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First Edition

Author Name(s)

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Foreword

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I

This is a Part



Introduction to Image Processing and the MATLAB Environment

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A COMPONENT PART for an electronic item is manufactured at one of three different factories, and then delivered to the main assembly line. Of the total number supplied, factory A supplies 50%, factory B 30%, and factory C 20%. Of the components manufactured at factory A, 1% are faulty and the corresponding proportions for factories B and C are 4% and 2% respectively. A component is picked at random from the assembly line.

- Checking various symbols in the current package configuration
- - — _

- `_` — `\textunderscore`
- `\` — `\textbackslash`
- `™` — `\texttrademark`
- `®` — `\textregistered`
- `<` — `\textless`
- `>` — `\textgreater`
- etc.
- Currently OK symbols with this package configuration
- `å` — `\aa`
- `å` — `\r{a}`
- `ü` — `\"u`
- `é` — `\'e`
- `è` — `\'e`
- `∅` — `\o`

1.1 INTRODUCTION

1.1.1 A Component Part

The term reliability usually refers to the probability that a component or system will operate satisfactorily either at any particular instant at which it is required or for a certain length of time. Fundamental to quantifying reliability is a knowledge of how to define, assess and combine probabilities [1]. This may hinge on identifying the form of the variability which is inherent in most processes. If all components had a fixed known lifetime there would be no need to model reliability.

A component part for an electronic item is manufactured at one of three different factories, and then delivered to the main assembly line. Of the total number supplied, factory A supplies 50%, factory B 30%, and factory C 20%. Of the components manufactured at factory A, 1% are faulty and the corresponding proportions for factories B and C are 4% and 2% respectively. A component is picked at random from the assembly line. What is the probability that it is faulty [4]? A component part for an electronic item is manufactured at one of three different factories, and then delivered to the main assembly line. Of the total number supplied, factory A supplies 50%, factory B 30%, and factory C 20%. Of the components manufactured at factory A, 1% are faulty and the corresponding proportions for factories B and C are 4% and 2% respectively. A component is picked at random from the assembly line.

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TABLE 1.1 Comparison of MATLAB and C Code for Simple Matrix Operations

Operations	Part of C Code	Hor. fts.	Ver. fts.
Ball	19, 221	4, 598	3, 200
Pepsi ^a	46, 281	6, 898	5, 400
Keybrd ^b	27, 290	2, 968	3, 405
Pepsi	14, 796	9, 188	3, 209

“A Process is a structured, measured set of activities designed to produce a specific output for a particular customer or market—A process is thus a specific ordering of work activities across time and space, with a beginning, an end, and clearly defined inputs and outputs: a structure for action.”

Thomas Davenport
Senior Adjutant to the Junior Marketing VP

MultiRelational k -Anonymity. Most works on k -anonymity focus on anonymizing a single data table; however, a real-life [2] database usually contains multiple relational tables. This has proposed a privacy model called *MultiR k -anonymity* to ensure k -anonymity on multiple relational tables. Their model assumes that a relational database contains a person-specific table PT and a set of tables T_1, \dots, T_n , where PT contains a person identifier Pid and some sensitive attributes, and T_i , for $1 \leq i \leq n$, contains some foreign keys, some attributes in QID , and sensitive attributes. The general privacy notion is to ensure that for each record owner o contained in the join of all tables $PT \bowtie T_1 \bowtie \dots \bowtie T_n$, there exists at least $k - 1$ other record owners share the same QID with o . It is important to emphasize that the k -anonymization is applied at the *record owner* level, not at the *record* level in traditional k -anonymity. This idea is similar to (X, Y) -anonymity, where $X = QID$ and $Y = \{Pid\}$.

1. Factual knowledge (“knowing that”) One family considers a privacy threat occurs when an attacker is able to link a record owner to a record in a published data table, to a sensitive attribute in a published data table, or to the published data table itself. We call them *record linkage*, *attribute linkage*.
 - (a) Conceptual knowledge (“knowing why”) One family considers a privacy threat occurs when an attacker is able to link a record owner to a record in

TABLE 1.2 Now we are engaged (a_g^a) (a_g^a) in a great civil war, testing whether that nation, or any nation so conceived.

Ball	19, 221	4, 598	3, 200
Pepsi	46, 281	6, 898	5, 400
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- ii. Spatial knowledge (“knowing what”)

In most literature on PPDP, they [5] consider a more relaxed, yet more practical, notion of privacy protection by assuming limited attacker’s background knowledge. Below, the term “victim” refers to the record owner being linked. We can broadly classify linking models to two families.

A component part for an electronic item is [3] manufactured at one of three different factories, and then delivered to the main assembly line. Of the total number supplied, factory A supplies 50%, factory B 30%, and factory C 20%. Of the components manufactured at factory A, 1% are faulty and the corresponding proportions for factories B and C are 4% and 2% respectively.

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published data table, or to the published data table itself. We call them *record linkage*, *attribute linkage*, and *table linkage*, respectively. In all types of linkages, we assume that the attacker knows the *QID* of the victim. In record and attribute linkages, we further assume that the attacker knows the presence of the victim's record in the released table, and seeks to identify the victim's record and/or sensitive information from the table [9]. In table linkage, the attack seeks to determine the present or absent of the victim's record in the released table. A data table is considered to privacy preserved if the table can effectively prevent the attacker from successfully performing these types of linkages on the table [6]. Sections 11.1-11.2 study this family of privacy models.

