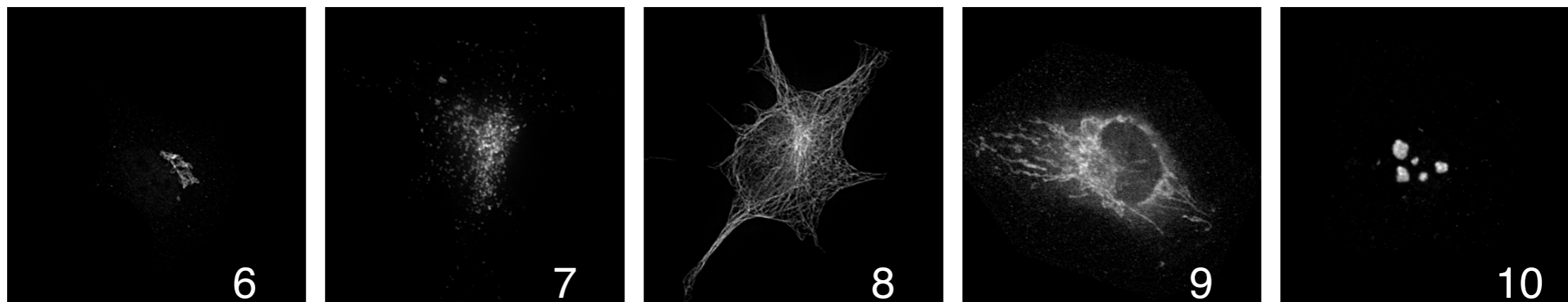
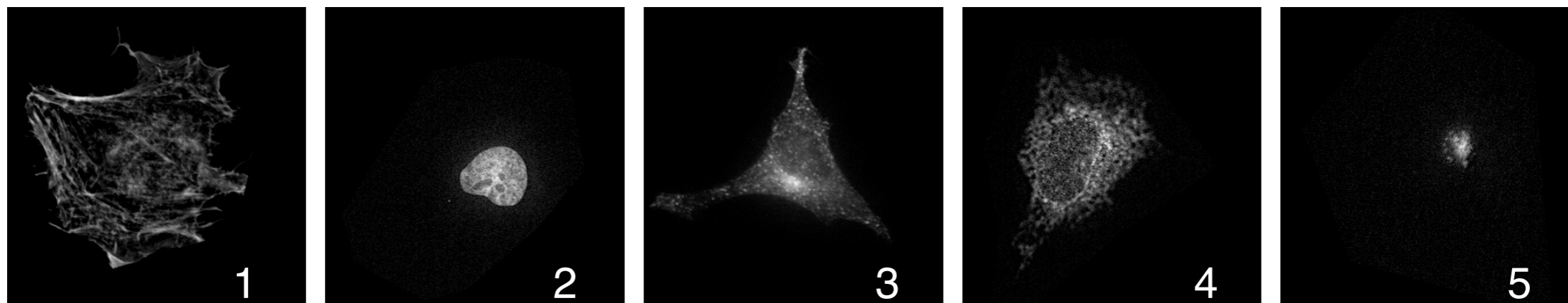
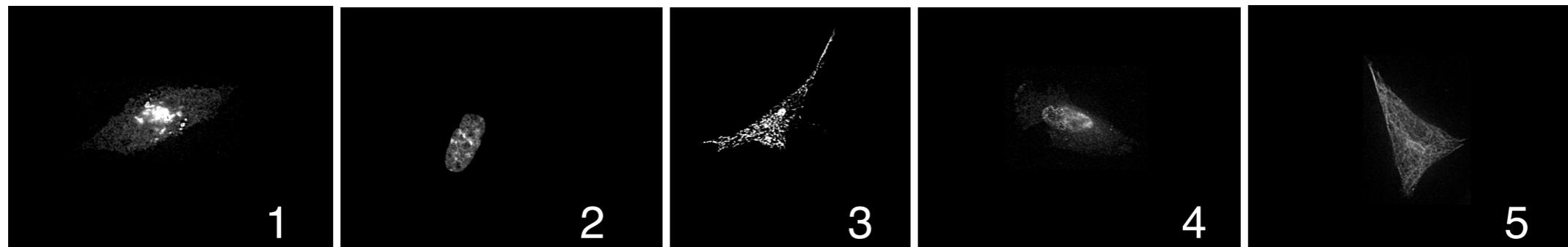
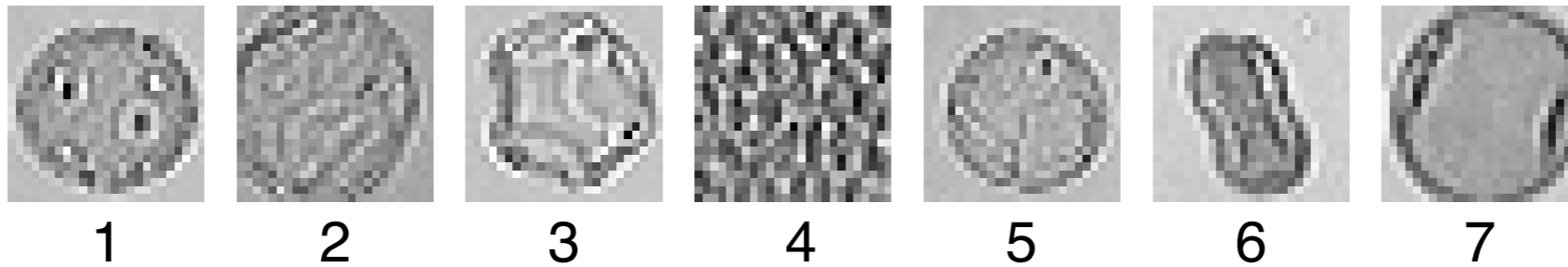


