行政院國家科學委員會專題研究計畫　成果報告

池設計和連接網路

計畫類別：個別型計畫
計畫編號：NSC92-2115-M-009-014-
執行期間：92 年 08 月 01 日至 94 年 07 月 31 日
執行單位：國立交通大學應用數學系(所)

計畫主持人：黃光明

報告類型：精簡報告

處理方式：本計畫可公開查詢

中　華　民　國 94 年 8 月 30 日

中文摘要(1)：

A construction of Pooling Designs with some Happy Surprises 一文是我和本系同仁翁志文與美籍和俄籍學者合作而成。此文已被 J. Computational Biology 雜誌接受(主編 Michael Waterman 是計算分子生物的開山祖師)，表示我們的研究成果已不僅是數學上的推論，也確有生物上的應用。此文討論如何用有限域的理論構造 DNA 上可糾錯的測試，有很多意外的結果。

中文摘要(2)：

Equivalence of the one-rate model to the classical model on strictly nonblocking switching networks 一文已刊於離散數學中著有聲譽的 SIAM J. Disc. Math. 此文證明了不阻塞通訊網路中一個令人意外的結果，即一個簡單模型和一個很複雜的模型等價。

A Construction of Pooling Designs with Some Happy Surprises

A. G. D'yachkov Frank K. Hwang* Antony J. Macula† Pavel A. Vilenkin Chih-wen Weng‡

December 9, 2003

Abstract

The screening of data sets for "positive data objects" is essential to modern technology. A (group) test that indicates whether or not a positive data object is in a specific subset or pool of the data set can greatly facilitate the identification of all the positive data objects. A collection of tested pools is called a pooling design. Pooling designs are standard experimental tools in many biotechnical applications. In this paper, we use the (linear) subspace relation coupled with general concept of a "containment matrix" to construct pooling designs with surprisingly high degrees of error-correction (detection.) Error-correcting pooling designs are important to biotechnical applications where error rates often are as high as 15%. What is also surprising is that the rank of the pooling design containment matrix is independent of the number of positive data objects in the data set.

Keywords: pooling designs, error-correction.

---

*This research was partially supported by a Republic of China NSC grant 92-2115-M-009-014.

†Corresponding author. This research was partially supported by NSF-DMS 0107179.

‡Corresponding author. This research was partially supported by a Republic of China NSC grant 91-2005-M-009-008.

1 Introduction

The screening of biological sets of objects, e.g., blood samples, cells, clones, macromolecules, is an essential but often laborious aspect of modern biotechnology. In a few instances, the screening of large libraries, e.g., peptide, cDNA, monoclonal antibody, for a relatively few number of positive objects has become a routine experimental procedure. See [2]. Similar approaches have also been proposed for contig sequencing [8], determination of exon boundaries in eukaryotic genes [17], detecting gene complex[18], micro-array quality control [3] and disease gene mapping [7].

Whenever the objective is to find "needles in a haystack" a test indicating whether at least one needle is in a specific part of the haystack can greatly facilitate the isolation of the "needles". Such tests are called *binary group tests* and the general mathematical method behind the identification of the "needles" using such tests is called *group testing* [6]. If we have a finite ground set or *population* containing elements that can be uniquely characterized as positive or negative, we refer to the collection of *positive elements* as the *positive subset* P. In the abstract group testing problem, P must be identified by performing 0, 1 tests on subsets of the population.

One applied aim is to consider screening situations where we have a biological set of objects containing a relatively small number data points (e.g., clones) which have a measurable attribute or function that can characterize them as "positive". This subcollection is initially unknown to the experimenter and it is the object of the search. A group of biological objects taken from a larger set of objects is called a *pool*. A *pool assay* is a 0, 1 test to determine if at least one member of the pool is positive. The practical goal here is to determine a large portion of P from the pool assays. The collection of pools taken from a biological set of objects is called a *pooling design*.

The following comes from [2].

"Much of the current effort of the Human Genome project involves the screening of a large recombinant DNA libraries to isolate clones containing a particular DNA sequence." "This screening is important for disease-gene mapping and also for large-scale clone mapping." "More generally, efficient screening techniques can facilitate a broad range of basic and applied biological research."