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Theorem 1.1 *Let m be a prime number. With the addition and multiplication as defined above, Z_m is a field.*

Proof 1.1 *Most of the proof of this theorem is routine. It is clear that $0 \in Z_m$ and $1 \in Z_m$ are the zero element and identity element. If $a \in Z_m$ and $a \neq 0$, then $m - a$ is the additive inverse of a . If $a \in Z_m$ and $a \neq 0$, then the greatest common divisor of a and m is 1, and hence there exist integers s and t such that $sa + tm = 1$. Thus $sa = 1 - tm$ is congruent to 1 modulo m . Let s^* be the integer in Z_m congruent to s modulo m . Then we also have $s^*a \equiv 1 \pmod{m}$. Hence s^* is the multiplicative inverse of a modulo m . Verification of the rest of the field properties is now routine.*

1.2 RECORD LINKAGE MODEL PART HEADING LENGTH LINE CHECK FOR LARGER TWO LINES EVERYWHERE

In the privacy attack of *record linkage*, some value *qid* on *QID* identifies a small number of records in the released table T , called a *group*. If the victim's *QID* matches the value *qid*, the victim is vulnerable to being linked to the small number of records in the group [7]. In this case, the attacker faces only a small number of possibilities for the victim's record, and with the help of additional knowledge, there is a chance that the attacker could uniquely identify the victim's record from the group.

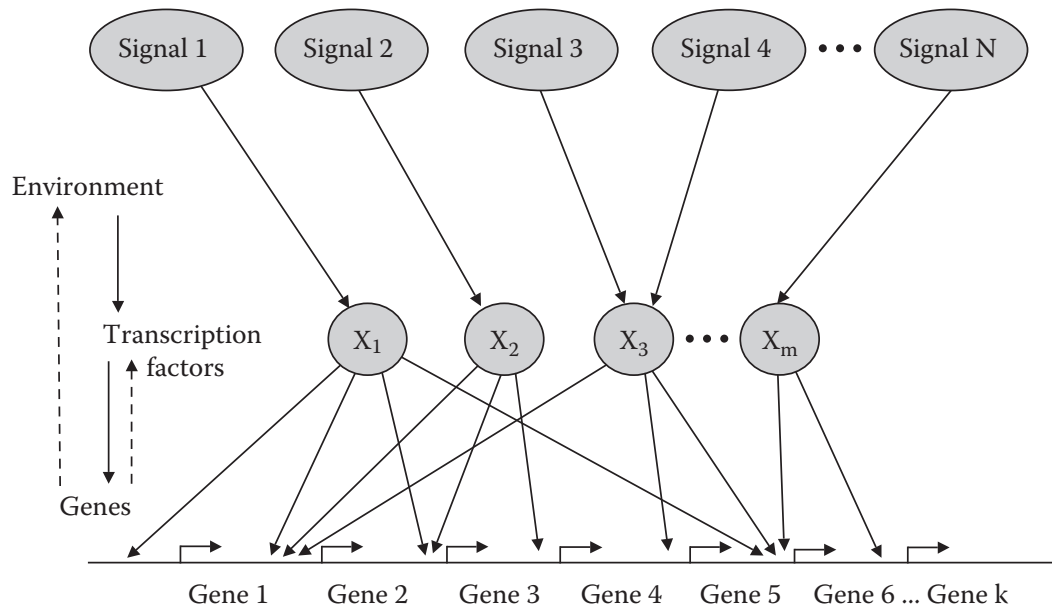


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1.2.1 A Component Part Heading Length Line Check for Larger Two Lines Everywhere

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Let u be in the subspace V . Because $0u = 0$, it follows that the zero vector is in V . Similarly, $-u$ is in V for all u in V . A simple example of a subspace of F^n is the set of all vectors $(0, a_2, \dots, a_n)$ with first coordinate equal to 0. The zero vector itself is a subspace.

Definition 1.1 Let $u^{(1)}, u^{(2)}, \dots, u^{(m)}$ be vectors in F^n , and let c_1, c_2, \dots, c_m be scalars. Then the vector

$$c_1u^{(1)} + c_2u^{(2)} + \dots + c_mu^{(m)}$$

is called a *linear combination* of $u^{(1)}, u^{(2)}, \dots, u^{(m)}$. If V is a subspace of F^n , then V is closed under vector addition and scalar multiplication, and it follows easily by induction that a linear combination of vectors in V is also a vector in V . Thus *subspaces are closed under linear combinations*; in fact, this can be taken as the defining property of subspaces. The vectors $u^{(1)}, u^{(2)}, \dots, u^{(m)}$ *span* V (equivalently, form a *spanning set* of V) provided every vector in V is a linear combination of $u^{(1)}, u^{(2)}, \dots, u^{(m)}$. The zero vector can be written as a linear combination of $u^{(1)}, u^{(2)}, \dots, u^{(m)}$ with all scalars equal to 0; this is a *trivial linear combination*. The vectors $u^{(1)}, u^{(2)}, \dots, u^{(m)}$ are *linearly dependent* provided there are scalars c_1, c_2, \dots, c_m , not all of which are zero, such that