# New Classifier: WND-CHARM

---

- No accuracy tradeoff for generality
- ~10x as many inputs as other classifiers
- Based on nearest-neighbor method
  - Not neural-nets or Bayes nets
  - WND-5: Weighted Neighbor Distance
  - WCD: Weighted Centroid Distance
- Pattern recognition applications
  - Worm Aging (Josiah Johnston)
  - Mouse Aging - AGEMAP (Tomasz Macura)
  - High-Density RNAi screens (Mark Eckley + Lior Shamir)
  - Lymphoma classification (Nikita Orlov)

# Benchmark classification problems



# Benchmark accuracy comparison

---

Data Set	Benchmark	BBN	WND5
Pollen	93%	78%	96%
CHO	88%	78%	95%
HeLa	83%	69%	86%

# New Classification Benchmarks



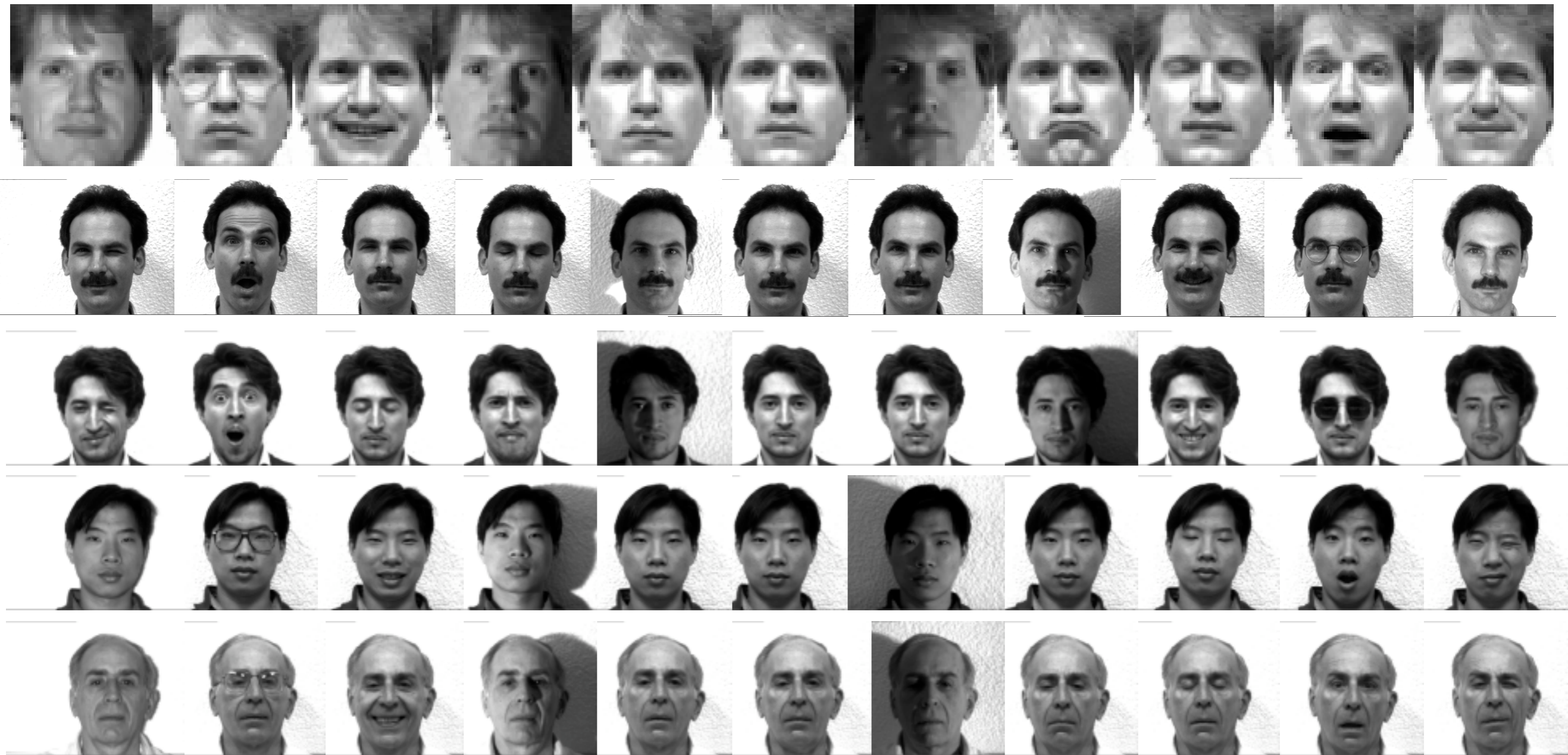
Cambridge University Computer Laboratory  
**The Database of Faces**



