BIOMETRIC SEARCH CODES

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Procedure

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

1. **Generation phase:** A biometric sequence $z^N(w)$ is generated for each individual w, hence

$$\Pr\{Z^N(w) = z^N\} = \prod_{n=1,N} Q(z_n), \text{ for all } z^N \in \mathcal{Z}^N.$$

2. **Enrollment phase:** Each individual is observed via an enrollment channel. The resulting enrollment-sequence $x^N(w)$, is added to a **database**. Now

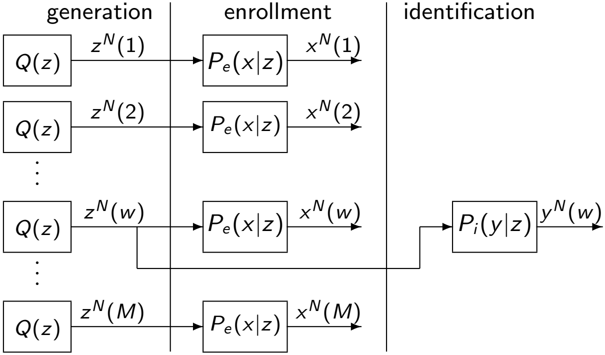
$$\Pr\{X^N(w) = x^N | Z^N(w) = z^N(w)\} = \prod_{n=1,N} P_e(x_n|z_n(w)) \text{ for all } x^N \in \mathcal{X}^N.$$

3. **Identification phase:** An unknown individual is observed via an identification channel. For individual w identification sequence y^N occurs with probability

$$\Pr\{Y^N = y^N | Z^N(w) = z^N(w)\} = \prod_{l=1,N} P_i(y_n|z_n(w)) \text{ for all } y^N \in \mathcal{Y}^N.$$

The observed identification-sequence y^N is now "compared" to all sequences x^N in the database and an **estimate** $\widehat{w}$ of the unknown individual is given.

Model


generation
enrollment
identification
$Q(z)$
$z^N(1)$
$P_e(x|z)$
$x^N(1)$
$Q(z)$
$z^N(2)$
$P_e(x|z)$
$x^N(2)$
$Q(z)$
$z^N(w)$
$P_e(x|z)$
$x^N(w)$
$P_i(y|z)$
$y^N(w)$
$Q(z)$
$z^N(M)$
$P_e(x|z)$
$x^N(M)$

Probabilistic structure

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

$$\begin{aligned}\Pr\{X^N(w) = x^N\} &= \prod_{n=1,N} Q_b(x_n)\\ \text{with } Q_b(x) &= \sum_{z \in \mathcal{Z}} Q(z)P_e(x|z) \text{ for all } x \in \mathcal{X},\end{aligned}$$

  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 $y^N \in \mathcal{Y}^N$,

$$\begin{aligned}\Pr\{Y^N = y^N|X^N(w) = x^N\} &= \prod_{n=1,N} Q_c(y_n|x_n)\\ \text{with } Q_c(y|x) &= \frac{\sum_{z \in \mathcal{Z}} Q(z)P_e(x|z)P_i(y|z)}{\sum_{z \in \mathcal{Z}} Q(z)P_e(x|z)},\\ &\quad \text{for all } x \in \mathcal{X}, y \in \mathcal{Y},\end{aligned}$$

  hence the channel $Q_c(y|x)$ between enrollment sequence and observation sequence is a DMC.

Capacity

Error probability is defined as

$$P_e \triangleq \sum_{w=1,M} \frac{1}{M} \Pr\{\widehat{W} \neq w | W = w\}$$

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

$$\begin{aligned} \frac{1}{N} \log_2 M &\geq C - \delta, \\ P_e &\leq \delta. \end{aligned}$$

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

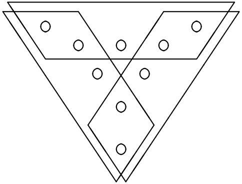
Proof

- Observe that the enrollment sequences $x^N(1), x^N(2), \cdots, x^N(M)$ form a **random code**.
- Ones of these codewords is observed via a DMC. The decoder looks for the unique index w such that $(x^N(\widehat{w}), y^N) \in \mathcal{A}_\varepsilon^N(XY)$.
- Standard arguments apply directly here and result in achievability.
- Converse is standard.

