BIOMETRIC SEARCH CODES

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A biometric identification system identifies individuals based on physical features. Let \( M \) individuals be indexed \( w \in \{1, 2, \ldots, M\} \). There are three operational phases:

1![](https://render.githubusercontent.com/render/math?math=\textbf{Generation phase:} \text{ A biometric sequence } z^N(w) \text{ is generated for each individual } w, \text{ hence } \Pr\{Z^N(w) = z^N\} = \prod_{n=1}^{N} Q(z_n), \text{ for all } z^N \in \mathcal{Z}^N.

2![](https://render.githubusercontent.com/render/math?math=\textbf{Enrollment phase:} \text{ Each individual is observed via an enrollment channel. The resulting enrollment-sequence } x^N(w), \text{ is added to a database. Now } \Pr\{X^N(w) = x^N|Z^N(w) = z^N(w)\} = \prod_{n=1}^{N} P_e(x_n|z_n(w)) \text{ for all } x^N \in \mathcal{X}^N.

3![](https://render.githubusercontent.com/render/math?math=\textbf{Identification phase:} \text{ An unknown individual is observed via an identification channel. For individual } w \text{ identification sequence } y^N \text{ occurs with probability } \Pr\{Y^N = y^N|Z^N(w) = z^N(w)\} = \prod_{l=1}^{N} P_i(y_l|z_n(w)) \text{ for all } y^N \in \mathcal{Y}^N.

The observed identification-sequence \( y^N \) is now ”compared” to all sequences \( x^N \) in the database and an estimate \( \hat{w} \) of the unknown individual is given.
A Standard Biometric Identification System

Descriptions and Definitions
Capacity Result, Proof

Search Complexity
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Search System Model
About the Ignorant Helper

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Model
Note that for all \( w \in \{1, 2, \cdots, M\} \), and \( x^N \in \mathcal{X}^N \),

\[ \Pr\{X^N(w) = x^N\} = \prod_{n=1}^{N} Q_b(x_n) \]

with \( Q_b(x) = \sum_{z \in \mathcal{Z}} Q(z)P_e(x|z) \) for all \( x \in \mathcal{X} \),

hence all enrollment sequences are IID with \( Q_b(x) \).

For all \( w \in \{1, 2, \cdots, M\} \), \( x^N \in \mathcal{X}^N \) and \( y^N \in \mathcal{Y}^N \),

\[ \Pr\{Y^N = y^N|X^N(w) = x^N\} = \prod_{n=1}^{N} Q_c(y_n|x_n) \]

with \( Q_c(y|x) = \frac{\sum_{z \in \mathcal{Z}} Q(z)P_e(x|z)P_i(y|z)}{\sum_{z \in \mathcal{Z}} Q(z)P_e(x|z)} \),

for all \( x \in \mathcal{X}, y \in \mathcal{Y} \),

hence the channel \( Q_c(y|x) \) between enrollment sequence and observation sequence is a DMC.
Error probability is defined as

\[ P_e \triangleq \sum_{w=1}^{M} \frac{1}{M} \Pr\{\hat{W} \neq w | W = w\} \]

We say that the capacity of a biometric system is \( C \) if for any \( \delta > 0 \) there exist, for all large enough \( N \), decoders that achieve

\[ \frac{1}{N} \log_2 M \geq C - \delta, \]

\[ P_e \leq \delta. \]

**Theorem**

O'Sullivan & Schmid [Allerton 2002], W., Kalker, Goseling & Linnartz [ISIT 2003]: The capacity of a biometric identification system is given by

\[ C = I(X; Y), \]

where \( P(x, y) = Q_b(x)Q_c(y|x) = \sum_{z \in Z} Q(z)P_e(x|z)P_i(y|z) \) for all \( x \in \mathcal{X}, y \in \mathcal{Y} \).
Proof

- Observe that the enrollment sequences $x^N(1), x^N(2), \ldots, x^N(M)$ form a random code.

- Ones of these codewords is observed via a DMC. The decoder looks for the unique index $w$ such that $(x^N(\hat{w}), y^N) \in A^N(\epsilon(XY))$.

- Standard arguments apply directly here and result in achievability.

- Converse is standard.
Can we somehow decrease the search complexity?

Note that to do the identification, the decoder has to check all enrollment sequences \( \{x^N(w), w = 1, 2, \cdots, M\} \) to find out whether \((x^N(w), y^N) \in \mathcal{A}_\varepsilon^N(XY)\).