$$c_1u^{(1)} + c_2u^{(2)} + \dots + c_mu^{(m)} = 0,$$

that is, the zero vector can be written as a *nontrivial linear combination* of $u^{(1)}, u^{(2)}, \dots, u^{(m)}$. For example, the vectors $(1, 4)$, $(3, -1)$, and $(3, 5)$ in \mathbb{R}^2 are linearly dependent since

$$3(1, 4) + 1(3, -2) - 2(3, 5) = (0, 0).$$

Vectors are *linearly independent* provided they are not linearly dependent. The vectors $u^{(1)}, u^{(2)}, \dots, u^{(m)}$ are a *basis* of V provided they are linearly independent and span V . By an *ordered basis* we mean a basis in which the vectors of the basis are listed in a specified order; to indicate that we have an ordered basis we write $(u^{(1)}, u^{(2)}, \dots, u^{(m)})$. A spanning set S of V is a *minimal spanning set* of V provided that each set of vectors obtained from S by removing a vector is not a spanning set for V . A linearly independent set S of vectors of V is a *maximal linearly independent set of vectors* of V provided that for each vector w of V that is not in S , $S \cup \{w\}$ is linearly dependent (when this happens, w must be a linear combination of the vectors in S). \square

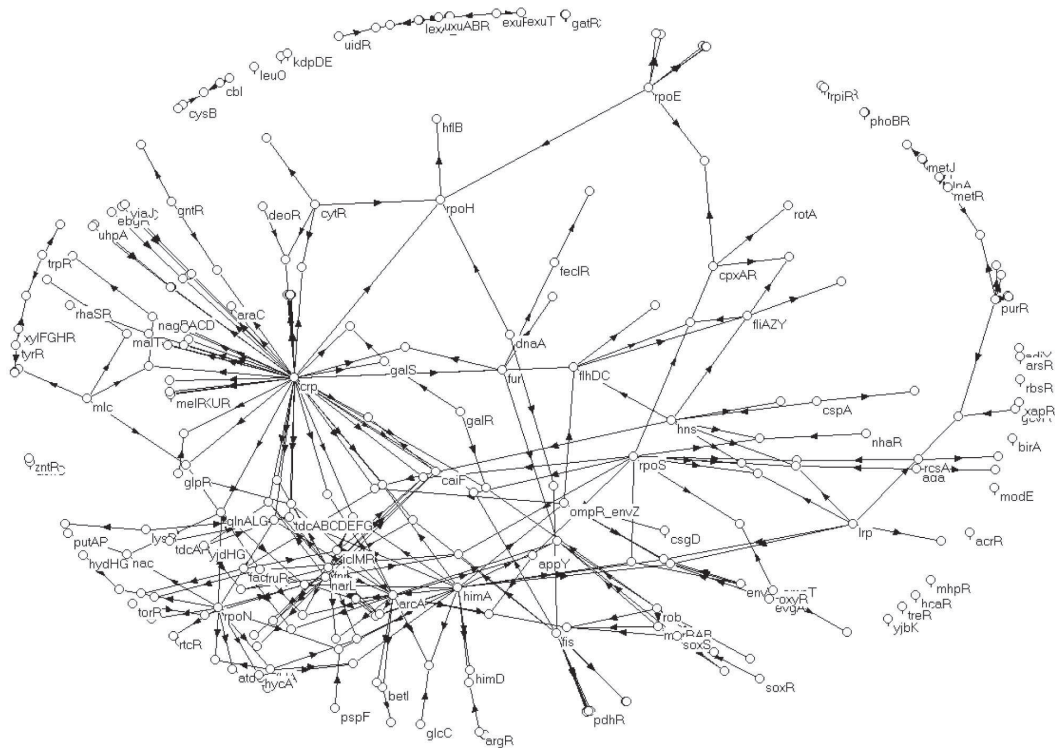


Figure 1.2 Figure caption goes hereq. Figure caption goes here. Figure caption goes here. Figure caption goes here. Figure caption goes here. Figure caption goes here.

In addition to matrix addition, subtraction, and multiplication, there is one additional operation that we define now. It's perhaps the simplest of them all. Let $A = [a_{ij}]$ be an m by n matrix and let c be a number [3]. Then the matrix $c \cdot A$, or simply cA , is the m by n matrix obtained by multiplying each entry of A by c :

$$cA = [ca_{ij}].$$

The matrix cA is called a *scalar multiple* of A .

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EXERCISES

- 1.1 *A change in production rate.* A gene Y with simple regulation is produced at a constant rate β_1 . The production rate suddenly shifts to a different rate β_2 .
- 1.2 *A change in production rate.* A gene Y with simple regulation is produced at a constant rate β_1 . The production rate suddenly shifts to a different rate β_2 .

