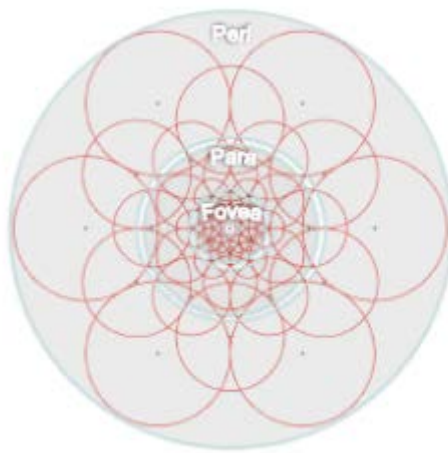


Freak: Fast retina keypoint.

In a nutshell, FREAK is similar to BRISK by having a handcrafted sampling pattern and also similar to ORB by using machine learning techniques to learn the optimal set of sampling pairs. FREAK also has an orientation mechanism that is similar to that of BRISK.

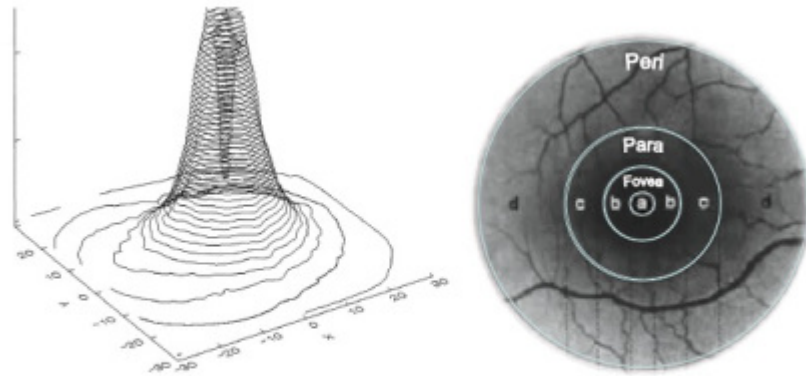
Retinal sampling pattern

FREAK suggests using the retinal sampling grid which is also circular with the difference of having higher density of points near the center. The density of points drops exponentially as can be seen in the following figure:



Each sampling point is smoothed with a Gaussian kernel where the radius of the circle illustrates the size of the standard deviation of the kernel.

As can be seen in the following figure, the suggested sampling grid corresponds with the distribution of receptive fields over the retina:

