3D Computer Vision

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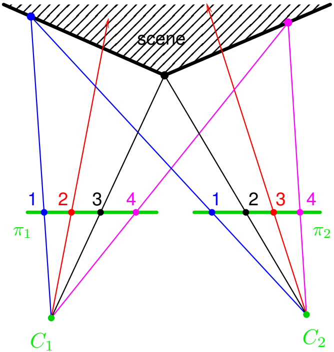
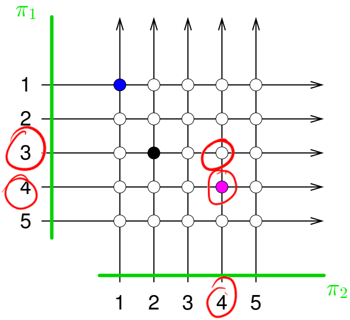
Open Informatics Master's Course

►Matching Table

Based on scene opacity and the observation on mutual exclusion we expect each pixel to match at most once.



rays in epipolar plane



matching table T

matching table

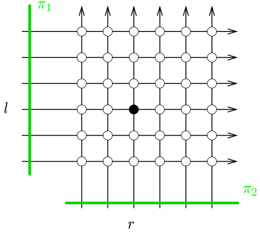
- rows and columns represent optical rays
- nodes: possible correspondence pairs
- full nodes: matches
- numerical values associated with nodes: descriptor similarities

see next

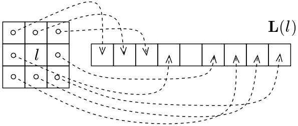
▶Constructing An Image Similarity Cost

- let $p_i = (l, r)$ and $\mathbf{L}(l)$, $\mathbf{R}(r)$ be (left, right) image descriptors (vectors) constructed from local image neighborhood windows

in matching table T:



'block' in the left image ↦ 'signal sample':



- a simple block similarity is $\mathrm{SAD}(l, r) = \|\mathbf{L}(l) - \mathbf{R}(r)\|_1$ L_1 metric (sum of absolute differences)
- a scaled-descriptor similarity is $\mathrm{sim}(l, r) = \dfrac{\|\mathbf{L}(l) - \mathbf{R}(r)\|^2}{\sigma_I^2(l, r)}$ SSD smaller is better
- σ_I^2 – the difference scale; a suitable (plug-in) estimate is $\frac{1}{2}\left[\mathrm{var}\big(\mathbf{L}(l)\big) + \mathrm{var}\big(\mathbf{R}(r)\big)\right]$, giving

$$\mathrm{sim}(l, r) = 1 - \underbrace{\frac{2\,\mathrm{cov}\big(\mathbf{L}(l), \mathbf{R}(r)\big)}{\mathrm{var}\big(\mathbf{L}(l)\big) + \mathrm{var}\big(\mathbf{R}(r)\big)}}_{\rho(\mathbf{L}(l), \mathbf{R}(r))} \tag{34}$$

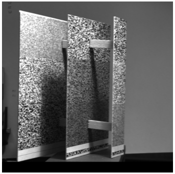
$\mathrm{var}(\cdot)$, $\mathrm{cov}(\cdot)$ is sample (co-)variance, not invariant to scale difference

- ρ – MNCC – Moravec's Normalized Cross-Correlation statistic bigger is better [Moravec 1977]

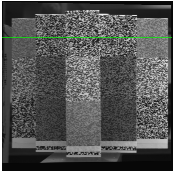
$$\rho^2 \in [0, 1], \qquad \mathrm{sign}\,\rho \sim \text{'phase'}$$

How A Scene Looks in The Filled-In Matching Table

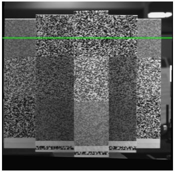
scene



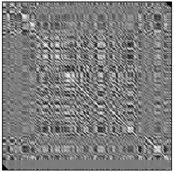
left image



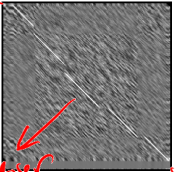
right image



5×5 window

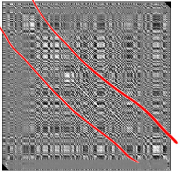


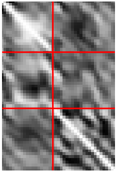
11×11 window



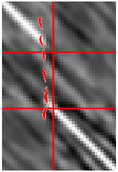
closer

3×3 window

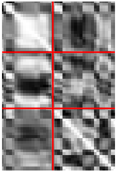




a good tradeoff



occlusion artefacts



undiscriminable

- MNCC ρ used ($\alpha = 1.5,\ \beta = 1$) →175
- high-correlation structures correspond to scene objects

constant disparity

- a diagonal in matching table
- zero disparity is the main diagonal   nonstd rectification

depth discontinuity

- horizontal or vertical jump in matching table

large image window

- better correlation
- worse occlusion localization

repeated texture

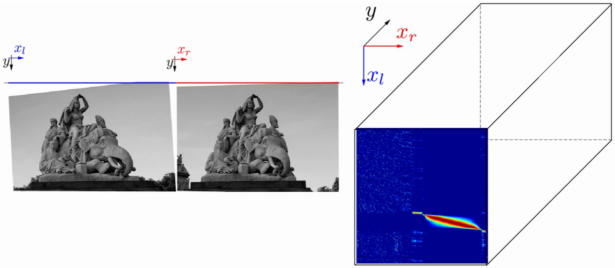
- horizontal and vertical block repetition

Image Point Descriptors And Their Similarity

Descriptors: Image points are tagged by their (viewpoint-invariant) physical properties:

- texture window [Moravec 77]
- a descriptor like DAISY [Tola et al. 2010]
- learned descriptors
- reflectance profile under a moving illuminant
- photometric ratios [Wolff & Angelopoulou 93-94]
- dual photometric stereo [Ikeuchi 87]
- polarization signature
- ...