For example, using probes to screen DNA libraries of clones fits the group testing paradigm in the following way: The population is the DNA library which consists of thousands of separate recombinant DNA clones each of which represents some contiguous piece of a contiguous superpiece of DNA. A unique, identifiable, predetermined, and contiguous DNA subpiece is called a *sequenced tagged site* (STS). A clone is called *positive* for an STS if it contains that STS. A pool is a subset of the clones that are mixed together and tested by exposing the entire group to a chemical probe. A pool is *labeled* positive for an STS if the probe chemically indicates its presence. In other words, if the tests are error-free, then a pool is labeled positive for an STS if and only if that pool contains at least one clone that contains that STS.

Generally because bioinformatic applications are often automated, parallel rather than sequential screening methods are generally preferred. See [6] for other screening cost factors. Long before the advent of bioinformatics, consideration of analogous factors in other testing, screening, or coding situations lead to the development of *nonadaptive group testing.* See [4]. In NGT, one must decide exactly which pools to test before any testing occurs. A NGT algorithm is sometimes referred to as a *one-stage* algorithm. A two-stage algorithm is a nearly nonadaptive algorithm. In a trivial two-stage algorithm, all non-trivial pools occur in the first stage. After the first stage is complete, one has a set the *candidate positives.* In the second stage, each candidate positive is individually tested to see whether or not it is an actual positive.

When screening biological sets errors almost always occur during the testing procedure. This paper addresses a new class of pooling designs that can cope with large numbers of errors.

2 d-disjunct matrices as nonadaptive pooling design models

We will use the terminology of clone library screening for convenience. Suppose there are n clones including at most d positive ones (others are negative). A pooling design M can be represented by a binary incidence matrix where the columns represent clones, the rows represent tests, and $m_{ij} = 1$ if and only if clone j is contained in the subset of test i.

Suppose there are n clones including at most d positive ones (others are negative). A (group) test is applicable to an arbitrary subset of clones with two possible outcomes: a negative outcome indicates all clones in the subset are negative, and a positive outcome indicates otherwise. A pooling design is a specification of all tests so that they can be performed simultaneously with the goal to identify all positive clones with a small number of tests. A pooling design M can be represented by a binary incidence matrix where the columns represent clones, the rows represent tests, and $m_{ij} = 1$ if and only if clone j is contained in the subset of test i.

Suppose M has t rows. Then the t outcomes can also be represented by a t-vector $V = (v_1, \cdots, v_t)^t$, where $v_i = 1$ if and only if the outcome of test i is positive ($v_i = 0$ otherwise). Note that V is the boolean sum of the set of positive clones. Therefore it is convenient to view a column vector C as a subset S of the base set $\{1, 2, \cdots, t\}$, where $i \in S$ if and only if C has an 1-entry in row i. Then we can say that V is the union of the set of positive clones.

M is called *d-disjunct* if no union of any d columns covers another column. A d-disjunct matrix not only identifies the up-to-d positive clones, but with a simple decoding. Namely, a clone is positive if and only if it (as a column) is contained by V. This is because a negative clone (column) has at least one row not covered by the union of the up-to-d positive clones; such a row then has a negative outcome which identifies the clone as negative. The notion of d-disjunctness was first raised by Kautz and Singleton[11] in the study of superimposed codes. It was also studied by Erdös, Frankl and Füredi[5] under the name of d-cover-free family in extremal set theory. d-disjunct matrices have become the most important tool in the construction of deterministic pooling designs. Although many constructions have been proposed, the existence of d-disjunct matrices is still sparse.

Macula [13] proposed a novel way of constructing d-disjunct matrices which uses the containment relation in a structure. More specifically, let $[m] := \{1, 2, \cdots, m\}$ be the base set. Then each of the n columns is labeled by a (distinct) k subset of $[m]$, assuming $n \leq \begin{pmatrix} m \\ k \end{pmatrix}$, and each of the $\begin{pmatrix} m \\ d \end{pmatrix}$ rows is labeled by a (distinct) d-subset of $[m]$, where $d < k < m$.

$m_{ij} = 1$ if and only if the label of row i is contained in the label of column j. He proved that M is d-disjunct.

Huang and Weng [9] generalized the construction to arbitrary atomic semi-lattice where the elements can be ranked. Again, label the columns by a subset of the rank k elements and label the rows by all rank d elements, $d < k$, then M is d-disjunct.

Ngo and Du [16] further extended the construction to some geometric structures like simplicial complexes, and some graph properties like matchings. It is safe to say the "containment matrix" method has opened a new door for constructing d-disjunct matrices from many mathematical structures. However, the basic result in all these constructions is invariably that, to obtain a d-disjunct matrix, use all rank d elements for rows.