... 40 Individuals, 10 images per subject

# New Classification Benchmarks

## The Yale Face Database

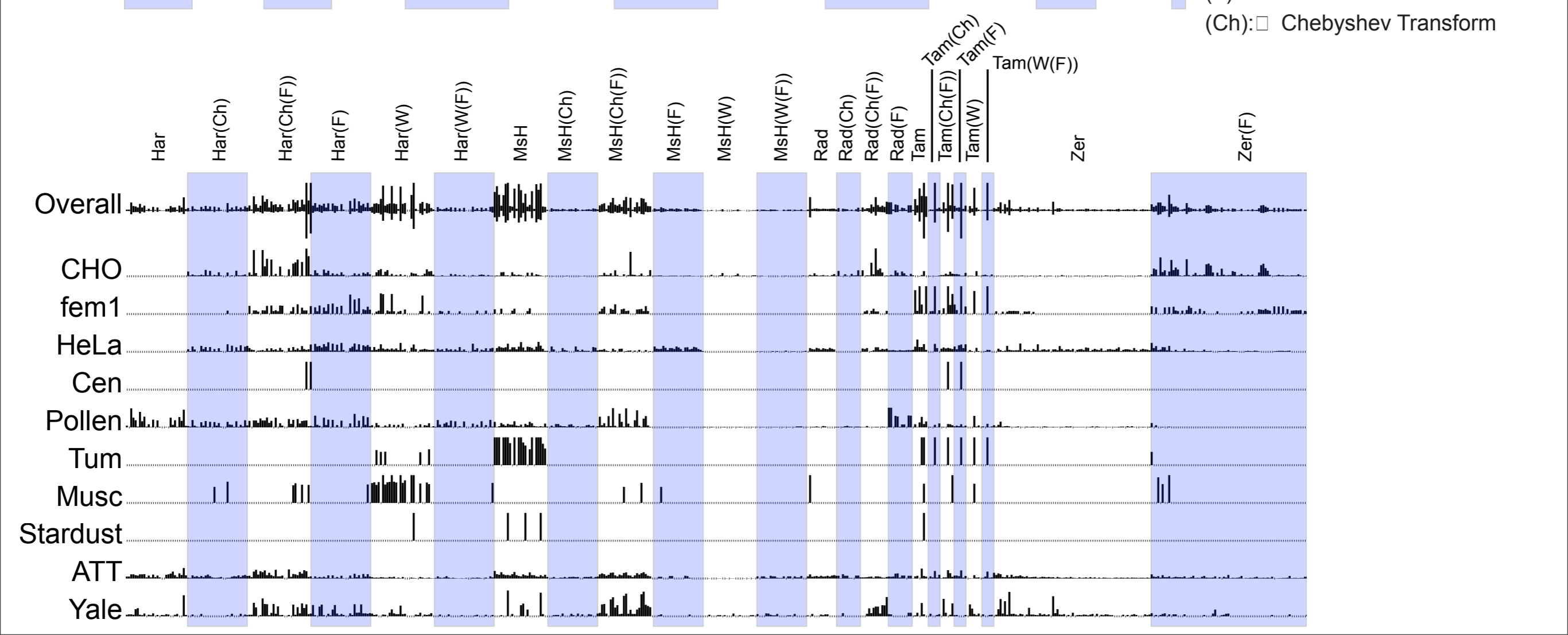
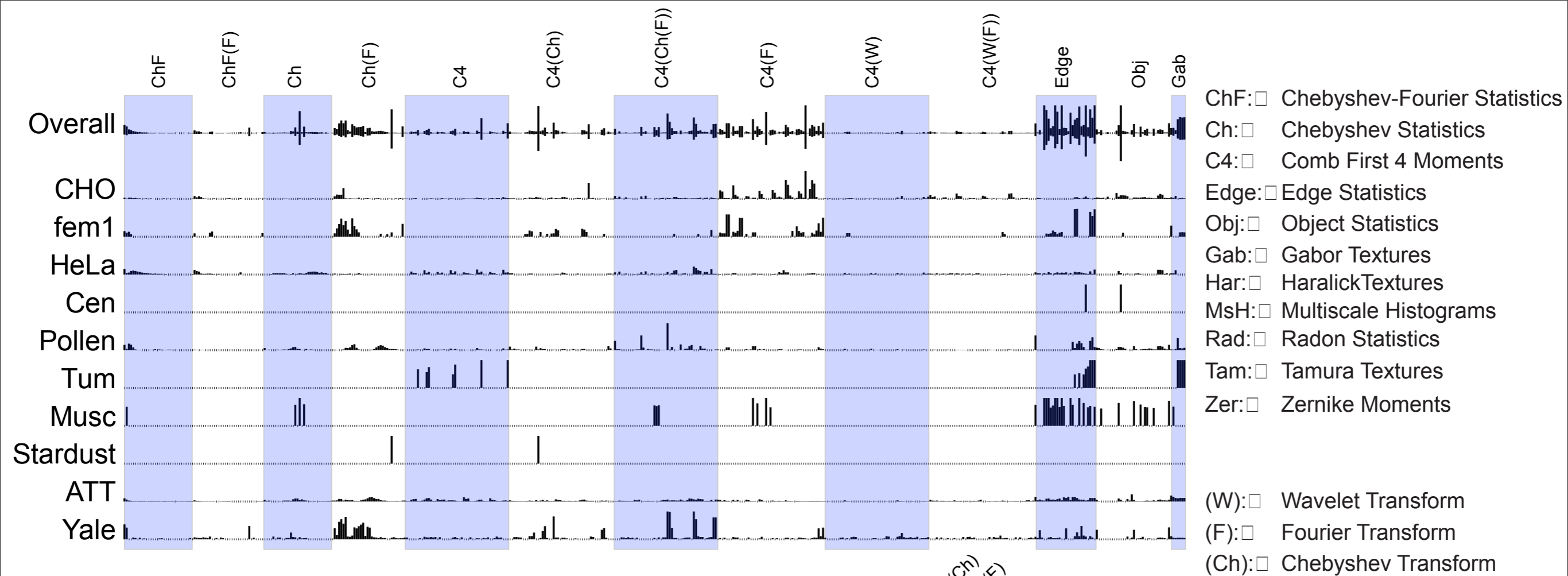