- similar points are more likely to match
- image similarity values for all 'match candidates' give the 3D matching table

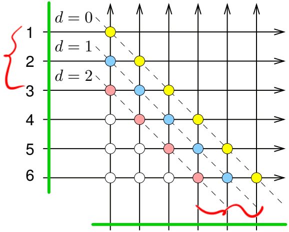


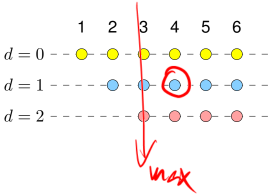
video

►Marroquin's Winner Take All (WTA) Matching Algorithm

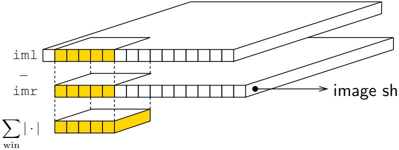
Alg: Per left-image pixel: The most SAD-similar pixel along the right epipolar line →168

1. select disparity range — this is a critical weak point
2. represent the matching table diagonals in a compact form





3. use an 'image sliding & cost aggregation algorithm'



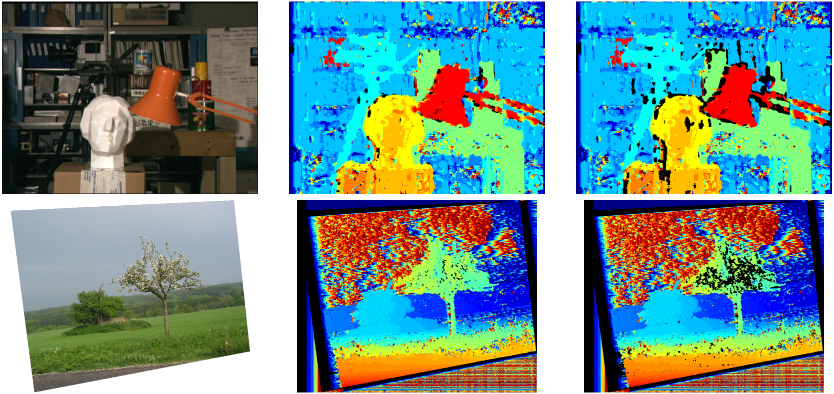
4. take the maximum over disparities d
5. threshold results by maximal allowed SAD dissimilarity

A Matlab Code for WTA

```
function dmap = marroquin(iml, imr, disparityRange)
%       iml, imr - rectified gray-scale images
% disparityRange - non-negative disparity range

% (c) Radim Sara (sara@cmp.felk.cvut.cz) FEE CTU Prague, 10 Dec 12

 thr = 20;                                          % bad match rejection threshold
 r = 2;
 winsize = 2*r+[1 1];                               % 5x5 window (neighborhood) for r=2
 N = boxing(ones(size(iml)), winsize);              % the size of each local patch is
                                                    % N = (2r+1)^2 except for boundary pixels

 % --- compute dissimilarity per pixel and disparity --->

 for d = 0:disparityRange                           % cycle over all disparities
  slice = abs(imr(:,1:end-d) - iml(:,d+1:end));     % pixelwise dissimilarity (unscaled SAD)
  V(:,d+1:end,d+1) = boxing(slice, winsize)./N;     % window aggregation
 end

 % --- collect winners, threshold, output disparity map --->

 [cmap,dmap] = min(V,[],3);                         % collect winners and their dissimilarities
 dmap(cmap > thr) = NaN;                            % mask-out high dissimilarity pixels
end % of marroquin

function c = boxing(im, wsz)
 % if the mex is not found, run this slow version:
 c = conv2(ones(1,wsz(1)), ones(wsz(2),1), im, 'same');
end % of boxing
```

WTA: Some Results

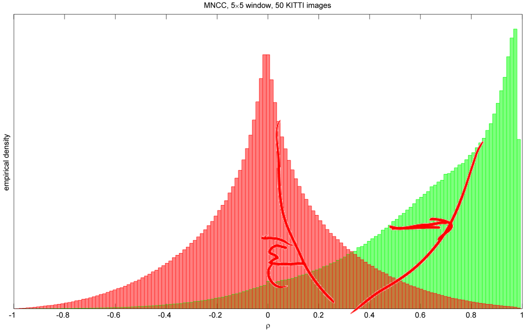
thr = 20 thr = 10



- results are fairly bad
- false matches in textureless image regions and on repetitive structures (book shelf)
- a more restrictive threshold (thr = 10) does not work as expected
- we searched the true disparity range, results get worse if the range is set wider
- chief failure reasons:
  - unnormalized image dissimilarity does not work well
  - no occlusion model (it just ignores the occlusion structure we have discussed →166)

▶A Principled Approach to Similarity

Empirical Distribution of MNCC ρ for Matches (green) and Non-Matches (red)



- histograms of ρ computed from 5×5 correlation window

ρ: bigger is better

- KITTI dataset
  - $4.2 \cdot 10^6$ ground-truth (LiDAR) matches for $p_1(\rho)$ (green),
  - $4.2 \cdot 10^6$ random non-matches for $p_0(\rho)$ (red)

Obs:

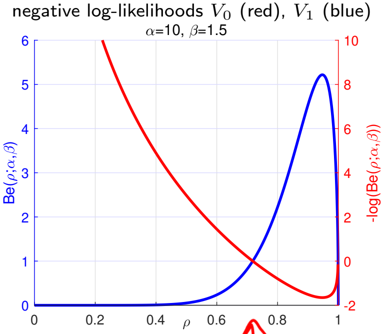
- non-matches (red) may have arbitrarily large ρ
- matches (green) may have arbitrarily low ρ
- $\rho = 1$ is improbable for matches

Match Likelihood

- ρ is just a normalized measurement
- we need a probability distribution on $[0, 1]$, e.g. Beta distribution

$$p_1(\rho) = \frac{1}{B(\alpha, \beta)} \, |\rho|^{\alpha-1} (1 - |\rho|)^{\beta-1}$$

- note that uniform distribution is obtained for $\alpha = \beta = 1$
- when $\alpha = 2$ and $\beta = 1$ then $p_1(\cdot) = 2|\rho|$



- the mode is at $\sqrt{\frac{\alpha-1}{\alpha+\beta-2}} \approx 0.9733$ for $\alpha = 10,\ \beta = 1.5$
- if we chose $\beta = 1$ then the mode was at $\rho = 1$
- perfect similarity is 'suspicious' (depends on expected camera noise level)
- from now on we will work with negative log-likelihood cost

$$V_1\big(\rho(l, r)\big) = -\log p_1\big(\rho(l, r)\big) \qquad \text{smaller is better} \tag{35}$$

- we should also define similarity (and negative log-likelihood $V_0(\rho(l, r))$) for non-matches

▶A Principled Approach to Matching

- given matching M what is the likelihood of observed data D?
- data – all cost pairs (V_0, V_1) in the matching table T
- matches – pairs $p_i = (l_i, r_i), \quad i = 1, \ldots, n$
- matching: partitioning matching table T to matched M and excluded E pairs

$$T = M \cup E, \quad M \cap E = \emptyset$$

- matching cost (negative log-likelihood, smaller is better)

$$V(D \mid M) = \sum_{p \in M} V_1(D \mid p) + \sum_{p \in E} V_0(D \mid p)$$

green red

$V_1(D \mid p)$ – negative log-probability of data D at matched pixel p (35)
$V_0(D \mid p)$ – ditto at unmatched pixel p →174 and →175

- matching problem

$$M^* = \arg \min_{M \in \mathcal{M}(T)} V(D \mid M)$$

$\mathcal{M}(T)$ – the set of all matchings in table T

- symmetric: formulated over pairs, invariant to left ↔ right image swap unlike in WTA

