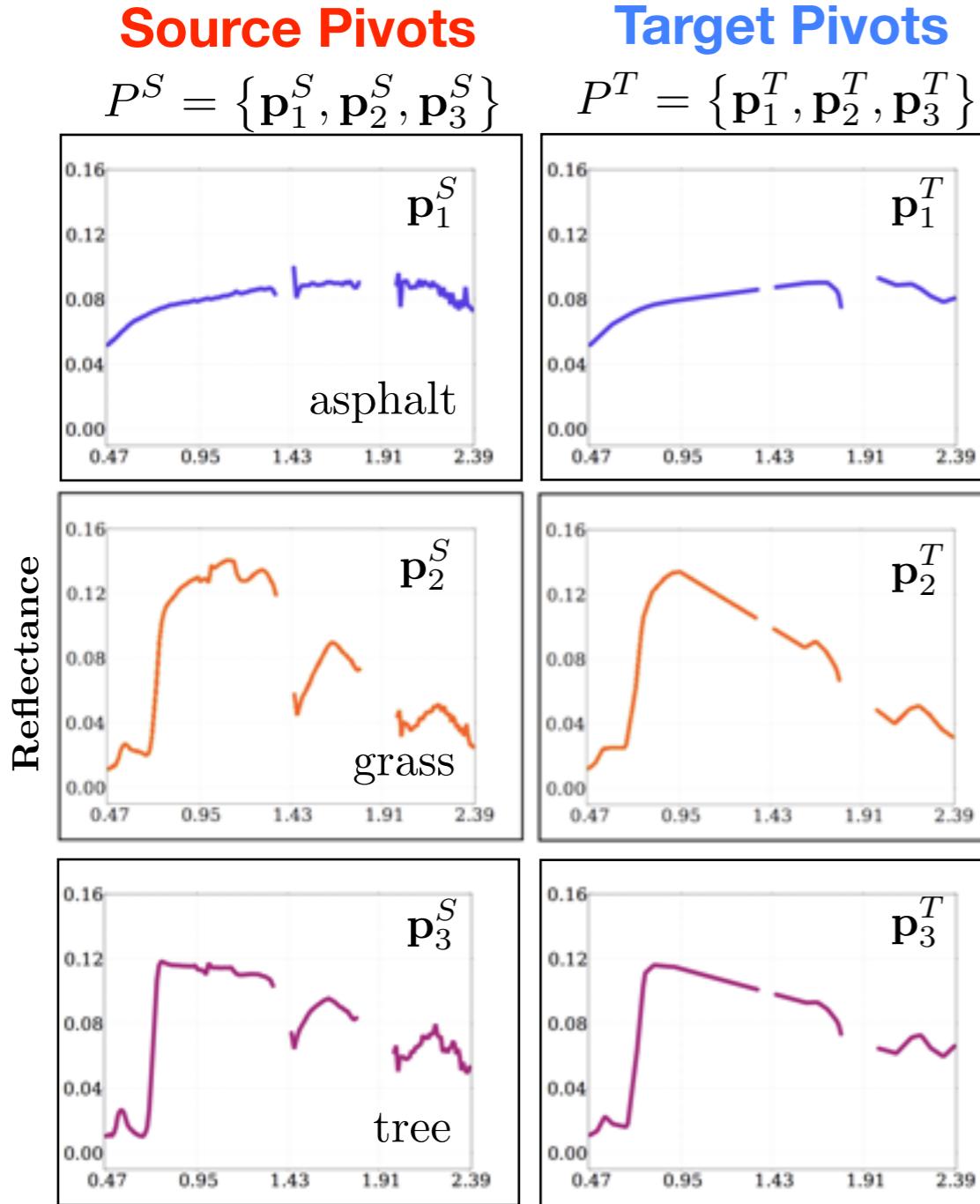
→  $l^{\text{th}}$  entry of  $R(\mathbf{x}^D, \mathbf{p}^D)$  = likelihood of distinguishing  $\mathbf{x}^D$  and  $\mathbf{p}_l^D$  from other pivots  $P^D$