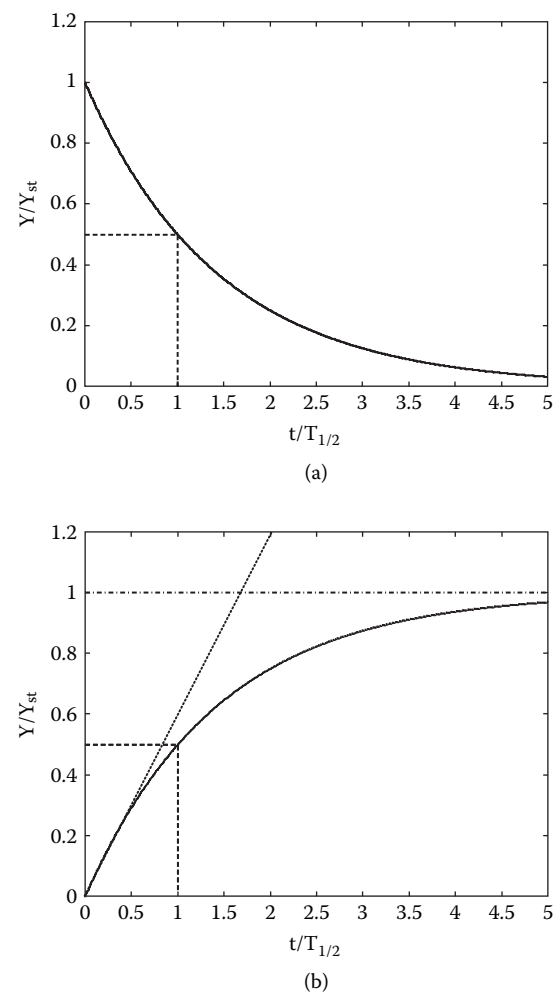


Figure 1.3 The bar charts depict the different risk contributions (top: 99% quantile, bottom: 99.9% quantile) of the business areas of a bank. The black bars are based on a Var/Covar approach, the white ones correspond to shortfall risk.

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- 1.8 *A change in production rate.* A gene Y with simple regulation is produced at a constant rate β_1 . The production rate suddenly shifts to a different rate β_2 .
- a. Calculate and plot the gene product concentration $Y(t)$.
- b. What is the response time (time to reach halfway between the steady states)?

Solution (for part a):

- a. Let us mark the time when the shift occurs as $t = 0$. Before the shift, Y reaches steady state at a level $Y(t = 0) = Y_{st} = \beta_1/\alpha$. After the shift,

$$dY/dt = \beta_2 - \alpha Y \quad (\text{P1.1})$$

The solution of such an equation is generally $Y = C_1 + C_2 e^{-\alpha t}$, where the constants C_1 and C_2 need to be determined so that $Y(t = 0) = \beta_1/\alpha$, and Y at long times reaches its new steady state, β_2/α . This yields the following sum of an exponential and a constant:

$$Y(t) = \beta_2/\alpha + (\beta_1/\alpha - \beta_2/\alpha) e^{-\alpha t} \quad (\text{P2.2})$$

Take the derivative with respect to time, dY/dt , and verify that Equation P2.1 is fulfilled.

- 1.9 *mRNA dynamics.* In the main text, we considered the activation of transcription of a gene (mRNA production) and used a dynamical equation to describe the changes in the concentration of the gene product, the protein Y. In this equation, $dY/dt = \beta - \alpha Y$, the parameter β describes the rate of protein production. In reality, mRNA needs to be translated to form the protein, and mRNA itself is also degraded by specific enzymes.
- a. Derive dynamical equations for the rate of change of mRNA and the rate of change of the protein product, assuming that mRNA is produced at rate β_m and degraded at rate α_m , and that each mRNA produces on average p protein molecules per unit time. The protein is degraded/diluted at rate α .

- b. Note that mRNA is often degraded at a much faster rate than the protein product $\alpha_m \gg \alpha$. Can this be used to form a quasi-steady-state assumption that mRNA levels are at steady state with respect to slower processes? What is the effective protein production rate β in terms of β_m , α_m , and p ? What would be the response time if the mRNA lifetime were much longer than the protein lifetime?

Solution:

- a. The dynamic equation for the concentration of mRNA of gene Y, Y_m , is:

$$dY_m / dt = \beta_m - \alpha_m Y_m \quad (\text{P1.2})$$

The dynamical equation for the protein product is due to production of p copies per mRNA and degradation/dilution at rate α :

$$dY_m / dt = \beta_m - \alpha_m Y_m \quad (\text{P1.3})$$

$$dY / dt = p Y_m - \alpha Y \quad (\text{P1.4})$$

- b. In the typical case that mRNA degradation is faster than the degradation/dilution of the protein product, we can assume that Y_m reaches steady state quickly in comparison to the protein levels. The reason is that the typical time for the mRNA to reach steady state is the response time $\log(2)/\alpha_m$, which is much shorter than the protein response time $\log(2)/\alpha$ because $\alpha_m \gg \alpha$. The steady-state mRNA level is found by setting $dY_m/dt = 0$ in Equation P2.3, yielding

Using this for Y_m in Equation P2.4 yields the following equation for the protein production rate:

In other words, the effective protein production rate, which is the first term on the right-hand side of the equation, is equal to the steady-state mRNA level times the number of proteins translated from each mRNA per unit time:

$$\beta = p \beta_m / \alpha_m \quad (\text{P1.5})$$

- 1.10 *Time-dependent production and decay.* A gene Y with simple regulation has a time-dependent production rate $\beta(t)$ and a time-dependent degradation rate $\alpha(t)$. Solve for its concentration as a function of time.

Think About It...