... 15 Individuals, 11 images per subject

# Face recognition accuracy

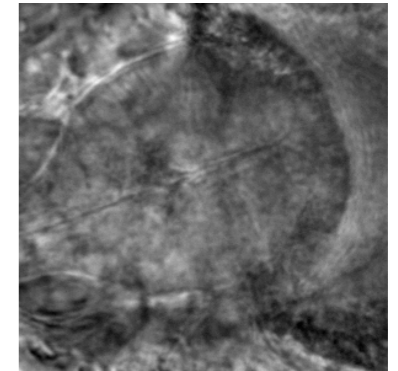
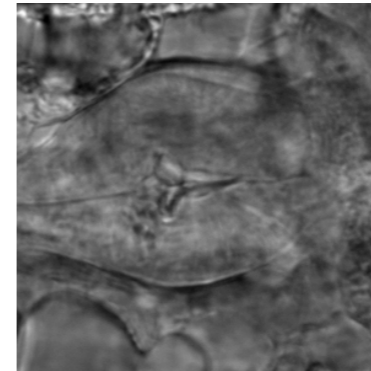
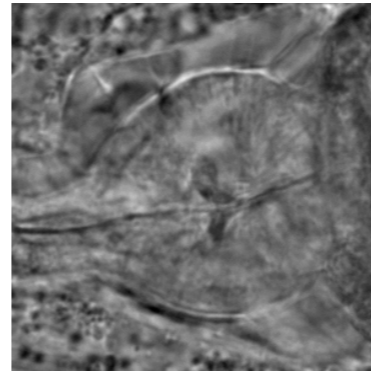
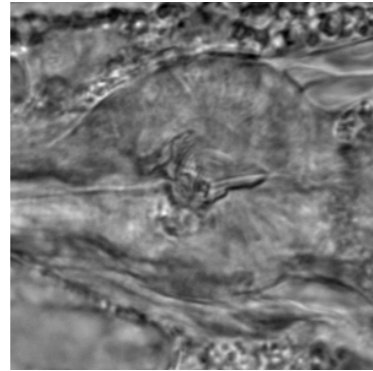
---

Data Set	Eigenfaces	Fisherfaces	DLDA	BBN	WND5
AT&T faces	90%	82.5%	89%	55%	99%
Yale faces	91%	80%	88%	58%	85%

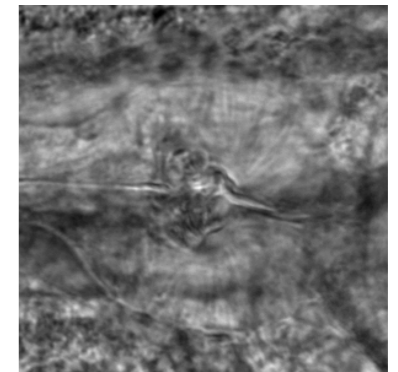
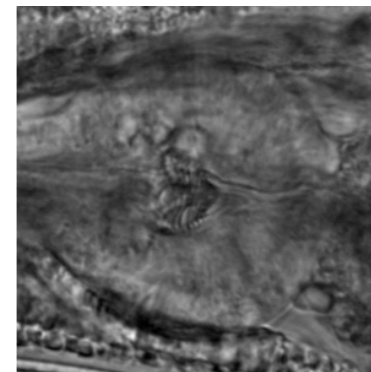
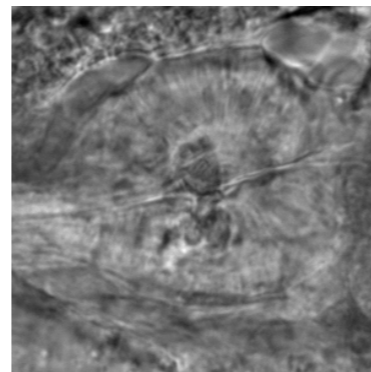
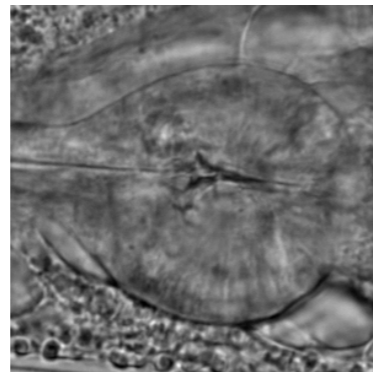


# Sarcopenia in the *C. elegans* Pharynx: Muscle degeneration in a synchronized isogenic population

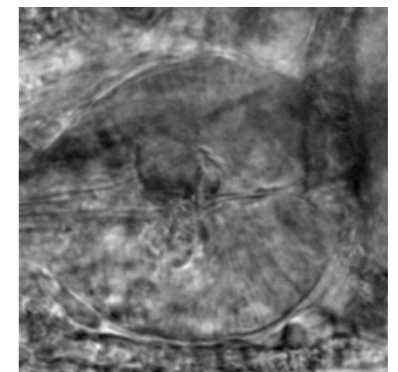
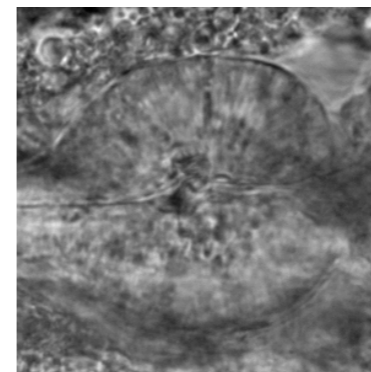
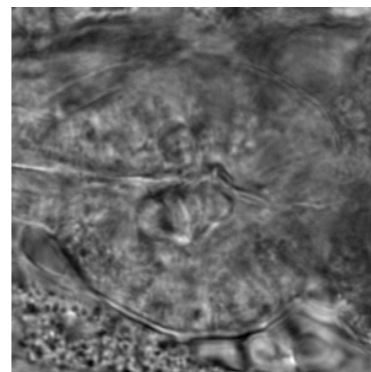
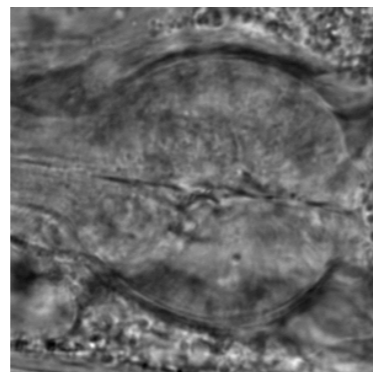
**Day 2**