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\*  $\mathbf{x}^D = \mathbf{x}^D / \|\mathbf{x}^D\|_2 \Rightarrow d(\mathbf{x}^D, \mathbf{p}^D) \Rightarrow$  spectral angle between  $\mathbf{x}^D$  and  $\mathbf{p}^D$

# Automatic Pivot Selection Relational (“R-space”) Transformation

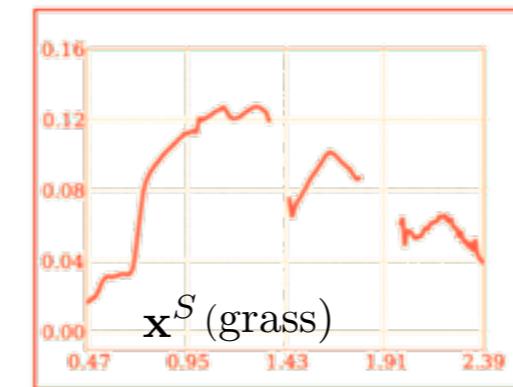
**Example:** number of classes  $K=3$ , pivots per class  $Q_k=1$



## R-transform

$$R(\mathbf{x}^D, P^D) = \left( \frac{d(\mathbf{x}^D, \mathbf{p}_1^D)}{\sum_{\ell=1}^Q d(\mathbf{x}^D, \mathbf{p}_\ell^D)}, \dots, \frac{d(\mathbf{x}^D, \mathbf{p}_Q^D)}{\sum_{\ell=1}^Q d(\mathbf{x}^D, \mathbf{p}_\ell^D)} \right)$$