▸(cont'd) Log-Likelihood Ratio

- we need to reduce matching to a standard polynomial-complexity problem
- convert the matching cost to an 'easier' sum

$$
\begin{aligned}
V(D \mid M) &= \sum_{p \in M} V_1(D \mid p) + \sum_{p \in E} V_0(D \mid p) + \overbrace{\sum_{p \in M} V_0(D \mid p) - \sum_{p \in M} V_0(D \mid p)}^{0} \\
&= \sum_{p \in M} \underbrace{\Big(V_1(D \mid p) - V_0(D \mid p)\Big)}_{-L(D \mid p)} + \underbrace{\sum_{p \in E} V_0(D \mid p) + \sum_{p \in M} V_0(D \mid p)}_{\sum_{p \in T} V_0(D \mid p) = \text{const}}
\end{aligned}
$$

- hence

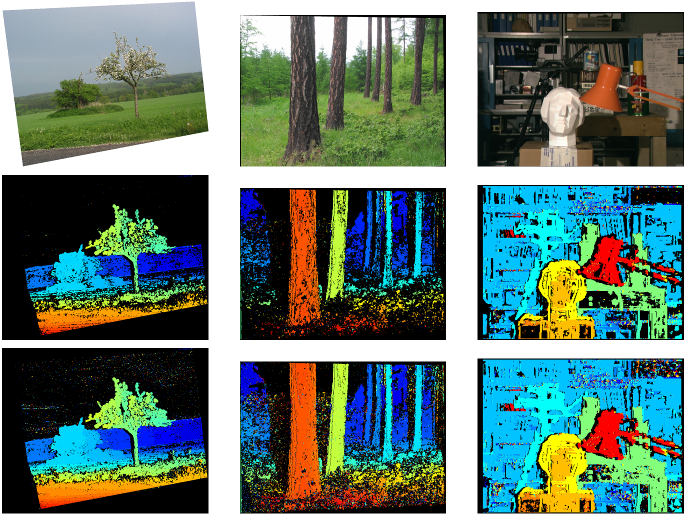
$$
\arg \min_{M \in \mathcal{M}(T)} V(D \mid M) = \boxed{\arg \max_{M \in \mathcal{M}(T)} \sum_{p \in M} L(D \mid p)} \tag{36}
$$

$L(D \mid p)$ – logarithm of matched-to-unmatched likelihood ratio (bigger is better)

why this way: we want to use maximum-likelihood but our measurement is all data D

- (36) is max-cost matching (maximum assignment) for the maximum-likelihood (ML) matching problem
  - use Hungarian (Munkres) algorithm and threshold the result with T: $L(D \mid p) > T \geq 0$
  - or step back: sacrifice symmetry to speed and use dynamic programming

Some Results for the Maximum-Likelihood (ML) Matching



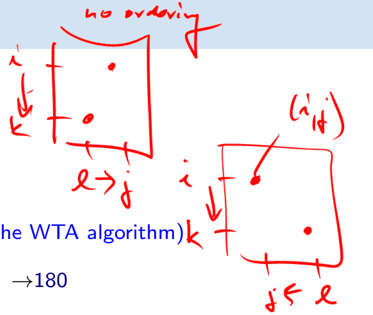
T threshol

- unlike the WTA we can efficiently control the density/accuracy tradeoff

black = no match

- middle row: threshold T for $L(D \mid p)$ set to achieve error rate of 3% (and 61% density results)
- bottom row: threshold T set to achieve density of 76% (and 4.3% error rate results)

▶Basic Stereoscopic Matching Models

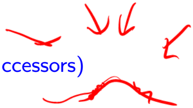


- notice many small isolated errors in the ML matching
- Q: how to reduce the noisiness? A: a stronger model

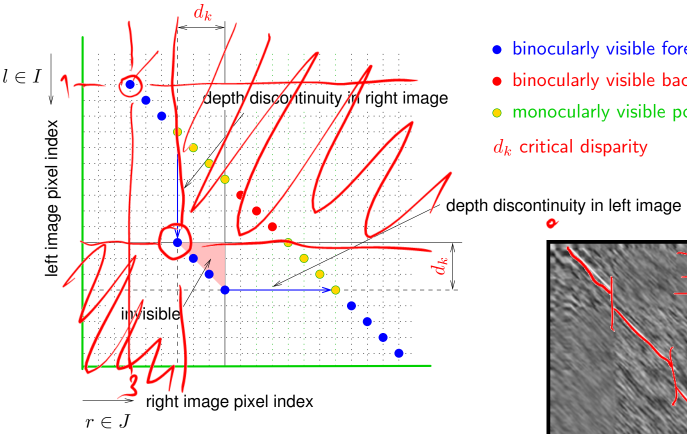
Potential models for M (from weaker to stronger)

1. Uniqueness: Every image point matches at most once
   - excludes semi-transparent objects
   - used in the ML matching algorithm (but not by the WTA algorithm)
2. Monotonicity: Matched pixel ordering is preserved →180
   - for all $(i, j) \in M, (k, l) \in M, \quad k > i \Rightarrow l > j$

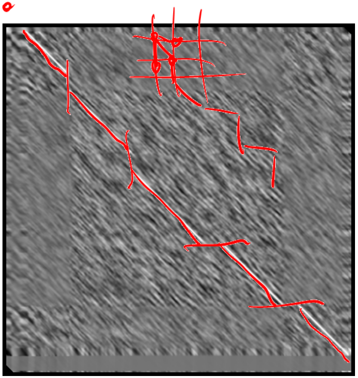
     Notation: $(i, j) \in M$ or $j = M(i)$ – left-image pixel i matches right-image pixel j
   - excludes thin objects close to the cameras
   - used in 3-Label Dynamic Programming (3LDP) [SP]
3. Coherence: Objects occupy well-defined 3D volumes
   - concept by [Prazdny 85]
   - algorithms are based on image/disparity map segmentation
   - a popular model (segment-based, bilateral filtering and their successors)
   - used in Stable Segmented 3LDP [Aksoy et al. PRRS 2008]



4. (Piecewise) binocular continuity: The scene images continuously w/o self-occlusions
   - disparities do not differ much in neighboring pixels (except at object boundaries)
   - full binocular continuity too strong, except in some applications
   - piecewise binocular continuity is combined with monotonicity in 3LDP

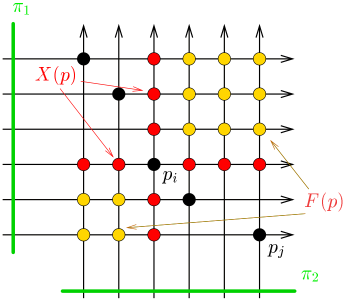


- binocularly visible foreground points
- binocularly visible background pts violating ordering
- monocularly visible points
- d_k critical disparity



- this leads to the concept of 'forbidden zone'