Commonly thought of as the first modern computer, ENTAC was built in 1944. It took up more space than an 18-wheeler's tractor trailer and weighed more than 17 Chevrolet Camaros. It consumed 140,000 watts of electricity while executing up to 5,000 basic arithmetic operations per second. One of today's popular microprocessors, the 486, is built on a tiny piece of silicon about the size of a dime.

With the continual expansion of capabilities, computing power will eventually exceed the capacity for human comprehension or human control.

The Information Revolution
Business Week

GLOSSARY

360 Degree Review: Performance review that includes feedback from superiors, peers, subordinates, and clients.

Abnormal Variation: Changes in process performance that cannot be accounted for by typical day-to-day variation. Also referred to as non-random variation.

Acceptable Quality Level (AQL): The minimum number of parts that must comply with quality standards, usually stated as a percentage.

Activity: The tasks performed to change inputs into outputs.

Adaptable: An adaptable process is designed to maintain effectiveness and efficiency as requirements change. The process is deemed adaptable when there is agreement among suppliers, owners, and customers that the process will meet requirements throughout the strategic period.

FURTHER READING

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Savageau, M.A. (1974). Comparison of classical and auto-genous systems of regulation in inducible operons. *Nature*, 252: 546–549.



Introduction to Image Processing and the MATLAB Environment

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Affiliation text1

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Author Name3

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Author Name4

Affiliation text4

CONTENTS

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11.2	Record Linkage Model	22
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11.2.1.1	H3 A Component Part	23

A COMPONENT PART for an electronic item is manufactured at one of three different factories, and then delivered to the main assembly line. Of the total number supplied, factory A supplies 50%, factory B 30%, and factory C 20%. Of the components manufactured at factory A, 1% are faulty and the corresponding proportions for factories B and C are 4% and 2% respectively. A component is picked at random from the assembly line.

11.1 INTRODUCTION

The term reliability usually refers to the probability that a component or system will operate satisfactorily either at any particular instant at which it is required or for a certain length of time. Fundamental to quantifying reliability is a knowledge of how to

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“A Process is a structured, measured set of activities designed to produce a specific output for a particular customer or market—A process is thus a specific ordering of work activities across time and space, with a beginning, an end, and clearly defined inputs and outputs: a structure for action.”

Thomas Davenport
Senior Adjutant to the Junior Marketing VP

MultiRelational k -Anonymity. Most works on k -anonymity focus on anonymizing a single data table; however, a real-life [2] database usually contains multiple relational tables. This has proposed a privacy model called *MultiR k -anonymity* to ensure k -anonymity on multiple relational tables. Their model assumes that a re-

lational database contains a person-specific table PT and a set of tables T_1, \dots, T_n , where PT contains a person identifier Pid and some sensitive attributes, and T_i , for $1 \leq i \leq n$, contains some foreign keys, some attributes in QID , and sensitive attributes. The general privacy notion is to ensure that for each record owner o contained in the join of all tables $PT \bowtie T_1 \bowtie \dots \bowtie T_n$, there exists at least $k - 1$ other record owners share the same QID with o . It is important to emphasize that the k -anonymization is applied at the *record owner* level, not at the *record* level in traditional k -anonymity. This idea is similar to (X, Y) -anonymity, where $X = QID$ and $Y = \{Pid\}$.

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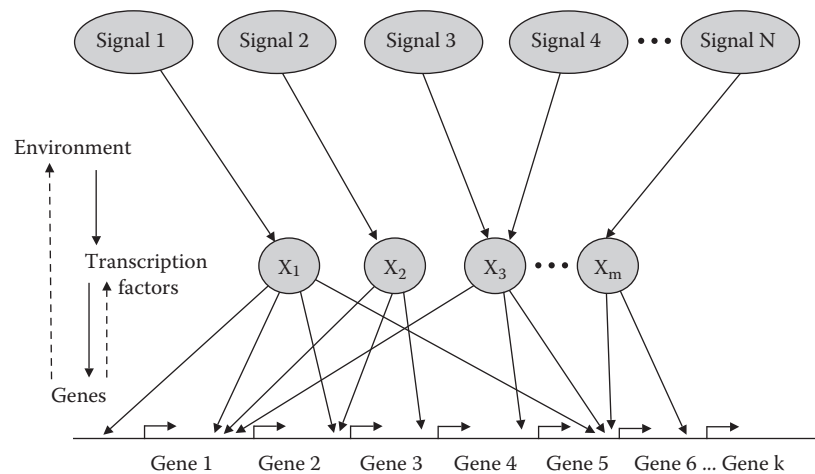