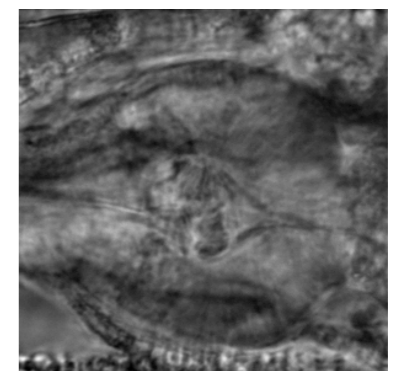
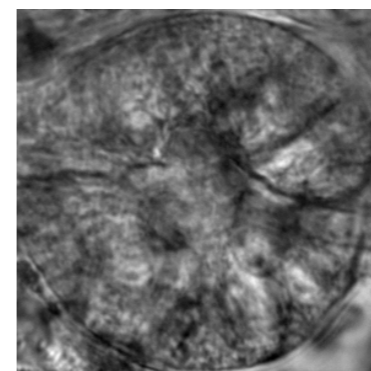
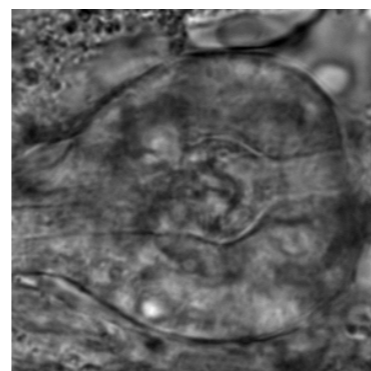
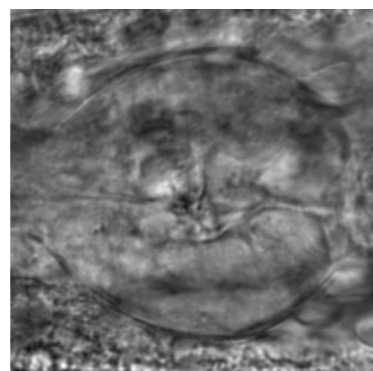
**Day 4**