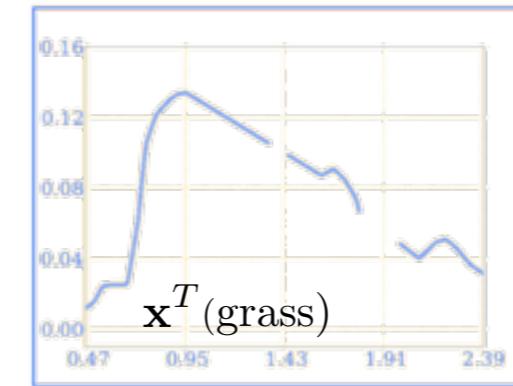
## Source Spectrum



$$R(\mathbf{x}^S, P^S)$$

$$R(\mathbf{x}^T, P^T)$$

## Target Spectrum



**Domain-specific Feature Space**

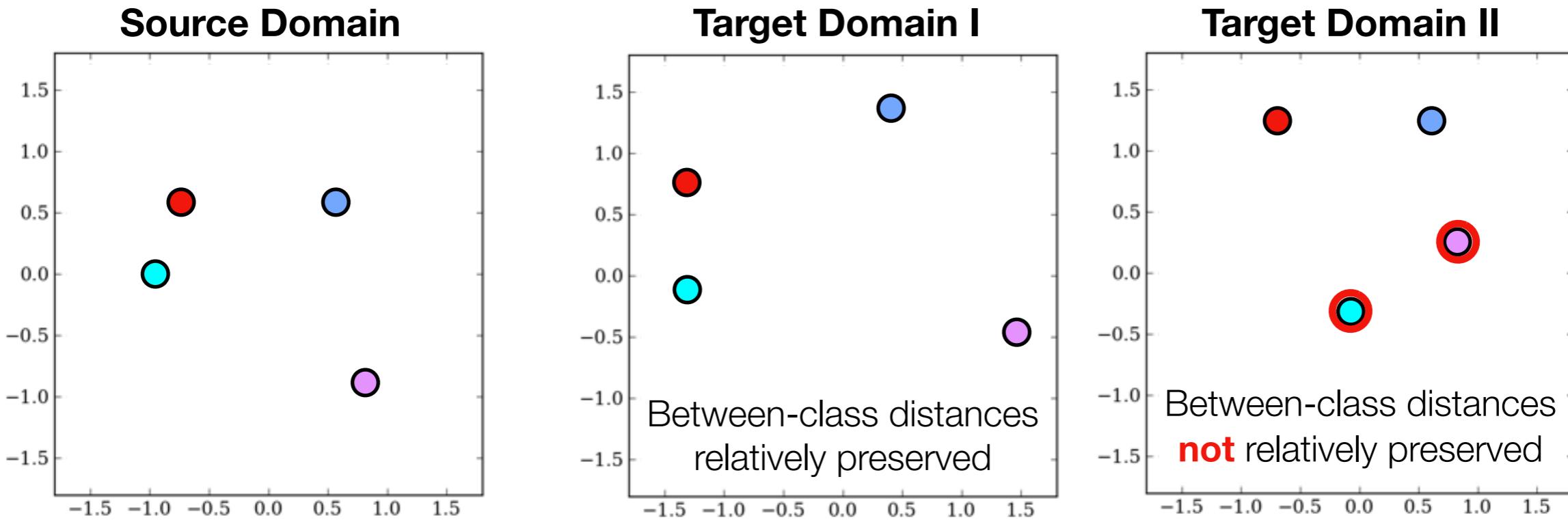
**Common Feature Space**

# Automatic Pivot Selection

[Bue and Thompson, NIPS  
Domain Adaptation workshop 2011]

## Multiclass Continuous Correspondence Learning (MCCL)

Assume between-class distances **relatively preserved** across domains



### Unsupervised Pivot Selection with MCCL:

For each source pivot  $\mathbf{p}_i^S$  in  $P^S$ , select *unique* target pivot  $\mathbf{p}_i^T = \mathbf{x}_\ell^T$  s.t.

$$\ell = \underset{j}{\operatorname{argmin}} \|R(\mathbf{p}_i^S, P^S) - R(\mathbf{x}_j^T, P^S)\|, \quad j \in \{1, \dots, N^T\}$$

# Mapping Source to Target Manifold

## Kabsch Algorithm / Procrustes Analysis

Given  $Q$  paired samples  $(P^S, P^T) = \{(\mathbf{p}_i^S, \mathbf{p}_i^T)\}_{i=1}^Q$