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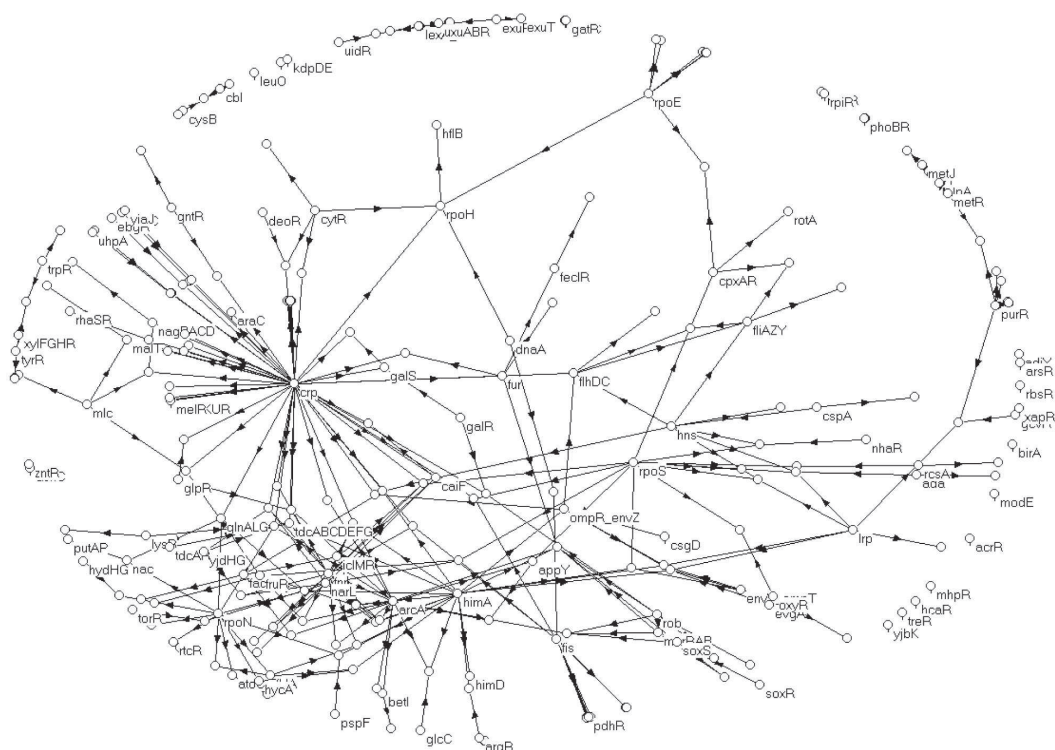


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Similarly, $-u$ is in V for all u in V . A simple example of a subspace of F^n is the set of all vectors $(0, a_2, \dots, a_n)$ with first coordinate equal to 0. The zero vector itself is a subspace.

Definition 11.1 Let $u^{(1)}, u^{(2)}, \dots, u^{(m)}$ be vectors in F^n , and let c_1, c_2, \dots, c_m be scalars. Then the vector

$$c_1 u^{(1)} + c_2 u^{(2)} + \dots + c_m u^{(m)}$$

is called a *linear combination* of $u^{(1)}, u^{(2)}, \dots, u^{(m)}$. If V is a subspace of F^n , then V is closed under vector addition and scalar multiplication, and it follows easily by induction that a linear combination of vectors in V is also a vector in V . Thus *subspaces are closed under linear combinations*; in fact, this can be taken as the defining property of subspaces. The vectors $u^{(1)}, u^{(2)}, \dots, u^{(m)}$ *span* V (equivalently, form a *spanning set* of V) provided every vector in V is a linear combination of $u^{(1)}, u^{(2)}, \dots, u^{(m)}$. The zero vector can be written as a linear combination of $u^{(1)}, u^{(2)}, \dots, u^{(m)}$ with all scalars equal to 0; this is a *trivial linear combination*. The vectors $u^{(1)}, u^{(2)}, \dots, u^{(m)}$ are *linearly dependent* provided there are scalars c_1, c_2, \dots, c_m , not all of which are zero, such that

$$c_1 u^{(1)} + c_2 u^{(2)} + \dots + c_m u^{(m)} = 0,$$

that is, the zero vector can be written as a *nontrivial linear combination* of $u^{(1)}, u^{(2)}, \dots, u^{(m)}$. For example, the vectors $(1, 4)$, $(3, -1)$, and $(3, 5)$ in \mathbb{R}^2 are linearly dependent since

$$3(1, 4) + 1(3, -2) - 2(3, 5) = (0, 0).$$

Vectors are *linearly independent* provided they are not linearly dependent. The vectors $u^{(1)}, u^{(2)}, \dots, u^{(m)}$ are a *basis* of V provided they are linearly independent and span V . By an *ordered basis* we mean a basis in which the vectors of the basis are listed in a specified order; to indicate that we have an ordered basis we write $(u^{(1)}, u^{(2)}, \dots, u^{(m)})$. A spanning set S of V is a *minimal spanning set* of V provided that each set of vectors obtained from S by removing a vector is not a spanning set for V . A linearly independent set S of vectors of V is a *maximal linearly independent set of vectors* of V provided that for each vector w of V that is not in S , $S \cup \{w\}$ is linearly dependent (when this happens, w must be a linear combination of the vectors in S). \square

In addition to matrix addition, subtraction, and multiplication, there is one additional operation that we define now. It's perhaps the simplest of them all. Let $A = [a_{ij}]$ be an m by n matrix and let c be a number [3]. Then the matrix $c \cdot A$, or simply cA , is the m by n matrix obtained by multiplying each entry of A by c :

$$cA = [ca_{ij}].$$

The matrix cA is called a *scalar multiple* of A .

```

<spec>      ::= <module> {<module>}

<module>    ::= <fun> | <init> | <host> | <channel> |

<fun>       ::= "fun" <funname> { ";" "fun" <funname> }

<funname>   ::= <name> <funpar>

<funpar>    ::= [ "(" <name> { "," <name> } ")" ]
               [ "[" <qop> { ";" <qop> } "]" ]