**Day 6**



**Day 8**



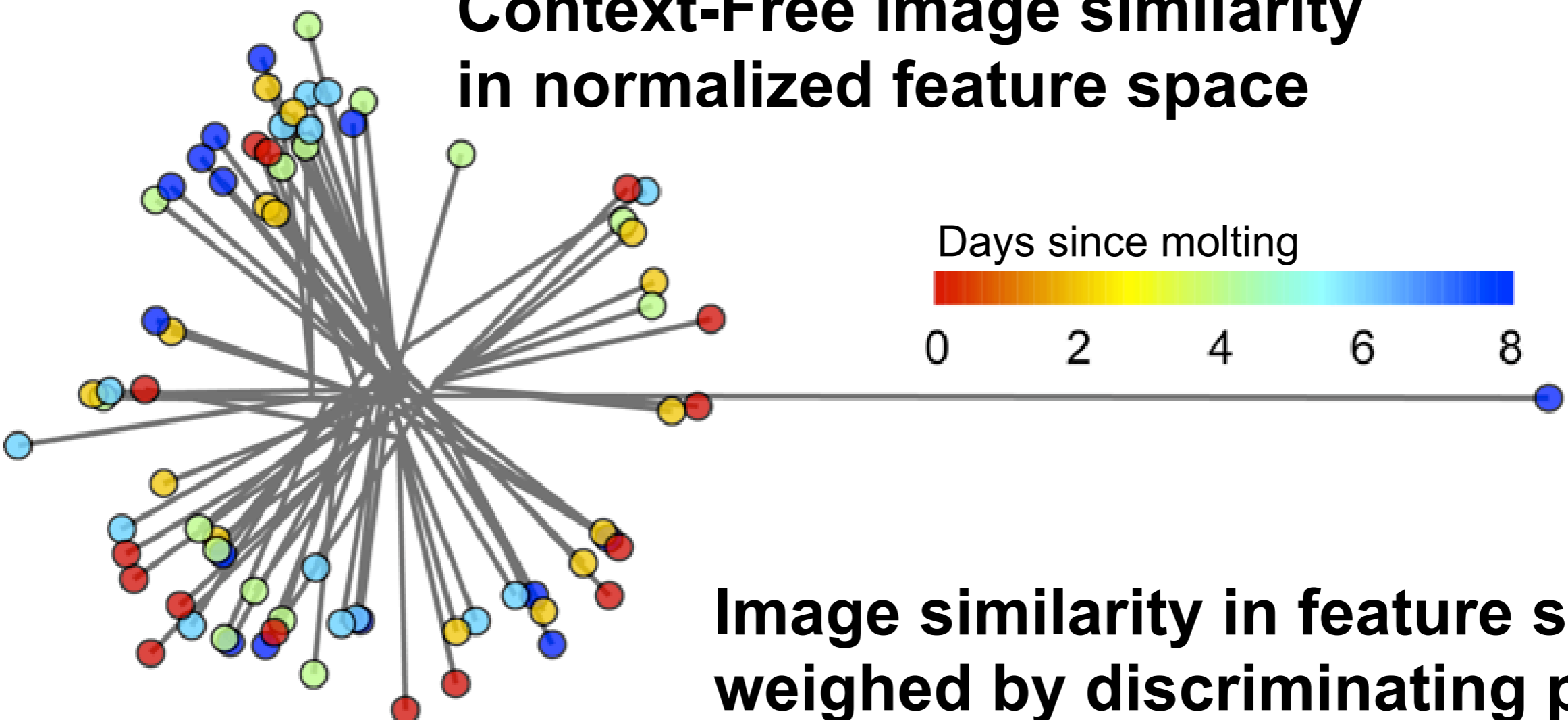


# Context-Free image similarity in normalized feature space

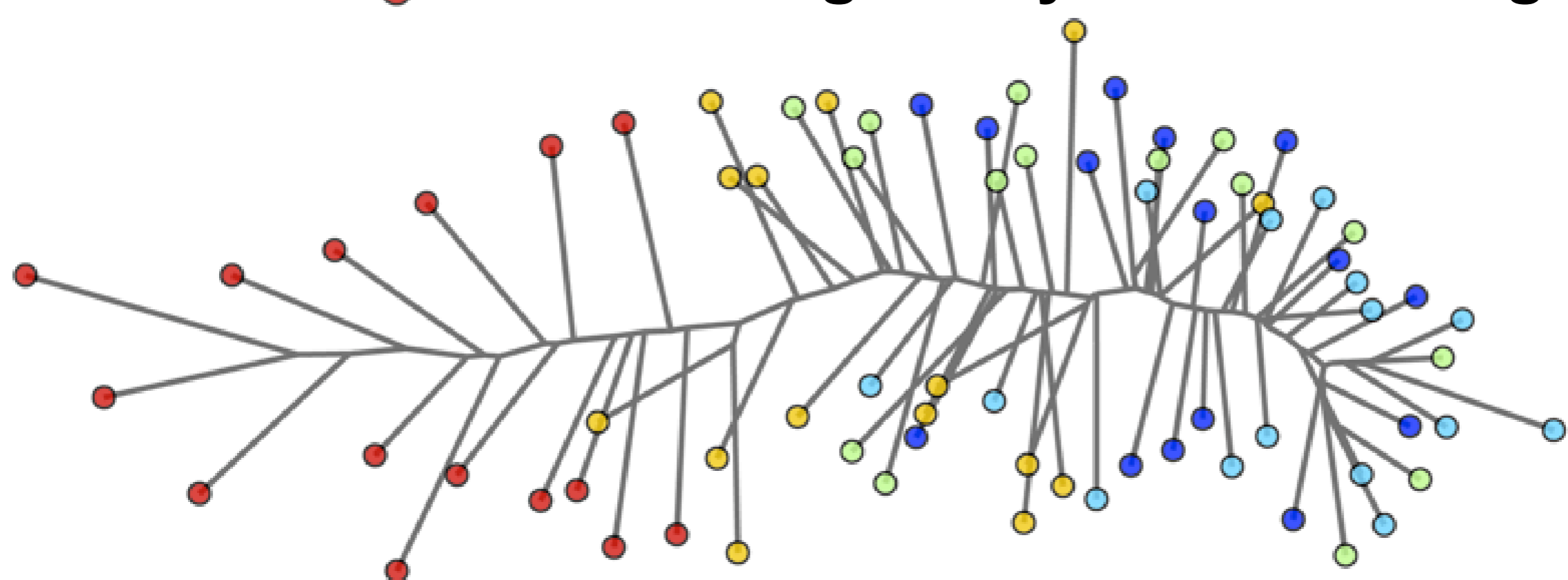
Days since molting



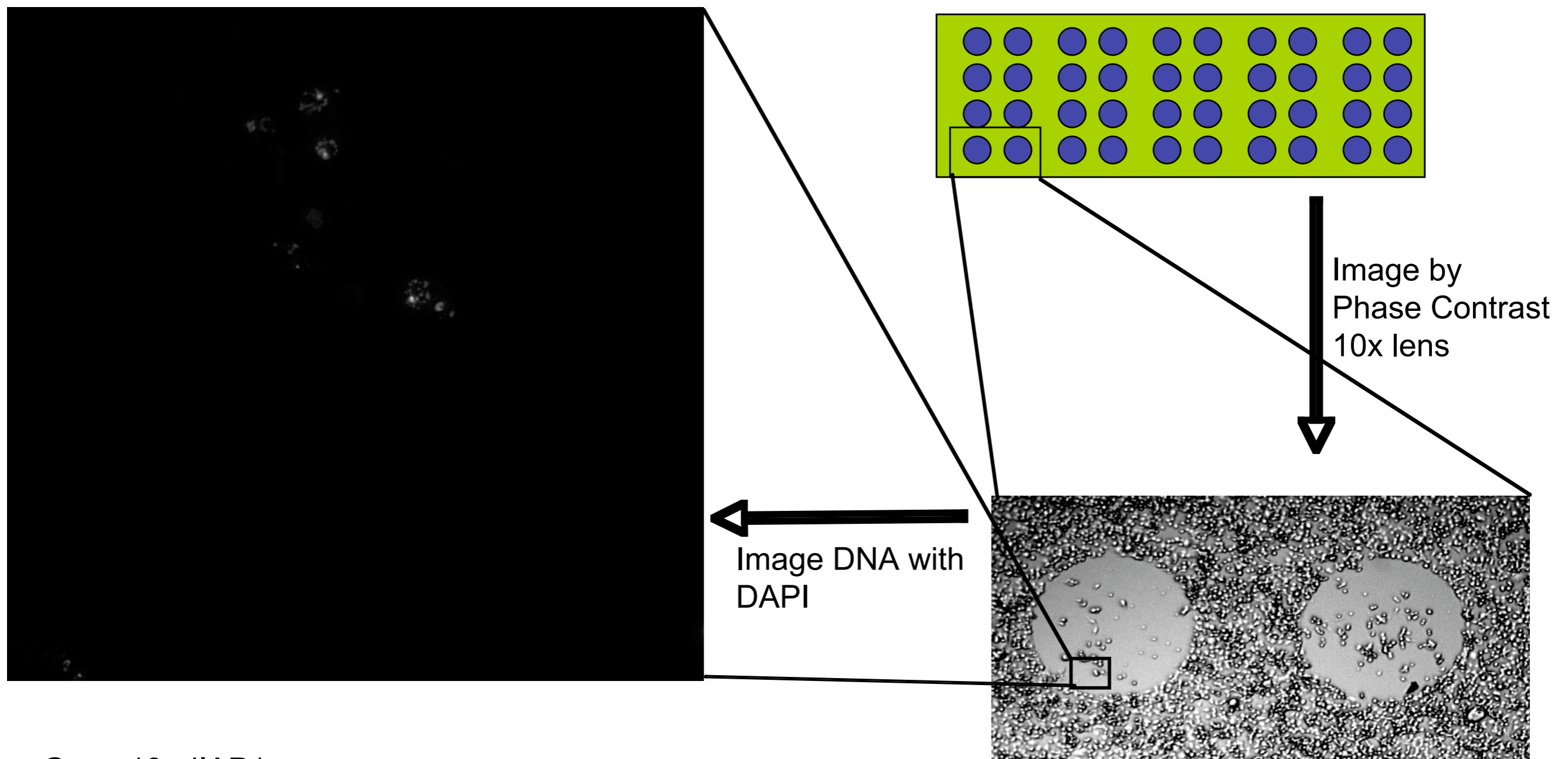
0 2 4 6 8