▶Formally: Uniqueness and Ordering in Matching Table T



$$p_j \notin X(p_i), \quad p_j \notin F(p_i)$$

- **Uniqueness Constraint:**

  A set of pairs $M = \{p_i\}_{i=1}^n$, $p_i \in T$ is a matching iff
  $$\forall p_i, p_j \in M : \; p_j \notin X(p_i).$$

  X-zone, $p_i \notin X(p_i)$

- **Ordering Constraint:**

  Matching M is monotonic iff
  $$\forall p_i, p_j \in M : \; p_j \notin F(p_i).$$

  F-zone, $p_i \notin F(p_i)$

- ordering constraint: matched points form a monotonic set in both images
- ordering is a powerful constraint: in $n \times n$ table we have monotonic matchings $O(4^n) \ll O(n!)$ all matchings

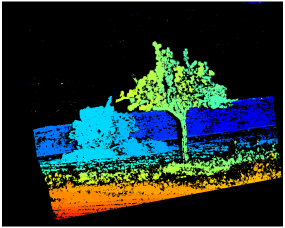
⊛ 2: how many are there maximal monotonic matchings? (e.g. 27 for $n = 4$; hard!)

- uniqueness constraint is a basic occlusion model
- ordering constraint is a weak continuity model and partly also an occlusion model
- monotonic matching can be found by **dynamic programming**

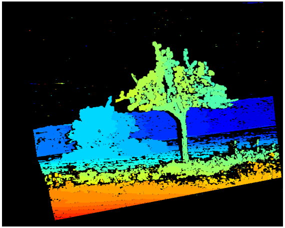
Some Results: AppleTree

left image

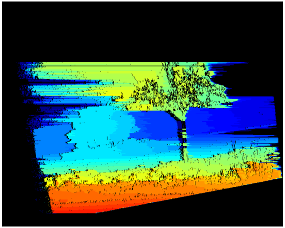
right image



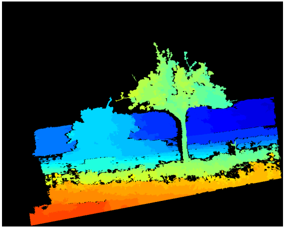
ML →177



3LDP w/ordering
[SP]



naïve DP
[Cox et al. 1992]



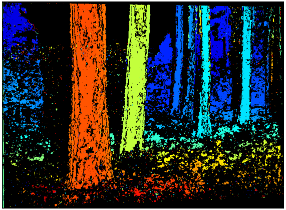
Stable Segmented 3LDP
[Aksoy et al. PRRS 2008]

- 3LDP parameters α_i, V_e learned on Middlebury stereo data http://vision.middlebury.edu/stereo/

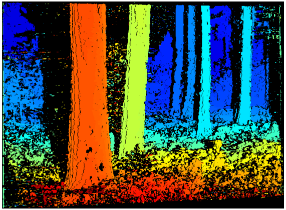
Some Results: Larch

left image

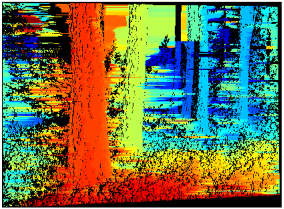
right image



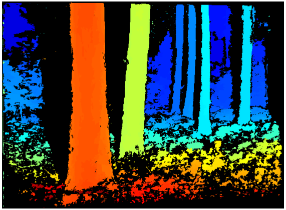
ML →177



3LDP w/ordering [SP]



naïve DP



Stable Segmented 3LDP

- naïve DP: no mutual occlusion model, ignores symmetry, has no similarity distribution model
- but even 3LDP has errors in mutually occluded region
- Stable Segmented 3LDP: few errors in mutually occluded region since it uses a coherence model

Algorithm Comparison

Marroquin's Winner-Take-All (WTA →171)

- the ur-algorithm — very weak model
- dense disparity map
- $O(N^3)$ algorithm, simple but it rarely works

Maximum Likelihood Matching (ML →177)

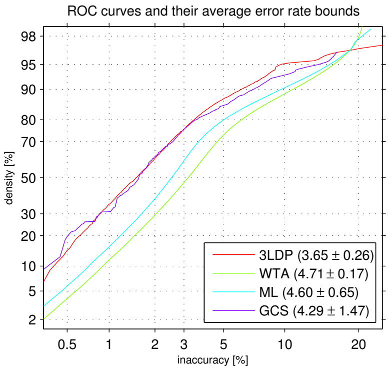
- semi-dense disparity map
- many small isolated errors
- models basic occlusion
- $O(N^3 \log(NV))$ algorithm — max-flow by cost scaling

MAP with Min-Cost Labeled Path (3LDP)

- semi-dense disparity map
- models occlusion in flat, piecewise binocularly continuous scenes
- has 'illusions' if ordering does not hold
- $O(N^3)$ algorithm

Stable Segmented 3LDP

- better than 3LDP — fewer errors at any given density
- $O(N^3 \log N)$ algorithm
- requires image segmentation — itself a difficult task



- ROC-like curve captures the density/accuracy tradeoff
- numbers: AUC (smaller is better)
- GCS is the one used in the exercises
- more algorithms at `http://vision.middlebury.edu/stereo/` (good luck!)