One practical problem with this type of construction is that a large n forces S to be large. Then the number of tests could be too large as there are too many rank d elements. This led Macula [15] to propose using the rank 2 elements for rows, regardless of the real d. He showed that while there is no guarantee to identify all positive clones, the probability of success is still satisfactory when d does not deviate too much from 2. Ngo and Du made a similar comment.

In this paper, we show that the containment matrix which use rank r of elements for rows has the degree d of disjunctness, where r can be much less than d. In fact r can be any number from 1 to $k - 1$ (k is the lever for columns), while $d \leq q^r$ for some constant q. This is the first happy surprise. Since we can choose $r = 1$, we also have better control on the number of tests.

3 The error-correcting capability

Biological experiments are notorious for producing erroneous outcomes. Therefore it would be wise for pooling designs to allow some outcomes to be affected by errors. Macula[14] proposed the notion of d^e-disjunct to reflect the error-correcting capability of a d-disjunct matrix. A d-disjunct matrix is d^e-disjunct if a column has at least $e + 1$ 1-entries not covered by the union of any other d columns. d^0-disjunct would then be the regular d-disjunct.

In [10] it was misclaimed that a d^e-disjunct matrix can correct e errors. The argument was that if we try all subsets E of up to e columns as the candidate set of errors and adjust the outcome set V to $V \cup E$, then when E is the true error set, a positive clone C must be contained in $V \cup E$. On the other hand, a negative clone C has at least $e+1$ 1-entries not covered by the set of up to d positive clones, i.e., C has at least $e+1$ negative outcomes. At most e of them can be converted to positive by errors, thus at least one negative outcome is not covered by V. The problem of this argument is that we need to show that C has at least one negative outcome not covered by $V \cup E$. The following is a counterexample.

Example 3.1. $d = 2$, $e = 1$. *Column* 1 *is the only positive clone while* v_3 *is an error.*

$$M = \begin{pmatrix} 1 & 0 & 0 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \\ 0 & 0 & 1 \end{pmatrix} \qquad V = \begin{pmatrix} 1 \\ 1 \\ 1 \\ 0 \\ 0 \\ 0 \end{pmatrix}$$

When $E = \{4\}$, $V \cup E = (1,1,1,1,0,0)^t$ *covers column* 1 *and* 2.

Thus the correct version should be

Theorem 3.2. *A* d^{2e}*-disjunct matrix is* e*-error-correcting.*

Proof. For a positive clone C the argument is as before that there exists a candidate set E such that $C \subseteq V \cup E$.

A negative clone C has at least $2e+1$ 1-entries not covered by the set D of up to d positive clones, hence at least $2e+1$ negative outcomes. e of them may be converted to positive by errors and another e of them by E, but at least one negative outcome is not covered by $V \cup E$. $\square$

For the reason that a d^e-disjunct matrix is not really e-correcting, and also that d^0-disjunct$=$ d-disjunct, is kind of uncustomary, we propose to use the term d^z-disjunct while z is the minimum (over C) number of 1-entries in C not covered by the union of any other d columns. Theorem 3.2 then can be restated as

Theorem 3.3. *A d^z-disjunct matrix can detect $z-1$ errors and correct $\lfloor \frac{z-1}{2} \rfloor$ errors.*

In particular, a d-disjunct matrix has no error-tolerance.

If an extra round of confirmatory tests is allowed, then a d^z-disjunct matrix can indeed correct $z-1$ errors. First, we need a lemma. Let $H(X,Y)$ denote the Hamming distance between two binary vectors X, Y of the same length.

Lemma 3.4. *Let M be a d^z-disjunct matrix and let S_1 S_2 be two distinct subsets of columns with $|S_1| \leq d, |S_2| \leq d$. Let U_i be the union of the set S_i for each $i = 1, 2$. Then*

1. $H(U_1, U_2) \geq z$ *if either* $S_1 \subseteq S_2$ *or* $S_2 \subseteq S_1$;
2. $H(U_1, U_2) \geq 2z$ *if otherwise.*

Proof. These are trivial by using the d^z-disjunct property. □

Theorem 3.5. *A d^z-disjunct matrix corrects $z-1$ errors with an extra round of at most d confirmatory tests.*