Can we somehow decrease the search complexity?

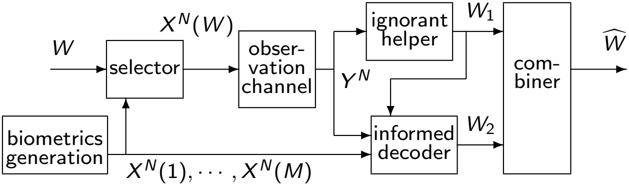
Note that to do the identification, the decoder has to check all enrollment sequences $\{x^N(w), w = 1, 2, \cdots, M\}$ to find out whether $(x^N(w), y^N) \in \mathcal{A}_\varepsilon^N(XY)$.

- **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):



- **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 $x^N(1), x^N(2), \cdots, x^N(M)$ 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 $\widehat{W}$.

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

$$\begin{aligned}\{(R_1, R_2, R) \quad : \quad & R_1 \geq I(Y;U), \\ & R_2 \geq \max(0, R - I(X;U)), \\ & 0 \leq R \leq I(X;Y), \\ & \textit{for } P(x,y,u) = Q_b(x)Q_c(y|x)P(u|y), \\ & \textit{where } |\mathcal{U}| \leq |\mathcal{Y}| + 1\}.\end{aligned}$$

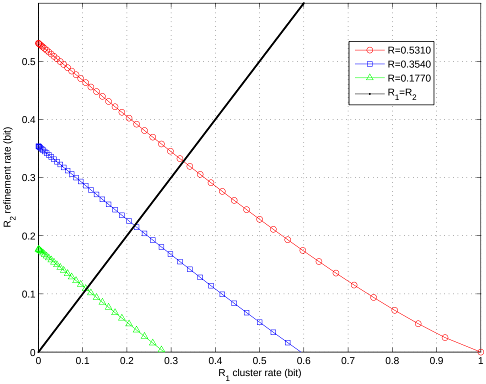
Proof outline

- 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.

Example: Binary uniform symmetric case

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:

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



Excess Rate

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

$$\begin{aligned}
\Delta = R_1 + R_2 - R &\geq I(U;Y) - I(U;X) \\
&= H(U|X) - H(U|Y,X) \\
&= I(U;Y|X) \\
&= H(Y|X) - H(Y|X,U).
\end{aligned}$$

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

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

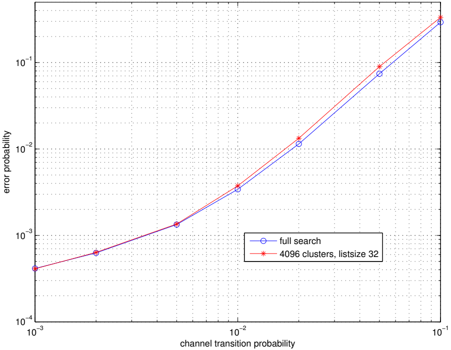
This maximum excess rate is achieved for $U = Y$, and this results in refinement rate $R_2 = 0$.
Note that the upper bound on the excess rate is larger for more noisy observation channels.
Noise-free observation channels allow for a zero-excess rate.

Concluding remarks

- Storage complexity (from the lists, which is $R_1 + R_2$) is not optimized here, and is Δ 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.

Search Complexity: Clustering Based on a Binary Golay Code

$N = 23$. Generate $M = 4096$ uniform binary biometric sequences ($R = 12/23$). Nr. of clusters $M_1 = 4096$. Refinement-list-size $M_2 = 32$. Error probability based on full search and on clustering. Complexity decrease $4096/32 = 128$.


error probability
10^{-1}
10^{-2}
10^{-3}
10^{-4}
10^{-3}
10^{-2}
10^{-1}
channel transition probability
full search
4096 clusters, listsize 32