- **QUESTION:** Can we speed up this process?
- **IDEA:** First we determine the “cluster” to which the unknown individual belongs, then we find out which individual “within the cluster” is the unknown individual we are looking for. (cluster-check must be as elementary as a refinement-check).
- **EXAMPLE:** 9 individuals in 3 clusters, 3 cluster-checks and 5 refinement-checks needed, 8 checks in total (6 would be better):

![Diagram of clusters and individuals]

- **QUESTION:** What is the fundamental trade-off between # of cluster-checks and # of refinement-checks here?
How do we model this search system?

First all enrollment-sequences \( X^N(1), X^N(2), \ldots, X^N(M) \) are generated, and this "code" is made available to informed decoder.

An individual \( W \) is chosen uniformly. Its enrollment sequence \( X^N(W) \) is transmitted via the observation channel, output is \( Y^N \).

The ignorant helper determines from \( Y^N \) the cluster index \( W_1 \), sends it to informed decoder and combiner.

The informed decoder determines from \( Y^N \) and \( W_1 \) the refinement-index \( W_2 \) and sends it to the combiner.

The combiner determines index \( \hat{W} \).
Why should the helper be ignorant?

If the helper would know the “code” it could do $\sqrt{M}$ cluster-checks, that each involve a typicality check for all $\sqrt{M}$ individuals in that cluster. In that case a cluster-check is not elementary anymore.
Fundamental trade-off

There are three rates. Rate $R$ corresponds to the number of individuals, cluster-rate $R_1$ to the number of clusters, and refinement-rate $R_2$ to the number of individuals in a cluster.

**Theorem**

The region of achievable rate triples for our biometric identification system is given by

$$\{(R_1, R_2, R) : \begin{align*}
R_1 &\geq I(Y; U), \\
R_2 &\geq \max(0, R - I(X; U)), \\
0 &\leq R \leq I(X; Y),
\end{align*}$$

for $P(x, y, u) = Q_b(x)Q_c(y|x)P(u|y)$, where $|U| \leq |Y| + 1$. 

Proof outline

- Generate $M_1$ covering sequences $u^N(1), u^N(2), \cdots, u^N(M_1)$.
- The ignorant helper determines which covering sequence $u^N(w_1)$ is jointly typical with $y^N$, and outputs $w_1$. There is always such a sequence if $R_1 \geq I(U; Y)$.
- The informed decoder has a list of individuals whose enrollment sequences are jointly typical with $u^N(w_1)$. The log-size of this list is $N(R - I(U; X))$. It finds out which of these sequences is jointly typical with $(y^N, u^N(w_1))$, and outputs its index $w_2$ within the list.
- If $R \leq I(X; Y)$, the probability that the enrollment sequence of some other individual is jointly typical with $(y^N, u^N(w_1))$, is negligible.
- Converse.
Consider a system with binary uniform biometric sequences and a binary symmetric observation channel with cross-over probability $q = 0.1$. Region of achievable triples:

$$\{(R_1, R_2, R) : R_1 \geq 1 - h(p), R_2 \geq \max(0, R - 1 + h(p \cdot q)),
0 \leq R \leq 1 - h(q), \text{ for } 0 \leq p \leq 1/2\}.$$
Excess Rate

Ideally $R_1 + R_2 = R$. However in general we can write for the excess rate $\Delta$ that

$$\Delta = R_1 + R_2 - R \geq I(U; Y) - I(U; X)$$
$$= H(U|X) - H(U|Y, X)$$
$$= I(U; Y|X)$$
$$= H(Y|X) - H(Y|X, U).$$

For $U$ such that $R \geq I(X; U)$ and for optimum cluster-refinement rate-pairs $(R_1, R_2)$ we get

$$\Delta = H(Y|X) - H(Y|X, U) \leq H(Y|X).$$

This maximum excess rate is achieved for $U = Y$, and this results in refinement rate $R_2 = 0$.

Note that the upper bound on the excess rate is larger for more noisy observation channels. Noise-free observation channels allow for a zero-excess rate.
Concluding remarks

- Storage complexity (from the lists, which is $R_1 + R_2$) is not optimized here, and is $\Delta$ larger than $R$. Compressed data bases are considered by Westover & O'Sullivan [2008], and Tuncel [2009].
- Implementation: Helper should use structured vector quantizer. In that case checking all the clusters is not needed, and only the refinement rate is of interest.
- Three or more steps.


![Graph showing channel transition probability vs. error probability for full search and clustering.](image)