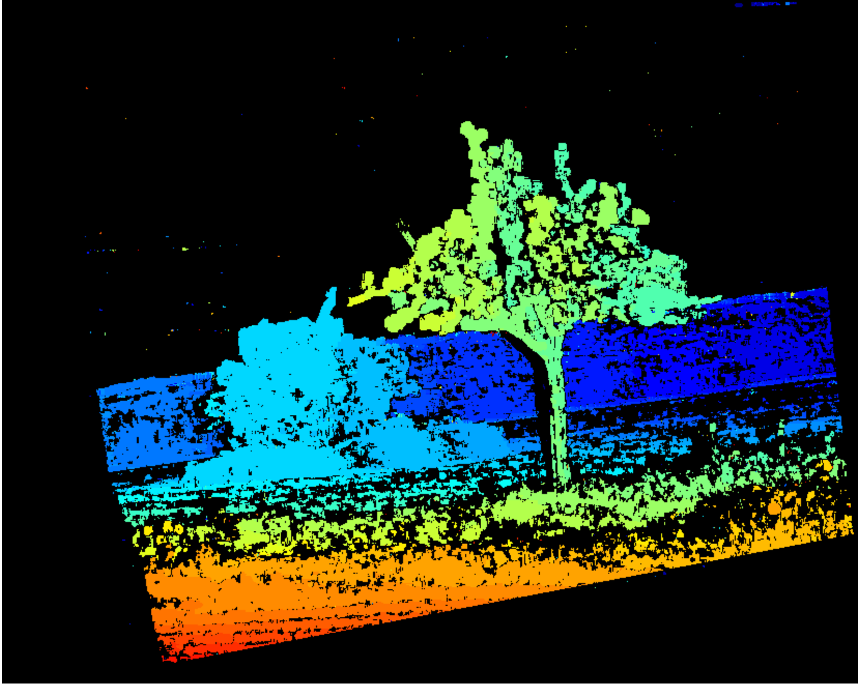
A Summary of This Course Highlights

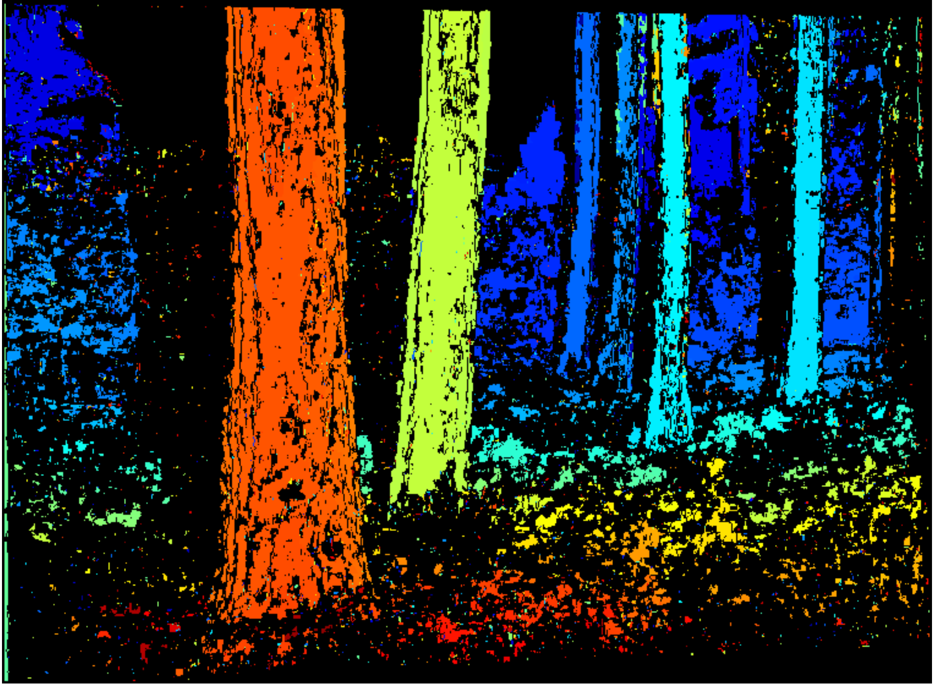
- homography as a two-image model
- epipolar geometry as a two-image model
- core algorithms for 3D vision:
  - simple intrinsic calibration methods
  - 6-pt alg for camera resection and 3-pt alg for exterior orientation (calibrated resection)
  - 7-pt alg for fundamental matrix, 5-pt alg for essential matrix
  - essential matrix decomposition to rotation and translation
  - efficient accurate triangulation
  - robust matching by RANSAC sampling
  - camera system reconstruction
  - efficient bundle adjustment
  - stereoscopic matching
- statistical robustness as a way to work with partially unknown information

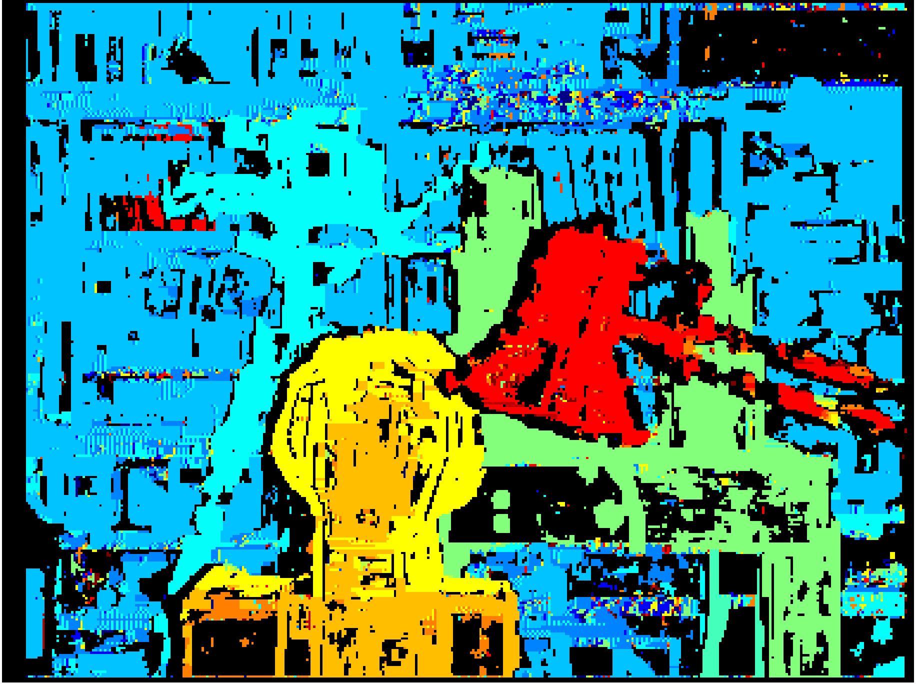
What can we do with these tools?

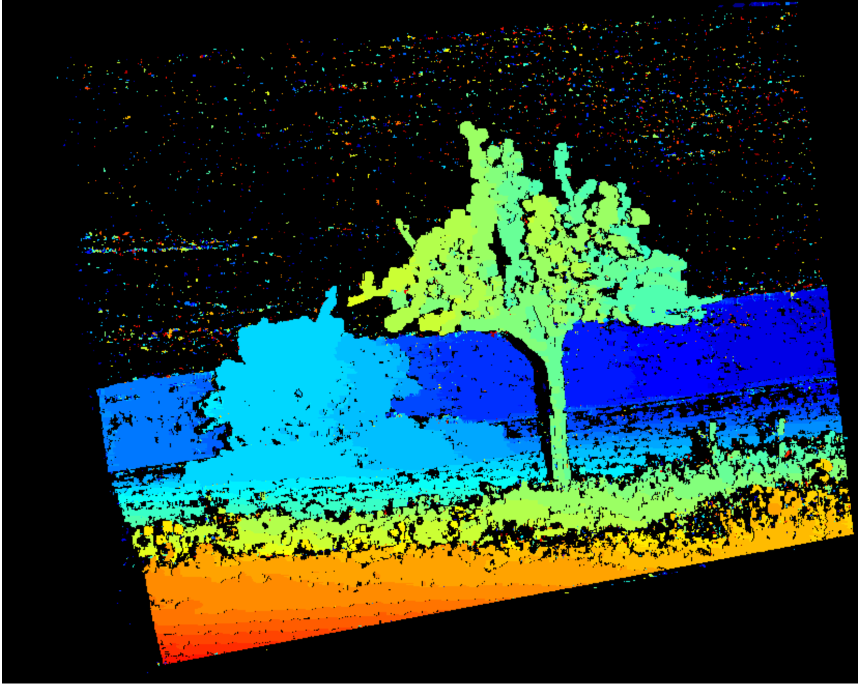
- 3D scene reconstruction
- visual odometry
- motion capture
- self-localization and mapping (not covered: 3D aggregation in scene maps)
- 3D scene measurement for robot motion planning
- automatic extrinsic calibration from motion (hand-eye calibration)