the transformation matrix  $\mathbf{T}$  minimizing

$$\varepsilon = \text{RMSD}^*(\mathbf{T} \cdot P^S, P^T)$$

is computed as follows

$$\mathbf{T} = \mathbf{W} \text{diag}(\mathbf{s}) \mathbf{V}^T$$

where

$$\mathbf{V} \mathbf{D} \mathbf{W}^T = \text{SVD}(\text{COV}(P^S, P^T))$$

$$\mathbf{s} = [1, \dots, 1, \text{sign}(\det(\mathbf{W} \mathbf{V}^T))]$$

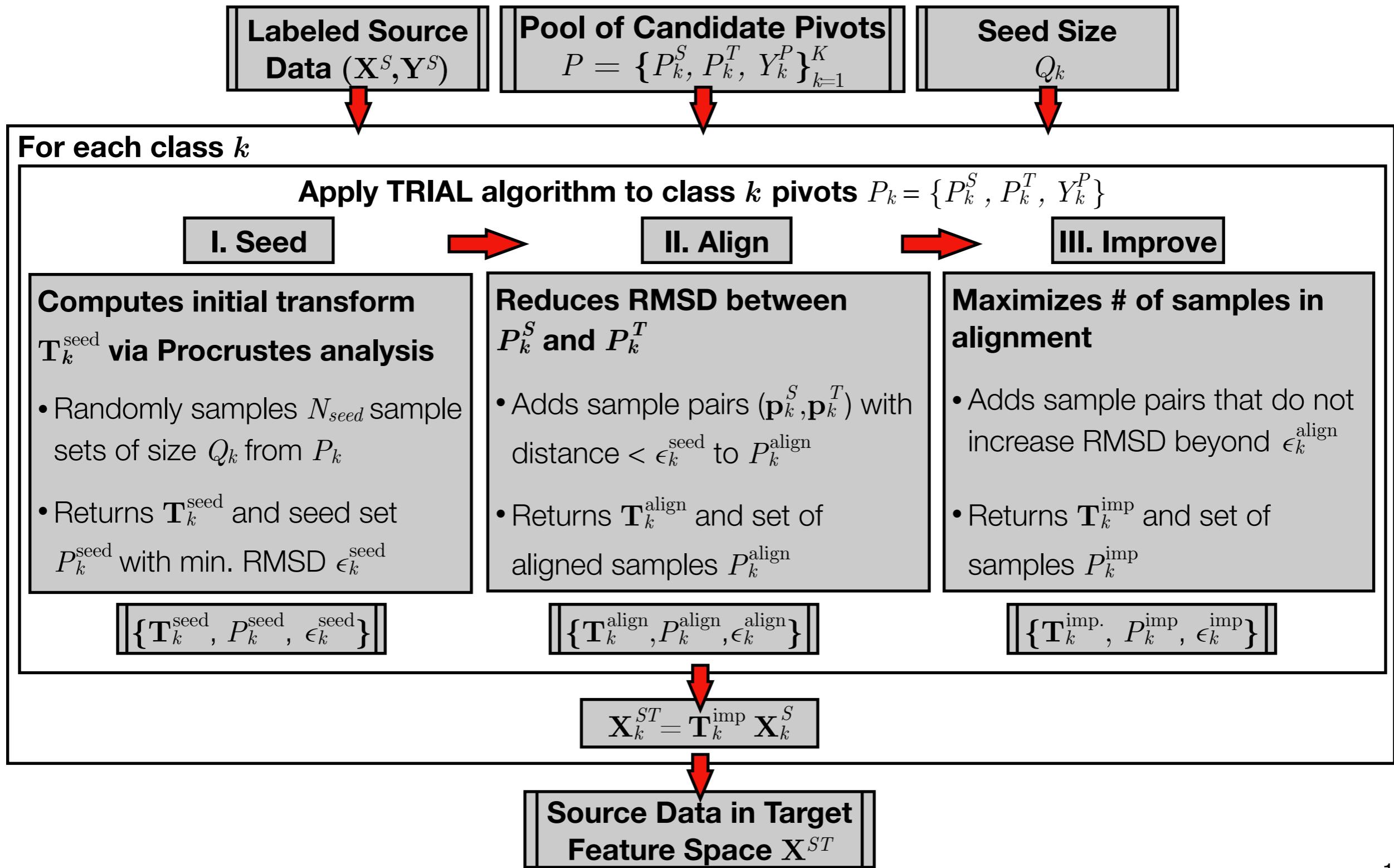


A Procrustean Transformation

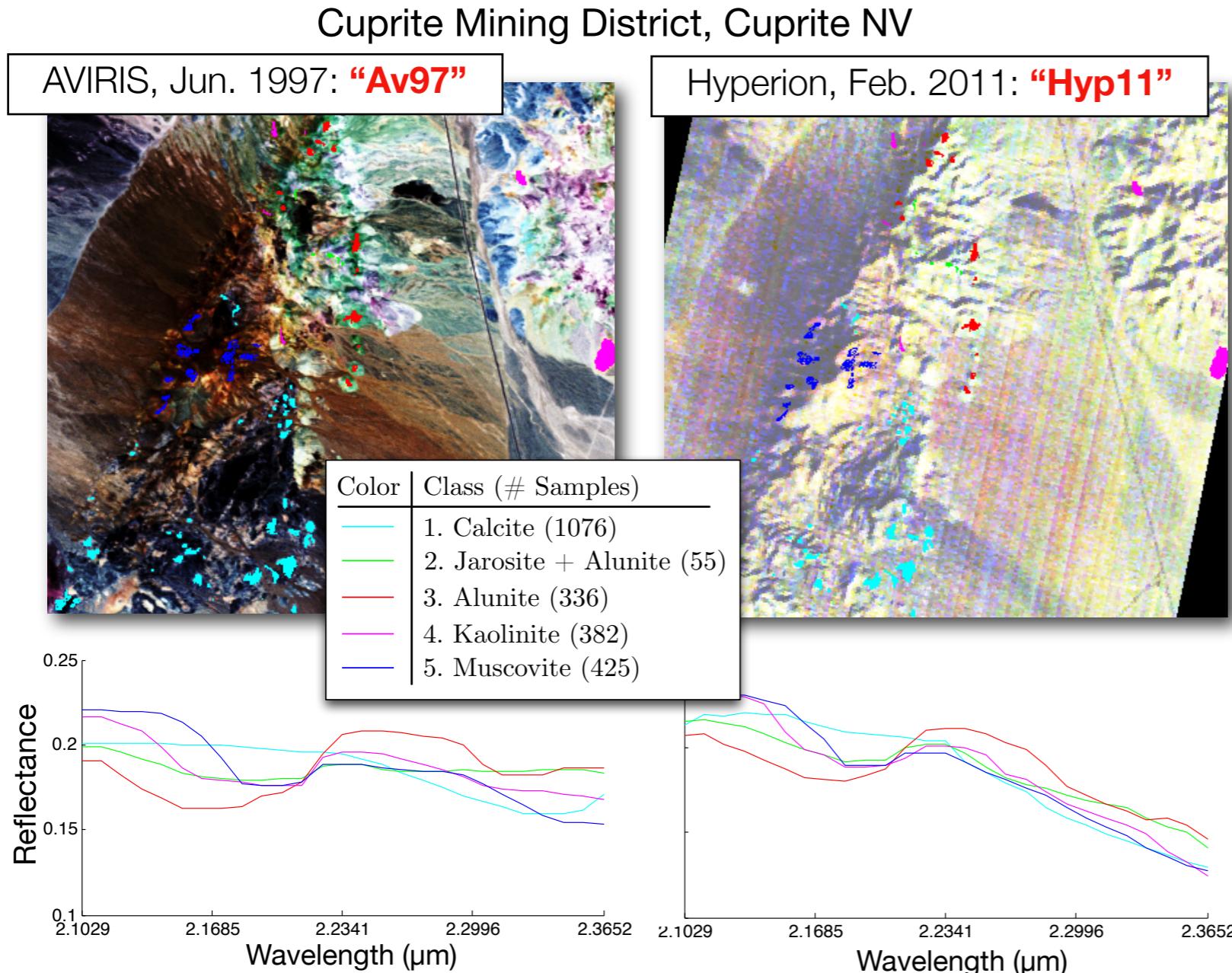
Credit: <http://www.mythweb.com/>

\*RMSD = Root Mean Square Deviation

# Aligning Source and Target Manifolds: Computing Per-class Transformations with TRIAL



# Cuprite, NV Imagery and Evaluation Methodology

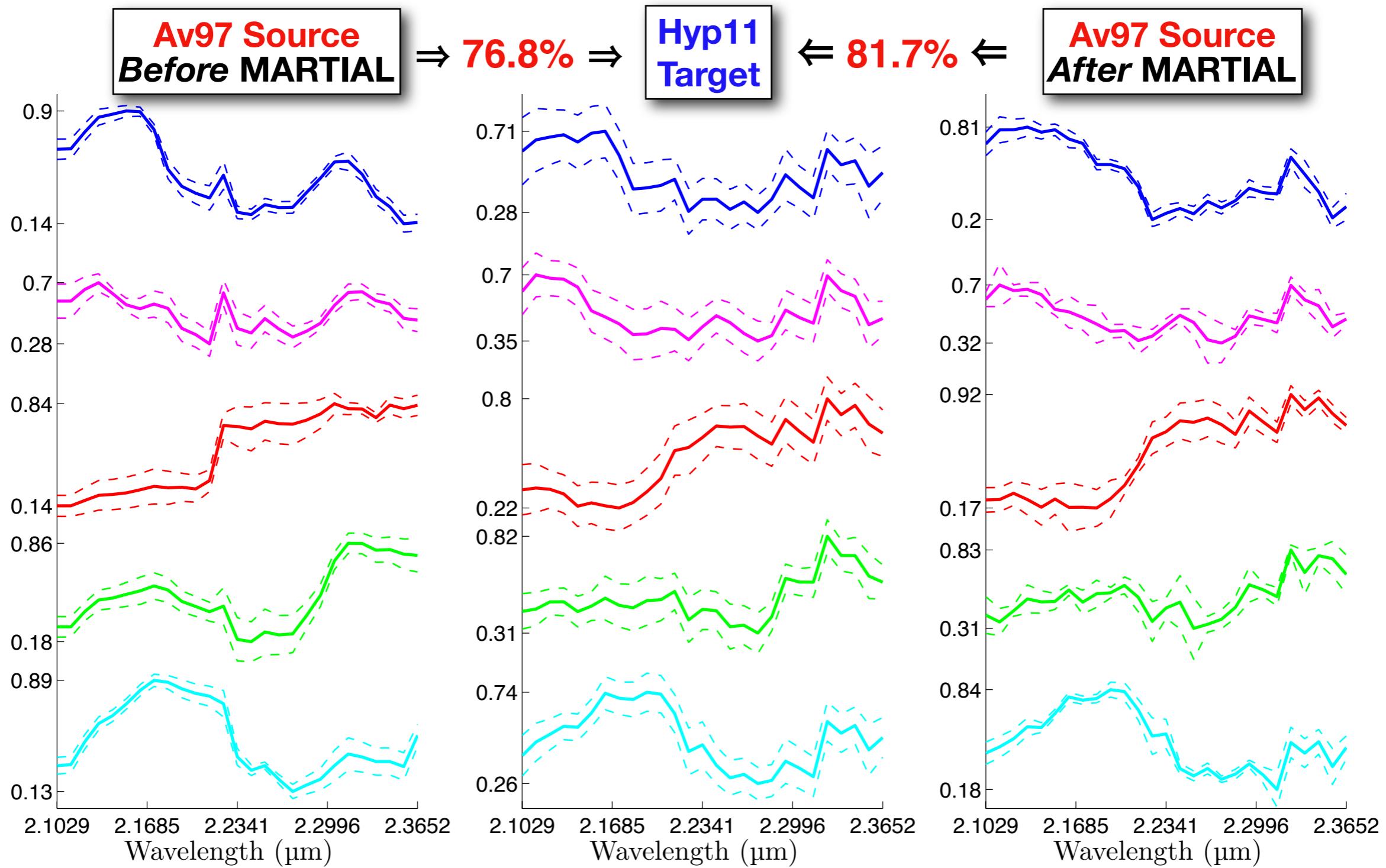


- ▶ Atmospheric compensation with ELM
- ▶ Each spectrum scaled by its  $L^2$  norm

- ▶ Scenarios:
  - ▶  $\text{Av97} \Rightarrow \text{Hyp11}$
  - ▶  $\text{Hyp11} \Rightarrow \text{Av97}$
- ▶ Classifier: linear SVM with 5-fold cross-validation
  - ▶ SVM C selected via cross-validation
- ▶ Compare to:
  - ▶ ST=source-to-target with no alignment
  - ▶ Procrustes alignment (single transform) using target pivots