```

In addition to matrix addition, subtraction, and multiplication, there is one additional operation that we define now. It's perhaps the simplest of them all. Let $A = [a_{ij}]$ be an m by n matrix and let c be a number [3]. Then the matrix $c \cdot A$, or simply cA , is the m by n matrix obtained by multiplying each entry of A by c :

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```

<letter>    ::= "a" | "b" | "c" | "d" | "e" | "f" | "g" |
               "h" | "i" | "j" | "k" | "l" | "m" | "n" |
               "o" | "p" | "q" | "r" | "s" |
               "v" | "w" | "x" | "y" | "z" | "A" | "B" |
               "C" | "D" | "E" | "F" | "G" |
               "J" | "K" | "L" | "M" | "N" | "O" | "P" |
               "Q" | "R" | "S" | "T" | "U" |
               "X" | "Y" | "Z" | "_"

<digit>     ::= "0" | "1" | "2" | "3" | "4" | "5" | "6" |
               "7" | "8" | "9"

<value>     ::= <digit> { <digit> } [ "." { <digit> } ]

<init>      ::= "init" "{" "version" <value> { "," <value> } "}"

<version>   ::= "version" <value> "{" <run> "}"
               { "version" <value> "{" <run> "}" }

<run>       ::= "run" <name> <par> [ <rep> ] [ <chrep> ] |
               "run" <name> <par> [ <rep> ] [ <chrep> ]
               "->" "run" <name> <par> [ <rep> ] [ <chrep> ]

<par>       ::= "(" [ <name> { "," <name> } | "*" ] ")"

```

```

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<chrep>        ::= "[" <name> "." <valuei>
                  { "," <name> "." <valuei> } "]"

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<hostpar>      ::= <name> "(" <sche> ")" "(" <hchan> ")"
                  "{" <hbody> "}"

<sche>         ::= "fifo" | "rr"

<hchan>        ::= <name> | "*"

<hbody>        ::= <process> | <#>

<process>      ::= "process" <name> <par> "{" <procpa> "}"
                  { "process" <name> <par>
                    "{" <procpa> "}" }

<inprocl>      ::= <var> | <in> | <out> | <if> | <do> |
                  <subproc> | <finish>