Proof. Take all subsets S of columns of M with $|S| \leq d$ and $H(U,V) \leq z-1$, where U is the union of S. Let S_1, S_2 be two such sets. The $H(U_1, U_2) \leq 2(z-1) < 2z$. By Lemma 3.4, either $S_1 \subseteq S_2$ or $S_2 \subseteq S_1$. Therefore the set $\{S\}$ is a chain. Hence $\{S\}$ has at most d members. Since $H(D,V) \leq z-1$, $D \in \{S\}$, D can be identified by testing at most d columns in the maximal chain of $\{S\}$. □

Not many constructions of d^z-disjunct matrices have been known. Macula [14], and also see [10], gave a construction for d^4, and recently Ngo and Du gave a construction for d^{d+1}. We will show that the construction delivering the first happy surprise mentioned in section 1 not only yields d-disjunct matrices, but also d^z-disjunct matrices with the z-value much greater than 4 or $d+1$. This is the second happy surprise.

4 The construction

Consider the m-dimensional space, or simply m-space, of $GF(q)$ where q is a prime or a prime power. Let $\begin{bmatrix} m \\ k \end{bmatrix}_q$ denote the number of k-dimensional subspaces, or simply k-space. It is well known [12, p. 291]

Lemma 4.1.

$$\begin{bmatrix} m \\ k \end{bmatrix}_q = \frac{(q^m-1)(q^{m-1}-1)\cdots(q^{m-k+1}-1)}{(q^k-1)(q^{k-1}-1)\cdots(q-1)}$$

and

$$\begin{bmatrix} m \\ k \end{bmatrix}_q = \begin{bmatrix} m \\ m-k \end{bmatrix}_q .$$

Definition 4.2. Fix integers $1 \le r < k < m$. Let $M(m,k,r)$ be the 01-matrix by taking all k-spaces (from an underlying m-space) as columns and all r-spaces as rows. $M(m,k,r)$ has a 1 in row i and column j if and only if i is contained in j.

$M(m,k,r)$ was first studied in [19] from a linear algebra point of view and in [16] from a pooling design point of view. $M(m,k,r)$ is easily checked to be a ranked atomic semi-lattice, thus the matrix is r-disjunct, hence [9] d^z-disjunct for some $1 \le d \le r$ and

$$z = \begin{bmatrix} k-d \\ r-d \end{bmatrix}_q .$$

Note that the construction still requires the row rank r being at least as large as the upper bound d of the number of positive clones. We now show that r can be much less than d. First, we give a lemma.

Lemma 4.3.

$$\begin{bmatrix} k \\ r \end{bmatrix}_q - \begin{bmatrix} k-1 \\ r \end{bmatrix}_q = q^{k-r} \begin{bmatrix} k-1 \\ r-1 \end{bmatrix}_q \qquad (0 \le r < k).$$

Proof.

$$\begin{aligned}
& \begin{bmatrix} k \\ r \end{bmatrix}_q - \begin{bmatrix} k-1 \\ r \end{bmatrix}_q \\
= \; & \frac{(q^k-1)(q^{k-1}-1)\cdots(q^{k-r+1}-1)}{(q^r-1)(q^{r-1}-1)\cdots(q-1)} - \frac{(q^{k-1}-1)(q^{k-2}-1)\cdots(q^{k-r}-1)}{(q^r-1)(q^{r-1}-1)\cdots(q-1)} \\
= \; & \frac{(q^k-1)-(q^{k-r}-1)}{q^r-1} \cdot \frac{(q^{k-1}-1)\cdots(q^{k-r+1}-1)}{(q^{r-1}-1)\cdots(q-1)} \\
= \; & q^{k-r} \begin{bmatrix} k-1 \\ r-1 \end{bmatrix}_q .
\end{aligned}$$

□

Theorem 4.4. *Suppose* $k-r \geq 2$ *and set* $p := \dfrac{q(q^{k-1}-1)}{q^{k-r}-1}$. *Then* $M(m,k,r)$ *is* d^z*-disjunct for* $1 \leq d \leq p$ *and*

$$z = q^{k-r}\begin{bmatrix} k-1 \\ r-1 \end{bmatrix}_q - (d-1)q^{k-r-1}\begin{bmatrix} k-2 \\ r-1 \end{bmatrix}_q .$$