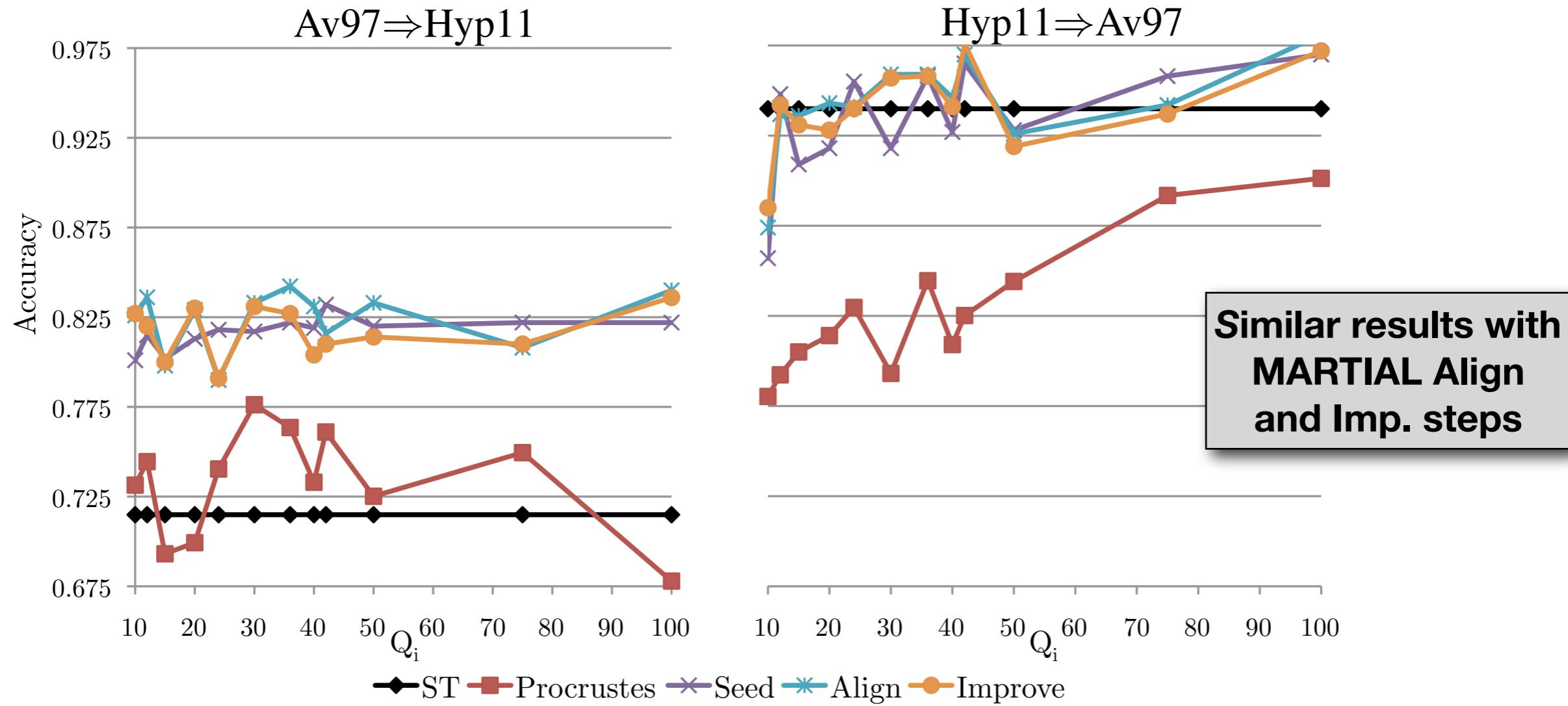
# Cuprite, NV Results

## Av97 $\Rightarrow$ Hyp11 classes before/after MARTIAL



# Cuprite, NV Results

## MARTIAL Accuracy vs. $Q_k$



Average Accuracy (%)	ST	Proc.	Seed	Align	Imp.
Av97 $\Rightarrow$ Hyp11	71.49	73.29	81.69	82.35	81.67
Hyp11 $\Rightarrow$ Av97	93.99	82.75	93.43	94.28	94.05

10%+ improvement over baseline (ST)