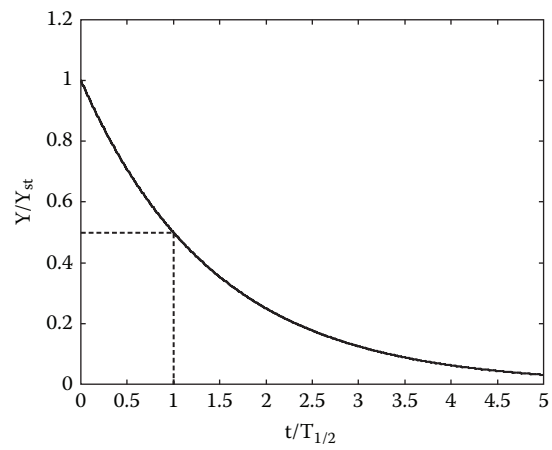
<subproc>      ::= "subprocess" <name> <par> "{" <procpa> "}"
                  { "subprocess" <name> <par>
                    "{" <procpa> "}" }

```

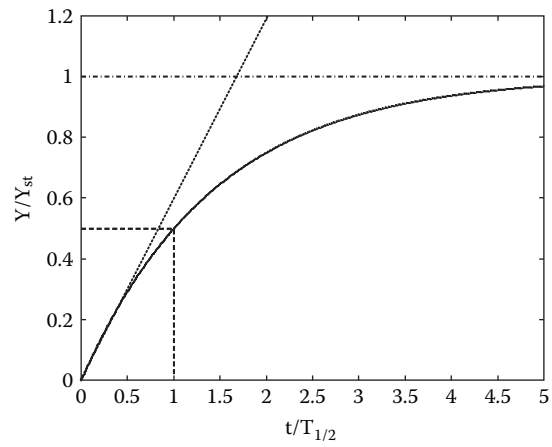
The term reliability usually refers to the probability that a component or system will operate satisfactorily either at any particular instant at which it is required or for a certain length of time. Fundamental to quantifying reliability is a knowledge of how to define, assess and combine probabilities [1]. This may hinge on identifying the form of the variability which is inherent in most processes. If all components had a fixed known lifetime there would be no need to model reliability.

EXERCISES

-
- 11.1 *A change in production rate.* A gene Y with simple regulation is produced at a constant rate β_1 . The production rate suddenly shifts to a different rate β_2 .
 - 11.2 *A change in production rate.* A gene Y with simple regulation is produced at a constant rate β_1 . The production rate suddenly shifts to a different rate β_2 .
 - 11.3 *A change in production rate.* A gene Y with simple regulation is produced at a constant rate β_1 . The production rate suddenly shifts to a different rate β_2 .
 - 11.4 *A change in production rate.* A gene Y with simple regulation is produced at a constant rate β_1 . The production rate suddenly shifts to a different rate β_2 .



(a)



(b)

Figure 11.3 The bar charts depict the different risk contributions (top: 99% quantile, bottom: 99.9% quantile) of the business areas of a bank. The black bars are based on a Var/Covar approach, the white ones correspond to shortfall risk.

- 11.5 *A change in production rate.* A gene Y with simple regulation is produced at a constant rate β_1 . The production rate suddenly shifts to a different rate β_2 .
- 11.6 *A change in production rate.* A gene Y with simple regulation is produced at a constant rate β_1 . The production rate suddenly shifts to a different rate β_2 .
- 11.7 *A change in production rate.* A gene Y with simple regulation is produced at a constant rate β_1 . The production rate suddenly shifts to a different rate β_2 .
- 11.8 *A change in production rate.* A gene Y with simple regulation is produced at a constant rate β_1 . The production rate suddenly shifts to a different rate β_2 .
- Calculate and plot the gene product concentration $Y(t)$.
 - What is the response time (time to reach halfway between the steady states)?

Solution (for part a):

- Let us mark the time when the shift occurs as $t = 0$. Before the shift, Y reaches steady state at a level $Y(t = 0) = Y_{st} = \beta_1/\alpha$. After the shift,

$$dY/dt = \beta_2 - \alpha Y \quad (\text{P11.1})$$

The solution of such an equation is generally $Y = C_1 + C_2 e^{-\alpha t}$, where the constants C_1 and C_2 need to be determined so that $Y(t = 0) = \beta_1/\alpha$, and Y at long times reaches its new steady state, β_2/α . This yields the following sum of an exponential and a constant:

$$Y(t) = \beta_2/\alpha + (\beta_1/\alpha - \beta_2/\alpha)e^{-\alpha t} \quad (\text{P2.2})$$

Take the derivative with respect to time, dY/dt , and verify that Equation P2.1 is fulfilled.

- 11.9 *mRNA dynamics.* In the main text, we considered the activation of transcription of a gene (mRNA production) and used a dynamical equation to describe the changes in the concentration of the gene product, the protein Y. In this equation, $dY/dt = \beta - \alpha Y$, the parameter β describes the rate of protein production. In reality, mRNA needs to be translated to form the protein, and mRNA itself is also degraded by specific enzymes.
- Derive dynamical equations for the rate of change of mRNA and the rate of change of the protein product, assuming that mRNA is produced at rate β_m and degraded at rate α_m , and that each mRNA produces on average p protein molecules per unit time. The protein is degraded/diluted at rate α .
 - Note that mRNA is often degraded at a much faster rate than the protein product $\alpha_m \gg \alpha$. Can this be used to form a quasi-steady-state assumption that mRNA levels are at steady state with respect to slower processes? What is the effective protein production rate β in terms of β_m , α_m , and p ? What would be the response time if the mRNA lifetime were much longer than the protein lifetime?

Solution:

- a. The dynamic equation for the concentration of mRNA of gene Y, Y_m , is:

$$dY_m / dt = \beta_m - \alpha_m Y_m \quad (\text{P11.2})$$

The dynamical equation for the protein product is due to production of p copies per mRNA and degradation/dilution at rate α :

$$dY_m / dt = \beta_m - \alpha_m Y_m \quad (\text{P11.3})$$

$$dY / dt = p Y_m - \alpha Y \quad (\text{P11.4})$$

- b. In the typical case that mRNA degradation is faster than the degradation/dilution of the protein product, we can assume that Y_m reaches steady state quickly in comparison to the protein levels. The reason is that the typical time for the mRNA to reach steady state is the response time $\log(2)/\alpha_m$, which is much shorter than the protein response time $\log(2)/\alpha$ because $\alpha_m \gg \alpha$. The steady-state mRNA level is found by setting $dY_m/dt = 0$ in Equation P2.3, yielding

Using this for Y_m in Equation P2.4 yields the following equation for the protein production rate:

In other words, the effective protein production rate, which is the first term on the right-hand side of the equation, is equal to the steady-state mRNA level times the number of proteins translated from each mRNA per unit time:

$$\beta = p \beta_m / \alpha_m \quad (\text{P11.5})$$

- 11.10 *Time-dependent production and decay.* A gene Y with simple regulation has a time-dependent production rate $\beta(t)$ and a time-dependent degradation rate $\alpha(t)$. Solve for its concentration as a function of time.

Think About It...

Commonly thought of as the first modern computer, ENIAC was built in 1944. It took up more space than an 18-wheeler's tractor trailer and weighed more than 17 Chevrolet Camaros. It consumed 140,000 watts of electricity while executing up to 5,000 basic arithmetic operations per second. One of today's popular microprocessors, the 486, is built on a tiny piece of silicon about the size of a dime.

With the continual expansion of capabilities, computing power will eventually exceed the capacity for human comprehension or human control.

The Information Revolution
Business Week

GLOSSARY

360 Degree Review: Performance review that includes feedback from superiors, peers, subordinates, and clients.

Abnormal Variation: Changes in process performance that cannot be accounted for by typical day-to-day variation. Also referred to as non-random variation.

Acceptable Quality Level (AQL): The minimum number of parts that must comply with quality standards, usually stated as a percentage.

Activity: The tasks performed to change inputs into outputs.

Adaptable: An adaptable process is designed to maintain effectiveness and efficiency as requirements change. The process is deemed adaptable when there is agreement among suppliers, owners, and customers that the process will meet requirements throughout the strategic period.

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