Proof. Let $C, C_1, \cdots, C_d$ be $d+1$ distinct columns (k-spaces) of M. By Lemma 3.1, C contains $\begin{bmatrix} k \\ r \end{bmatrix}_q$ r-spaces. To obtain the maximum coverage of these r-spaces, we may assume that each C_i intersects C at a $(k-1)$-space by the observation

$$C \cap \bigcup_{i=1}^{d} C_i = \bigcup_{i=1}^{d} (C \cap C_i).$$

Then each C_i covers $\begin{bmatrix} k-1 \\ r \end{bmatrix}_q$ r-spaces of C. However, the coverage of each pair of C_i and C_j overlaps at a $(k-2)$-space. Therefore only C_1 covers the full $\begin{bmatrix} k-1 \\ r \end{bmatrix}_q$ r-spaces, while each of $C_2, \cdots, C_d$ can cover a maximum of $\begin{bmatrix} k-1 \\ r \end{bmatrix}_q - \begin{bmatrix} k-2 \\ r \end{bmatrix}_q$ r-spaces not covered by C_1. Consequently the number of r-spaces of C not covered by $C_1, \cdots, C_d$ is at least

$$\begin{aligned} z &= \begin{bmatrix} k \\ r \end{bmatrix}_q - \begin{bmatrix} k-1 \\ r \end{bmatrix}_q - (d-1)(\begin{bmatrix} k-1 \\ r \end{bmatrix}_q - \begin{bmatrix} k-2 \\ r \end{bmatrix}_q) \\ &= q^{k-r}\begin{bmatrix} k-1 \\ r-1 \end{bmatrix}_q - (d-1)q^{k-r-1}\begin{bmatrix} k-2 \\ r-1 \end{bmatrix}_q . \end{aligned}$$

Note that for $M(m,k,r)$ to be d^z-disjunct, z must be positive, which implies

$$d < \frac{q^{k-r}\begin{bmatrix} k-1 \\ r-1 \end{bmatrix}_q}{q^{k-r-1}\begin{bmatrix} k-2 \\ r-1 \end{bmatrix}_q} + 1,$$

or $d \leq p$. □

Suppose $d \leq q+1$. The following corollary shows the above z is optimal.

Corollary 4.5. *Suppose* $k - r \geq 2$ *and* $1 \leq d \leq q + 1$. *Then* $M(m, k, r)$ *is not* d^{z+1}*-disjunct, where* z *is as in Theorem 4.4.*

Proof. We prove this by showing that a maximum coverage of r-spaces in the proof of Theorem 4.4 is obtained. We reverse the arguments. Let U be a $(k-2)$-space contained in C. Then the number of $(k-1)$-spaces between U and C is

$$\begin{bmatrix} k-(k-2) \\ k-1-(k-2) \end{bmatrix}_q = q+1.$$

We choose d distinct ones among them, say T_i $(1 \leq i \leq d)$. For each T_i, we choose a k-space C_i such that $C \cap C_i = T_i$. Hence each pair of C_i and C_j overlaps at the same $(k-2)$-space U. $\square$

Lemma 4.6. *Suppose* $r \leq \dfrac{k}{2}$. *Then with referring to the definition of* p *in Theorem 4.4,* $d = q^r$ *is the largest integer less or equal to* p.

Proof. Note that $q^{r-1} < q^r \leq q^{k-r}$. Hence

$$\begin{aligned} p - q^r &= \frac{q(q^{k-1}-1)}{q^{k-r}-1} - q^r \\ &= \frac{q^k - q - q^k + q^r}{q^{k-r}-1} \\ &= \frac{q(q^{r-1}-1)}{q^{k-r}-1} \\ &< \frac{qq^{r-1}}{q^{k-r}} \\ &\leq 1. \end{aligned}$$

Then $p - 1 < q^r \leq p$. $\square$

Corollary 4.7. *Suppose* $k - r \geq 2$ *and* $d = q^r$. *Then* $M(m, k, r)$ *is* d^z*-disjunct with*

$$z = \begin{bmatrix} k-1 \\ r-1 \end{bmatrix}_q + (q^r - 1)\begin{bmatrix} k-2 \\ r \end{bmatrix}_q.$$