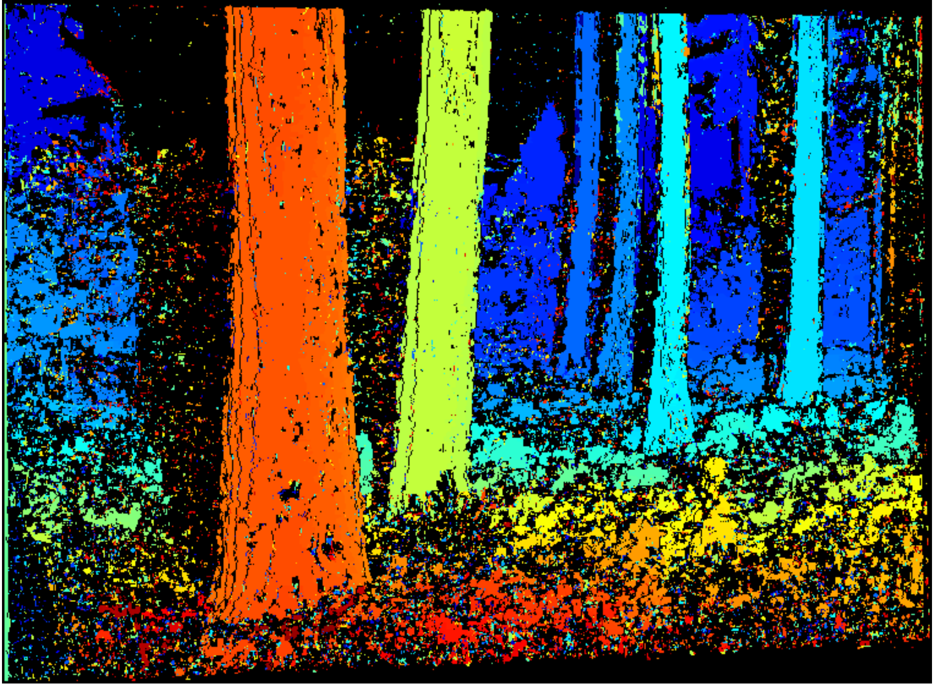
Thank You

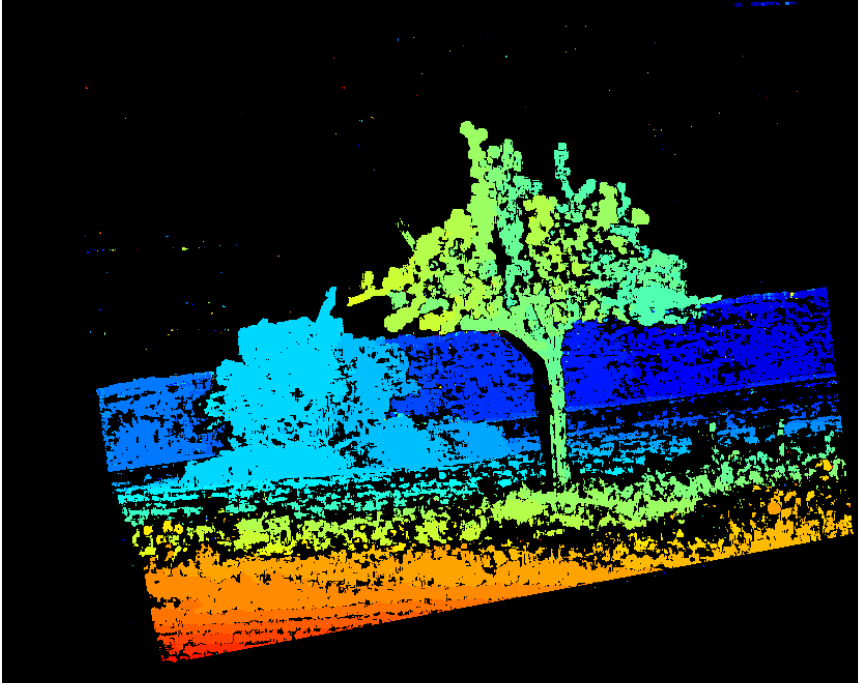


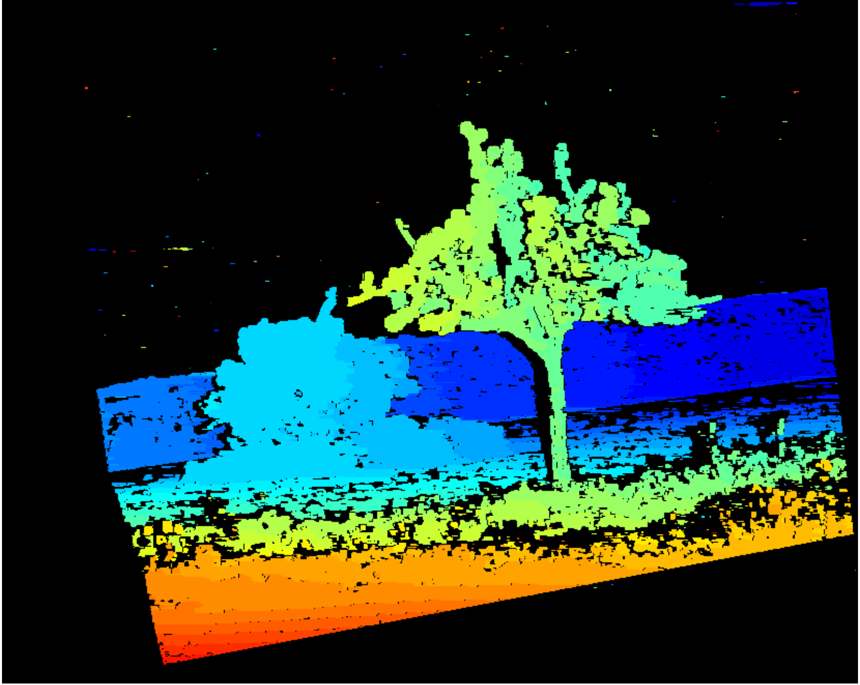


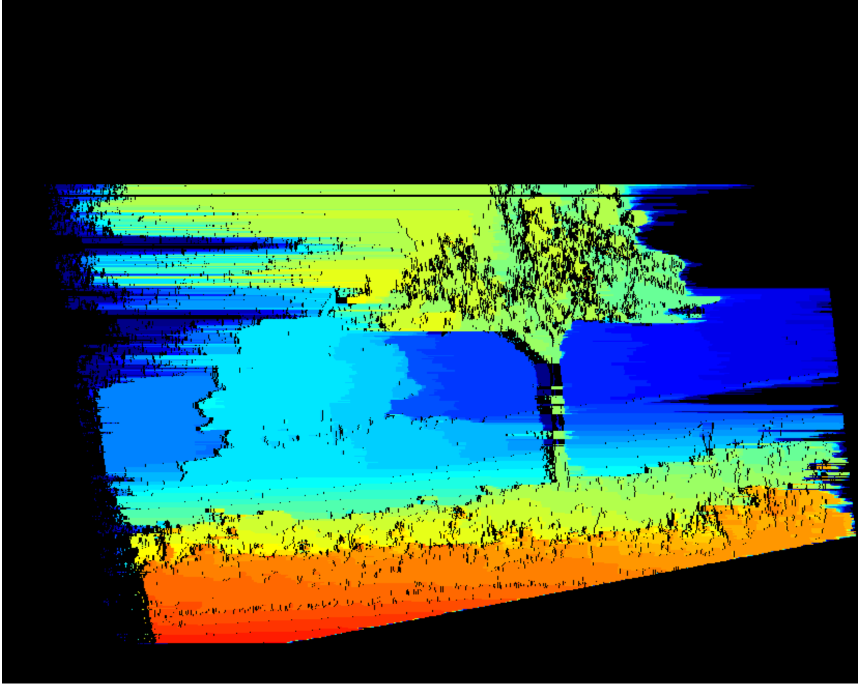


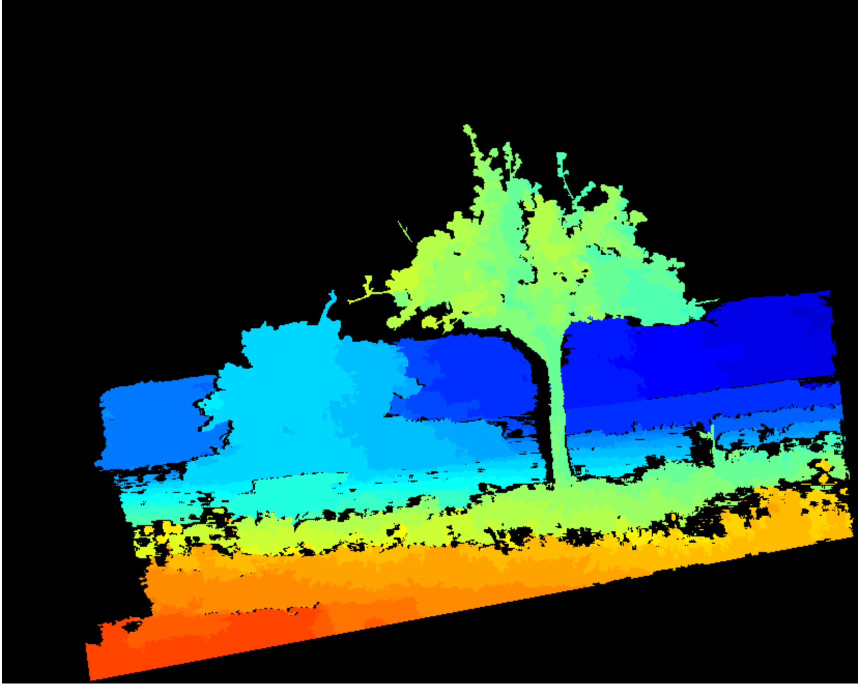