no degradation / small improvement

Procrustes (single transform) alignment susceptible to pivot misalignment

# Unsupervised Domain Adaptation

## Intraclass Distance and Domain Adaptation Accuracy

**Why >10% difference in Av97⇒Hyp11 vs. Hyp11⇒Av97 accuracy?**

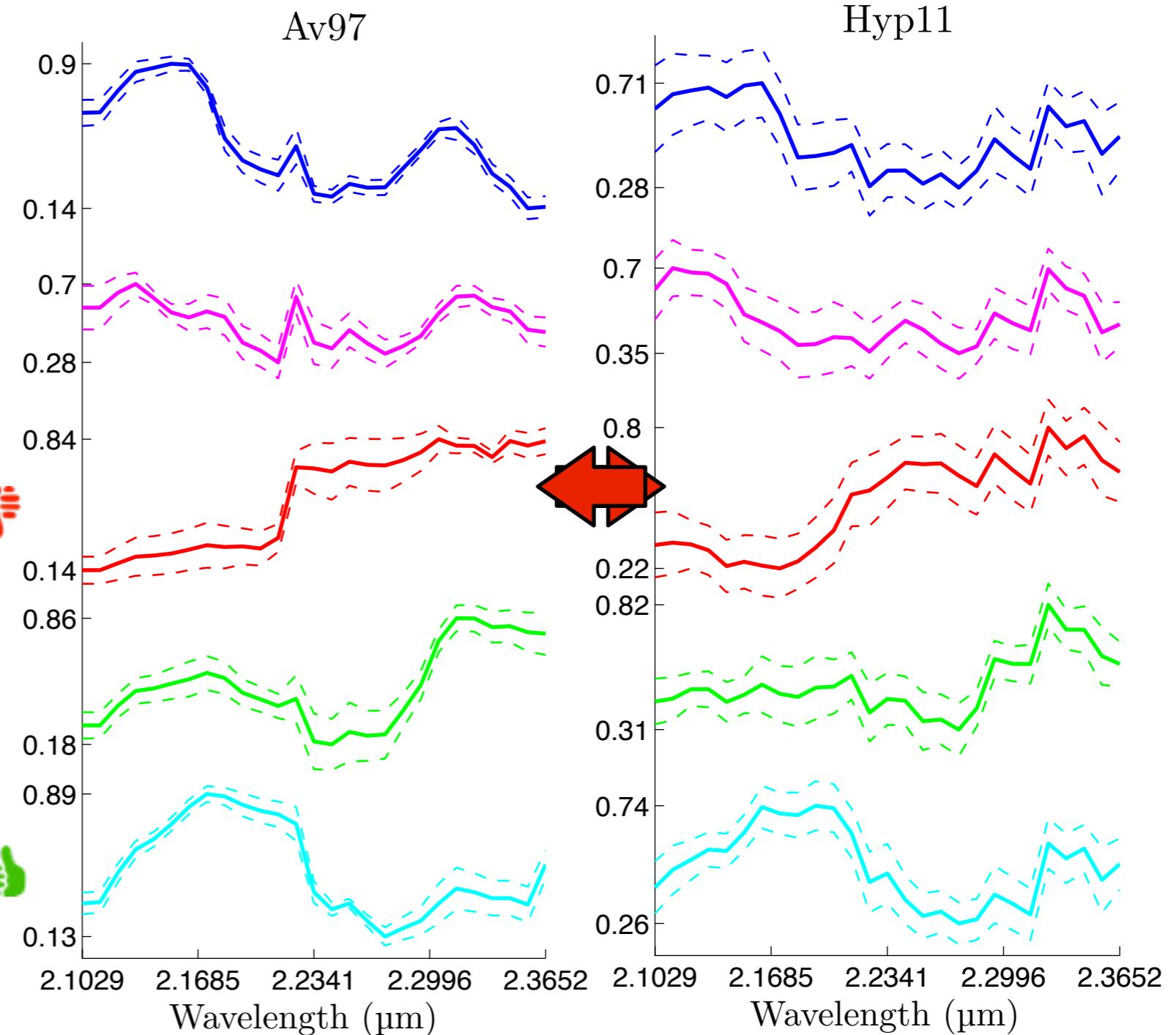
Accuracy limited by the amount of target variance the source-selected pivots can explain

Av97⇒Hyp11

Low source class variance +  
High target class variance =  
Source⇒Target accuracy = **Low** 🚫

Hyp11⇒Av97

High source class variance +  
Low target class variance =  
Source⇒Target accuracy = **High** 🤗



# Summary and Future Work

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- ▶ Proposed the **MARTIAL** algorithm for **unsupervised, multiclass** domain adaptation
  - ▶ Extended TRIAL protein alignment algorithm to high-dimensional, unsupervised manifold alignment problems
- ▶ Computing per-class transforms often more robust to misalignments than a single source-to-target transform
- ▶ Domain adaptation performance limited by similarity and separability of source and target domains
- ▶ Future work:
  - ▶ Analyze results using MARTIAL align and improve steps
  - ▶ Assess pivot misalignment vs. prediction accuracy
- ▶ MATLAB code available at: <http://tinyurl.com/martial-code>

Thank you 