Proof. Setting $d = q^r$ in Theorem 4.4 and referring to Lemma 4.1, Lemma 4.3,

$$\begin{aligned}
z &= q^{k-r}\begin{bmatrix} k-1 \\ r-1 \end{bmatrix}_q - (q^r-1)q^{k-r-1}\begin{bmatrix} k-2 \\ r-1 \end{bmatrix}_q \\
&= \begin{bmatrix} k \\ r \end{bmatrix}_q - \begin{bmatrix} k-1 \\ r \end{bmatrix}_q - (q^r-1)(\begin{bmatrix} k-1 \\ r \end{bmatrix}_q - \begin{bmatrix} k-2 \\ r \end{bmatrix}_q) \\
&= \begin{bmatrix} k \\ r \end{bmatrix}_q - q^r\begin{bmatrix} k-1 \\ r \end{bmatrix}_q + (q^r-1)\begin{bmatrix} k-2 \\ r \end{bmatrix}_q \\
&= \begin{bmatrix} k \\ k-r \end{bmatrix}_q - q^{k-(k-r)}\begin{bmatrix} k-1 \\ r \end{bmatrix}_q + (q^r-1)\begin{bmatrix} k-2 \\ r \end{bmatrix}_q \\
&= \begin{bmatrix} k-1 \\ k-r \end{bmatrix}_q + (q^r-1)\begin{bmatrix} k-2 \\ r \end{bmatrix}_q \\
&= \begin{bmatrix} k-1 \\ r-1 \end{bmatrix}_q + (q^r-1)\begin{bmatrix} k-2 \\ r \end{bmatrix}_q .
\end{aligned}$$

□

When $r = 1$, the z in Theorem 4.4 is in a neater form.

Corollary 4.8. *Suppose* $k \geq 3$, $d \leq q$ *and* $z = q^{k-2}(q-d+1)$. *Then* $M(m,k,1)$ *is* d^z*-disjunct, but is not* d^{z+1}*-disjunct.*

Proof. Setting $r = 1$ in the z formula of Theorem 4.4, we obtain

$$\begin{aligned}
z &= q^{k-1}\begin{bmatrix} k-1 \\ 0 \end{bmatrix}_q - (d-1)q^{k-2}\begin{bmatrix} k-2 \\ 0 \end{bmatrix}_q \\
&= q^{k-2}(q-d+1).
\end{aligned}$$

The second statement follows from Corollary 4.5. □

Example 4.9. *Fix* $q = 5$. *Then* $M(8,4,1)$ *is a* 5^{25}*-disjunct matrix with* 97656 *rows and* 200525284806 *columns. This means that we can use around* 10^5 *pools with* 25 *errors allowed to determine the positives when the number of items is around* 2×10^{11} *with at most* 5 *positives.*

References

[1] Barrllot, E., Lacroix, B. and Cohen, D. 1995. Theoretical analysis of library screening using an n-dimensional pooling strategy. *Nucleic Acids Res.* 19:6241-6247.

[2] Bruno, W. J., Knill, E., Balding, D. J., Bruce, D. C., Doggett, N. A., Sawhill, W. W., Stallings, R. L., Whittaker C. C., and Torney E. C. 1995. Effective pooling designs of library screening. *Genomics* 26:21-30.

[3] Colburn, C., Ling, A., Tompa, M. 2002. Construction of optimal quality control ogilio arrays, *Bioinformatics*, 18, no. 4, 529-535.

[4] Du, D. and Hwang, F. K. 2000. *Combinatorial Group Testing and Its Applications*, 2$^{\text{nd}}$ Ed., World Scientific, Singapore.

[5] Erdös, P., Frankl, and Füredi, D. 1985. Families of finite sets in which no set is covered by the union of r others. *Israel J. Math.* 51:79–89.

[6] Farach, et al. 1997. Group testing problems with sequences experimental molecular biology, *Proceedings of Compression and Complexity of Sequences, 1997, B. Carpentieri, et al. (Eds.)* IEEE Press, 357-367.

[7] Flodman, P., Macula, A., Spence, A. and Torney, D. 2001. A new data mining technique for the analysis of simulated genetic data. *Proceedings of Genetic Analysis Workshop 12, Wiley-Liss, 2001*; *Genet Epidemiol (Genetic epidemiology.)* 21 Suppl 1: S390-5 (2001.)

[8] Grebinski, V. and Kucherov, G. 1998. Reconstructing a Hamiltonian cycle by querying the graph:application to DNA physical mapping. *Disc. Appli. Math..* 88:147-165.

[9] Huang, T. and Weng, C. 2004. Pooling Spaces and Non-Adaptive Pooling Designs. *Disc. Math.* 282(1-3):163-169.

[10] Hwang, F. K. 2003. On Macula's Error-Correcting Pool Designs. *Disc. Math.* 267:311-314.

[11] Kautz, W. H. and Singleton, R. C. 1964. Nonadaptive binary superimposed codes. *IEEE Trans. Inform. Theory* 10:363–377.