# Image similarity in feature space weighed by discriminating power



# Living cell microarrays - apoptosis control



Gene 13, dIAP1

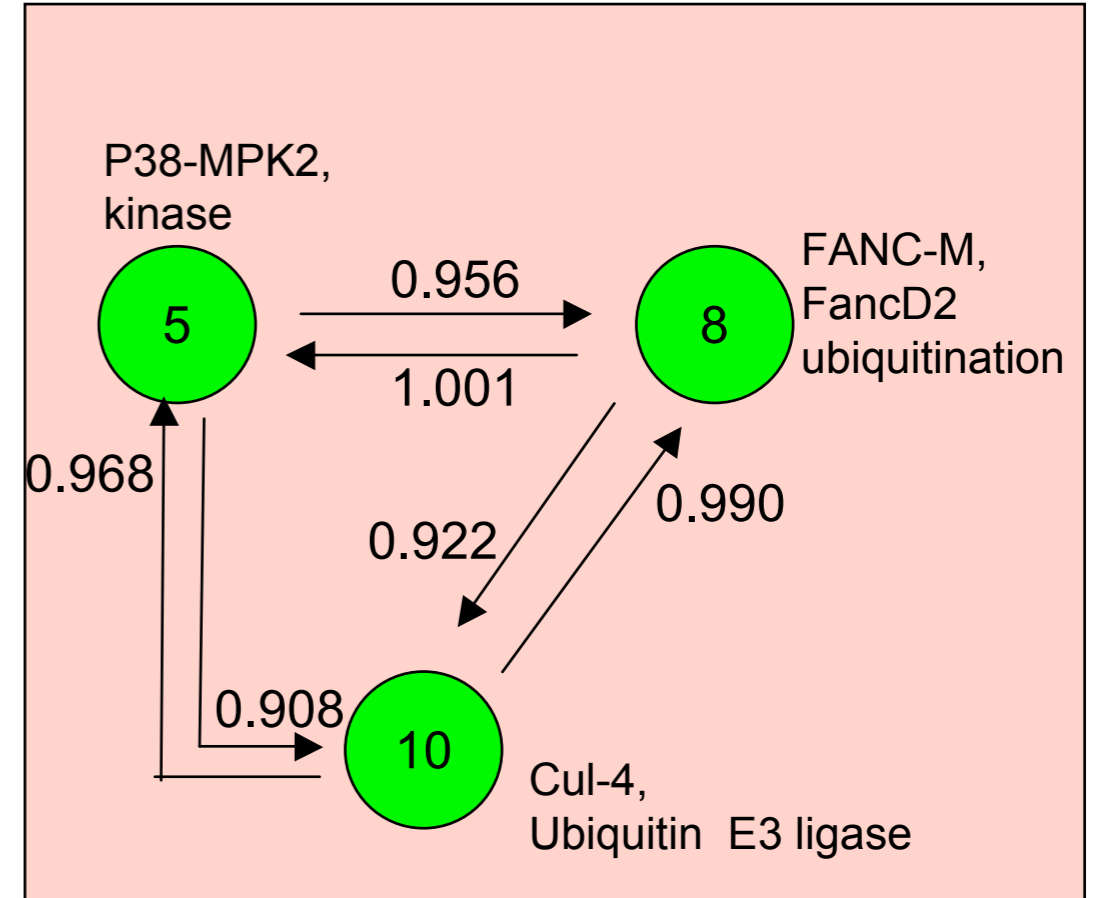
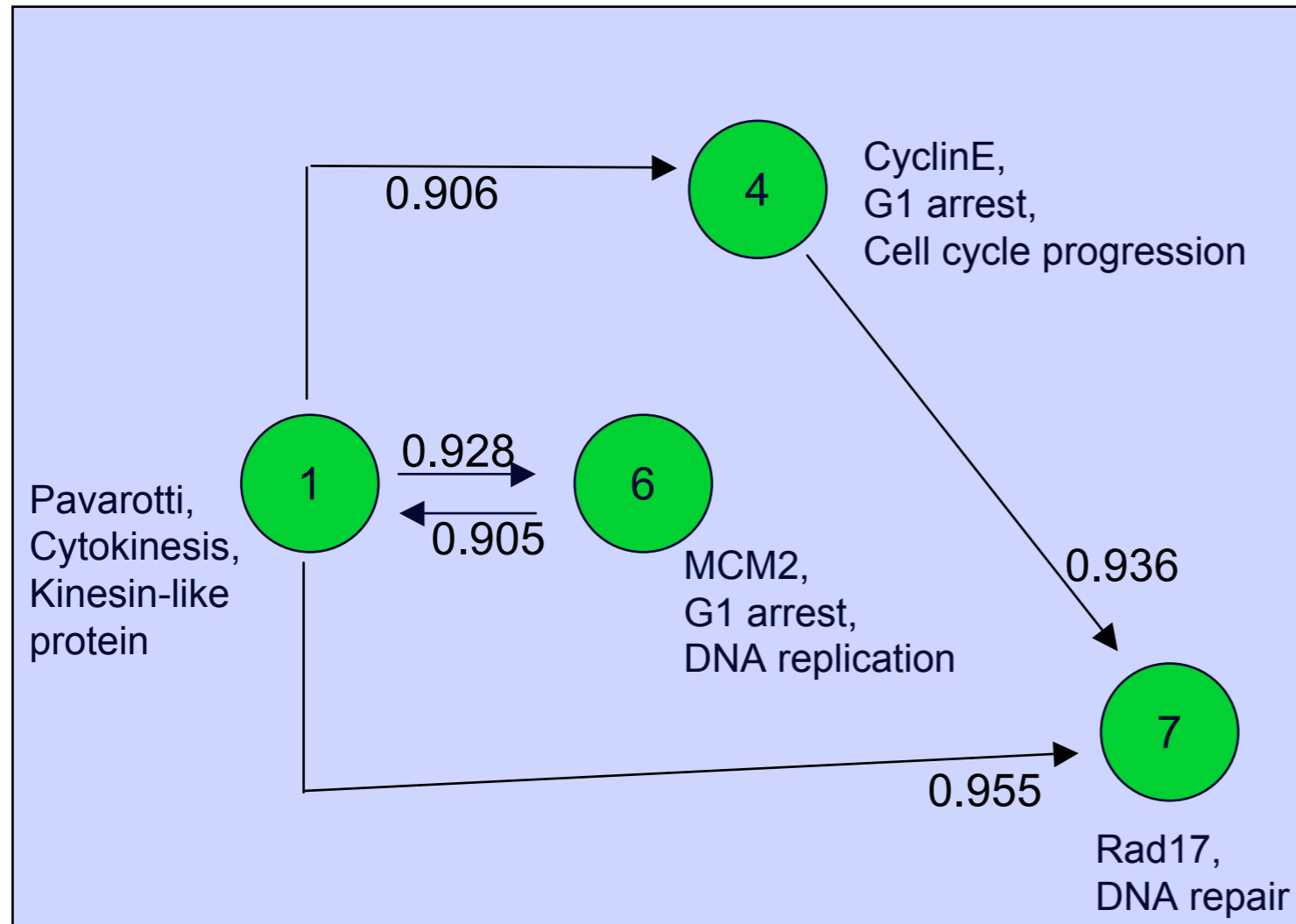
# Phenotype similarities