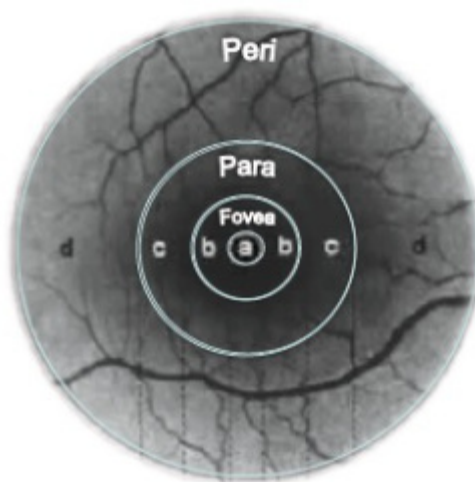


(a) Density of ganglion cells over the retina (b) Retina areas

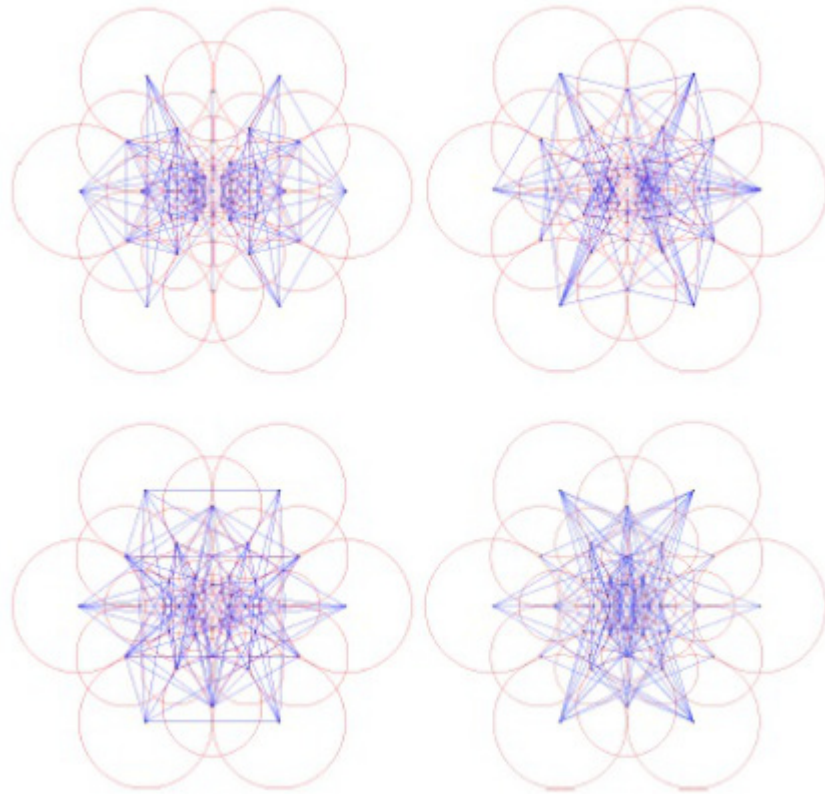
Learning the sampling pairs

With few dozen sampling points, thousands of sampling pairs can be considered. However, many of the pairs might not be useful efficiently describe a patch. A possible strategy can be to follow BRISK's approach and select pairs according to their spatial distance. However, the selected pairs can be highly correlated and not discriminant. Consequently, FREAKS follows ORB's approach and tries to learn the pairs by maximizing variance of the pairs and taking pairs that are not correlated.

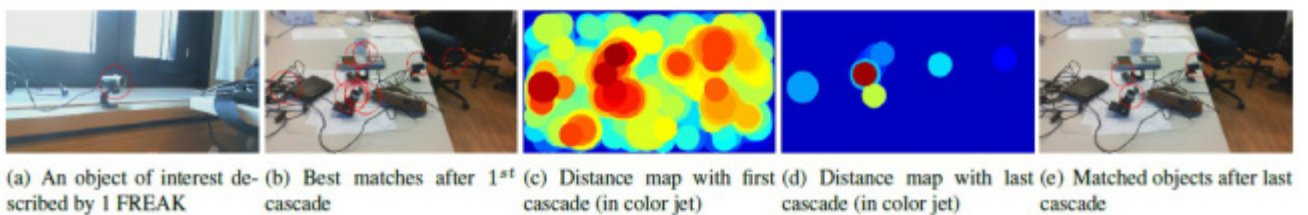
Interestingly, there is a structure in the resulting pairs – a coarse-to-fine approach which matches our understanding of the model of the human retina. The first pairs that are selected mainly compare sampling points in the outer rings of the pattern where the last pairs compare mainly points in the inner rings of the pattern. This is similar to the way the human eye operates, as it first use the perifoveal receptive fields to estimate the location of an object of interest. Then, the validation is performed with the more densely distributed receptive fields in the fovea area.



The sampling pairs are illustrated in the following figure, where each figure contains 128 pairs (from left to right, top to bottom):

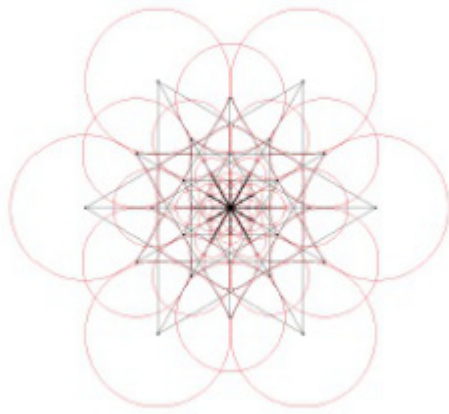


FREAKS takes advantage of this coarse-to-fine structure to further speed up the matching using a cascade approach: when matching two descriptors, we first compare only the first 128 bits. If the distance is smaller than a threshold, we further continue the comparison to the next 128 bits. As a result, a cascade of comparisons is performed accelerating even further the matching as more than 90% of the candidates are discarded with the first 128 bits of the descriptor. The following figure illustrates the cascade approach:



Orientation assignment

To somewhat compensate for rotation changes, FREAK measures the orientation of the keypoint and rotates the sampling pairs by measure angle. FREAK's mechanism for measuring the orientation is similar to that of BRISK only that instead of using long distance pairs, FREAK uses a predefined set of 45 symmetric sampling pairs:



OpenCV implementation

C++:

```
FREAK(bool orientationNormalized=true, bool scaleNormalized=true, float  
patternScale=22.0f, int nOctaves=4, const vector<int>& selectedPairs=vector<int>() )
```

Parameters:

orientationNormalized – Enable orientation normalization.

scaleNormalized – Enable scale normalization.

patternScale – Scaling of the description pattern.

nOctaves – Number of octaves covered by the detected keypoints.

selectedPairs – (Optional) user defined selected pairs indexes,

FREAK is descriptor only. There is no corresponding feature detector.

You can combine it with FAST, ORB, SIFT, SURF, MSER or use goodFeaturesToTrack function