[12] van Lint, J. H., and Wilson, R. M. 1992. *A Course in Combinatorics.* Cambridge, Victoria.

[13] Macula, A. J. 1996. A simple construction of d-disjunct matrices with certain constant weights. *Disc. Math.* 162:311–312.

[14] Macula, A. J. 1996. Error-correcting nonadaptive group testing with d^e-disjunct matrices. *Disc. Appl. Math.* 80:217-222.

[15] Macula, A. J. 1999. Probabilistic nonadaptive and two-stage group testing with relatively small pools and DNA library screening. *J. Comb. Opt.* 2:385–397.

[16] Ngo, H., and Du, D. 2002. New Constructions of Non-Adaptive and Error-Tolerance Pooling Designs. *Disc. Math.* 243:161–170.

[17] Pevzner, P. A. 2000. *Computational Molcular Biology: an algorithmic approach.* MIT Press, Mass Sec. 9.5-9.6.

[18] Torney, D. C. 1999. Sets pooling designs. *Ann. Combin.* 3:95–101.

[19] Yakir, A. 1993. Inclusion matrix of k vs 1 affine subspaces and a permutation module of the general affine group. *J. Combin. Theory, Ser. A* 63:301–317.

A. G. D'yachkov
Faculty of Mechanics and Mathematics
Department of Probability Theory
Moscow State University
Moscow 119899, Russia
email: `dyachkov@artist.math.msu.su`

Frank K. Hwang
Department of Applied Mathematics
National Chiao Tung University
1001 Ta Hsueh Road
Hsinchu 30050, Taiwan

email: `fhwang@math.nctu.edu.tw`

Antony J. Macula*
Department of Mathematics
College at Geneseo
State University of New York
Geneseo, NU 14454, USA
email: `macula@geneseo`

Pavel A. Vilenkin
Faculty of Mechanics and Mathematics
Department of Probability Theory
Moscow State University
Moscow 119899, Russia
email: `paul@vilenkin.dnttm.ru`

Chih-wen Weng
Department of Applied Mathematics
National Chiao Tung University
1001 Ta Hsueh Road
Hsinchu 30050, Taiwan
email: `weng@math.nctu.edu.tw`

EQUIVALENCE OF THE ONE-RATE MODEL TO THE CLASSICAL MODEL ON STRICTLY NONBLOCKING SWITCHING NETWORKS

W.R.CHEN AND F.K.HWANG* AND XUDING ZHU†

Abstract. In the one-rate(f) network, each link can carry up to f messages for some integer f. The classical model is the special case when $f = 1$. We show that a network is strictly nonblocking under the one-rate(f) model if and only if it is strictly nonblocking under the classical model.

Key words. Switching network, one-rate network, multirate network, graph coloring, flow, strictly nonblocking

AMS subject classifications. 68M10, 15C15, 90B18

1. Introduction.

A switching network consists of a set of nodes and a set of (directed) links. Typically, an outlink of a node is the inlink of another node, and vice versa. There are two special types of nodes: the *inputs* and the *outputs*. Each input (output) is a node which has no inlink (outlink) and exactly one outlink (inlink).

We view a network as a directed graph $G = (V, E)$, where each vertex is a node and each edge is a link. The inputs and outputs are subsets I, O of V. To emphasize the special roles of the inputs and outputs, we denote a network as $G = (V, E, I, O)$. A network is called *acyclic* if the directed graph G is acyclic, i.e., G contains no directed cycles.

Let $G = (V, E, I, O)$ and f a positive integer. The 1-rate(f) network, denoted by (G, f), is a network G together with the capacity constraint that each edge can carry up to f messages. If $f = 1$, then the 1-rate network $(G, 1)$ is the *classical model*. In other words, a classical model is a network in which each edge can carry at most 1 message. In this paper, we only consider 1-rate networks.

A *traffic* of (G, f) is a sequence of input-output pairs (i, j), where $i \in I$ and $j \in O$. There are two types of traffics: requests and cancellations. A *request* is a pair (i, j) neither of i, j has appeared in more than $f - 1$ previous uncancelled requests. Namely, the pair requests a connection in the network. A *cancellation* is a previous request whose connection in the network is to be removed. A request (i, j) is *routed* if a directed i-j-path is chosen, without exceeding the capacity of the edges. So a request (i, j) can be routed in the network (which has already routed many previous requests) if and only if there exists a directed i-j-path each of whose edges has not been used more than $f - 1$ times.