---

	1	2	3	4	5	6	7	8	9	10	11	12	13	14
Gene1	1.000	0.839	<b>0.913</b>	<b>0.906</b>	0.730	<b>0.928</b>	<b>0.955</b>	0.730	0.597	0.782	0.853	0.822	0.653	0.571
Gene2	0.571	1.000	0.637	0.592	0.510	0.513	0.505	0.506	0.595	0.509	0.470	0.442	0.651	0.533
Gene3	0.446	0.353	1.000	0.364	0.279	0.454	0.304	0.293	0.197	0.360	0.499	0.400	0.169	0.218
Gene4	0.868	0.812	0.766	1.000	0.737	0.836	<b>0.936</b>	0.726	0.671	0.745	0.753	0.735	1.124	0.639
Gene5	0.743	0.749	0.598	0.746	1.000	0.753	0.754	<b>0.956</b>	<b>0.980</b>	<b>0.908</b>	0.833	0.888	0.626	1.027
Gene6	<b>0.905</b>	0.733	<b>0.966</b>	0.830	0.695	1.000	0.840	0.705	0.562	0.782	0.870	0.823	0.569	0.534
Gene7	0.792	0.668	0.659	0.792	0.681	0.791	1.000	0.683	0.636	0.694	0.714	0.713	0.755	0.560
Gene8	0.788	0.755	0.659	0.759	1.001	0.796	0.774	1.000	<b>0.929</b>	<b>0.922</b>	0.890	<b>0.958</b>	0.586	<b>0.960</b>
Gene9	0.427	0.568	0.299	0.459	0.603	0.450	0.497	0.606	1.000	0.537	0.417	0.459	0.569	0.819
Gene10	0.841	0.882	0.828	0.825	<b>0.968</b>	0.839	0.814	<b>0.990</b>	<b>0.978</b>	1.000	<b>0.922</b>	<b>0.946</b>	0.722	<b>0.936</b>
Gene11	0.832	0.683	<b>0.964</b>	0.769	0.783	0.861	0.764	0.802	0.579	0.833	1.000	<b>0.973</b>	0.506	0.585
Gene12	0.830	0.644	0.835	0.788	0.865	0.851	0.751	0.889	0.646	0.876	<b>0.980</b>	1.000	0.495	0.662
Gene13	0.248	0.333	0.162	0.353	0.265	0.232	0.328	0.262	0.355	0.251	0.167	0.184	1.000	0.330
Untreated	0.387	0.394	0.301	0.376	0.564	0.400	0.382	0.542	0.668	0.502	0.443	0.485	0.360	1.000

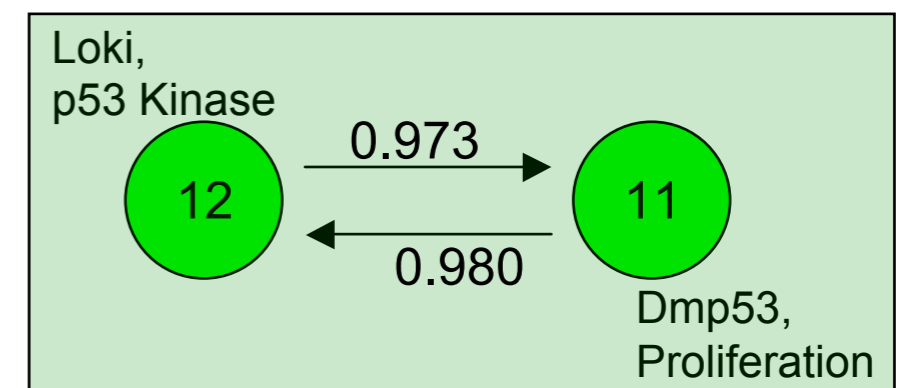
# Phenotype similarity network

The network is deduced based on symmetric similarities between phenotypes. A link between two phenotypes represents similarity > 0.90 of the similarity of each phenotype to itself (1.0).



- Node 2: MAPk-AK2, G2 delay
- Node 3: CHD1, chromodomain, helicase domain protein, Unknown phenotype

- Node 9: Pebble, Cytokinesis, RhoGEF



- Node 13: dIAP1, apoptosis