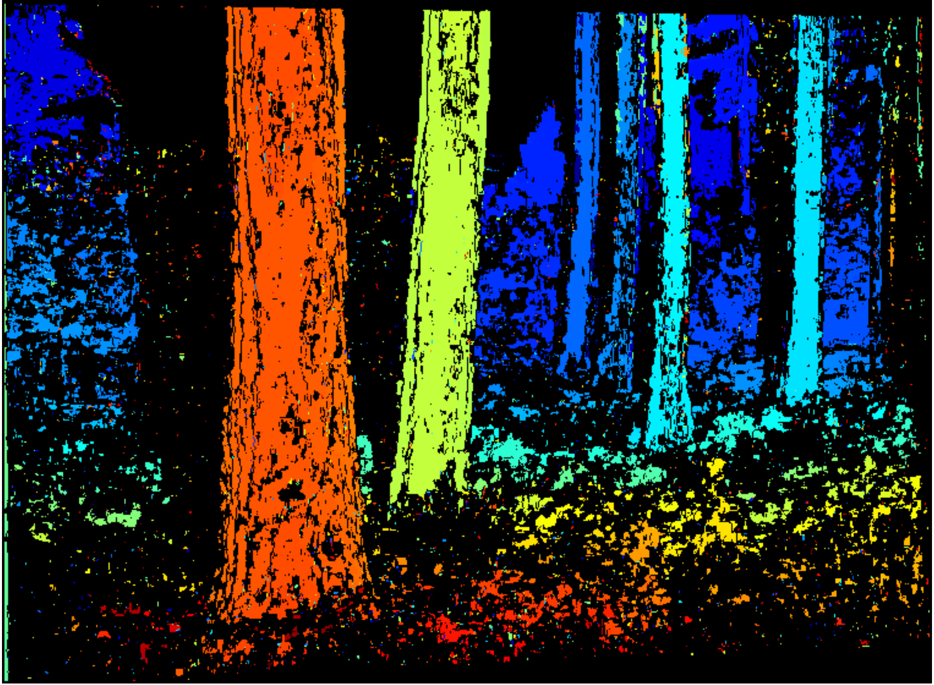


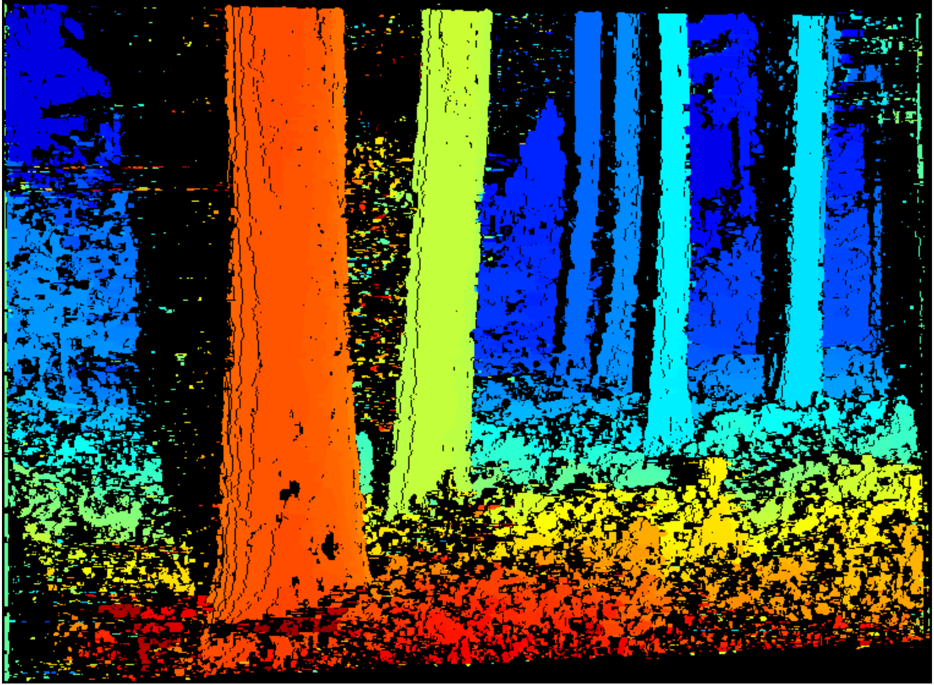


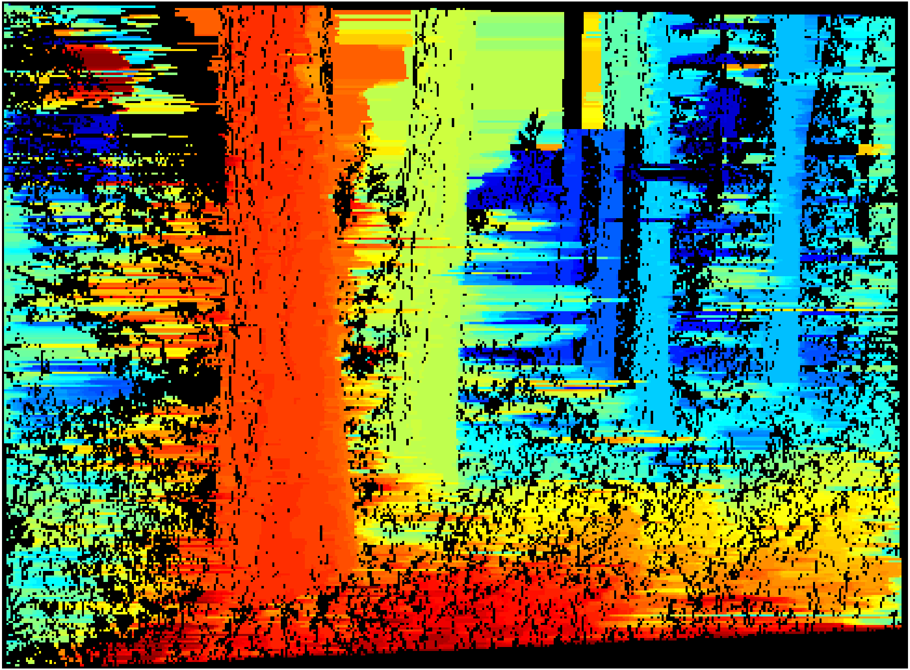


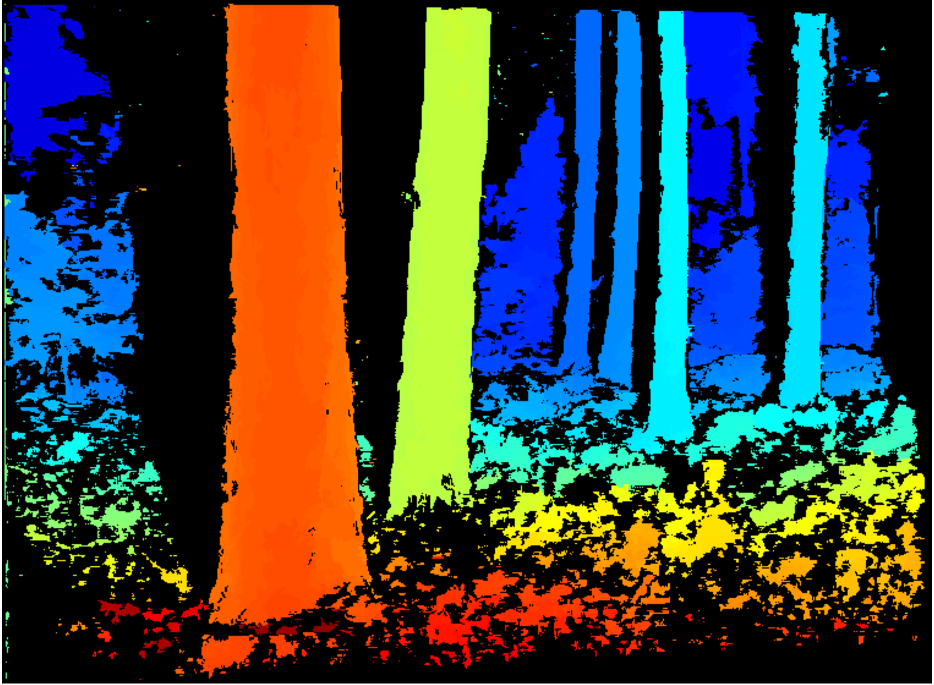


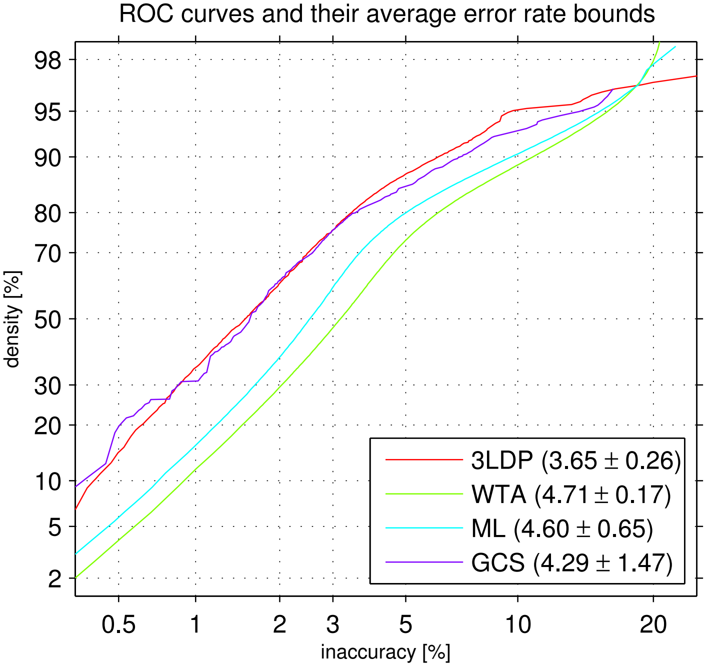











ROC curves and their average error rate bounds
98
95
90
80
70
50
30
20
10
5
2
density [%]
0.5
1
2
3
5
10
20
inaccuracy [%]
3LDP (3.65 ± 0.26)
WTA (4.71 ± 0.17)
ML (4.60 ± 0.65)
GCS (4.29 ± 1.47)