A *state* S of (G, f) is a collection of (not necessarily distinct) directed paths of G joining vertices of I to vertices of O, such that each edge e is contained in at most f directed paths. Given a state S, let $S(e)$ denote the number of directed paths containing e. Then $0 \leq S(e) \leq f$. A state is *blocking* if there exists a vertex $i \in I$ and $j \in O$ such that both i and j are contained in fewer than f directed paths in S, and every directed i-j-path of G contains an edge e with $S(e) = f$. We say that (G, f) is strictly nonblocking if there is no blocking state.

---

*Department of Applied Mathematics, National Chiao Tung University, Research partially supported by ROC National science council grant NSC 91-2115-M-009-010 and the National Chiao Tung University Lee-MTI center.

†Department of Applied Mathematics, National Sun Yat-sen University, Taiwan, `zhu@math.nsysu.edu.tw`, Research partially supported by ROC National science council grant NSC 91-2115-M-110-003.

The classical model is of course the dominating model in the study of switching networks. Recently, the multirate network has received increasing attention due to the popular attempt to integrate multimedia service into one network. Since the theory of the classical model is well established, it is profitable to ask how much of it can be extended to the multirate model. The 1-rate model is the simplest multirate model, but also has its own application. It is used in the *digital symmetrical matrices* in time-space switching [7, 10]. The principle of providing more links between two nodes, known as *statistical line grouping* in [8], was promoted as a major technique to cut down network blocking. On the other hand, strict nonblockingness is one of the most fundamental property of a switching network. Therefore, asking whether one model implies the other on this property can serve as a natural start to explore the relation between the classical model and the multirate model. In this paper we prove that if $G = (V, E, I, O)$ is an acyclic network, then the strict nonblockingness of a 1-rate network (G, f) is equivalent to that of the classical model $(G, 1)$.

2. Strictly nonblocking for (G, f) implies the same for $(G, 1)$.

We first prove the implication in one direction.

THEOREM 2.1. *If (G, f) is strictly nonblocking for some positive integer f, then $(G, 1)$ is strictly nonblocking.*

Proof. It suffices to prove that if $(G, 1)$ has a blocking state, then (G, f) has a blocking state. Suppose S is a blocking state of $(G, 1)$. Let S' be the collection of directed paths of G which is obtained by duplicating f times each directed path of S. Then S' is a state of (G, f) and for each edge e of G, $S'(e) = f \times S(e)$. As S is a blocking state of $(G, 1)$, there is an input $i \in I$ and an output $j \in O$ such that none of i, j is contained in any directed path of S, and any directed i-j-path of G contains an edge e with $S(e) = 1$. Then both of i and j are contained in no directed paths of S', and every directed i-j-path of G contains an edge e with $S'(e) = f$. Therefore S' is a blocking state of (G, f). □

In the remainder, we shall prove the other direction, i.e., if for some integer $f \geq 1$, (G, f) has a blocking state, then $(G, 1)$ has a blocking state. Let S be a blocking state of (G, f). Then there exist $i \in I$ and $j \in O$ such that both i, j are contained in at most $f - 1$ directed path of S, and any directed i-j-path contains an edge e with $S(e) = f$. We need to construct a blocking state S' for $(G, 1)$. One may attempt to partition the directed paths in S into f classes such that

(i) Directed paths which share an edge belong to different classes.

(ii) There exists a class C not containing any directed path with end vertex i or j.

If such a partition exists, then it is easy to verify that the class C is a blocking state of $(G, 1)$. However, such a partition may not exist. Consider the following network: Fig. 1 shows an example of $(G, 2)$, where G is a simple digraph (a pair of double links indicates a link carrying two paths). The collection of directed paths $S = \{P_1, P_2, P_3, P_4\}$ in Figure 1 is a blocking state for $(G, 2)$, where input i and output j each has generated one path and hence a new request (i, j) is legitimate. However, it is impossible to partition the paths into 2 classes in such a way that directed paths sharing an edge belong to different classes, because every two directed paths share an edge. Thus to construct the blocking state S' for $(G, 1)$, we need to use directed paths not contained in the collection S.

3. Strictly nonblocking for $(G, 1)$ implies the same for $(G, 2)$.

In this section, we consider the case $f = 2$.

THEOREM 3.1. *Suppose G is acyclic. If $(G, 1)$ is nonblocking, then $(G, 2)$ is nonblocking.*

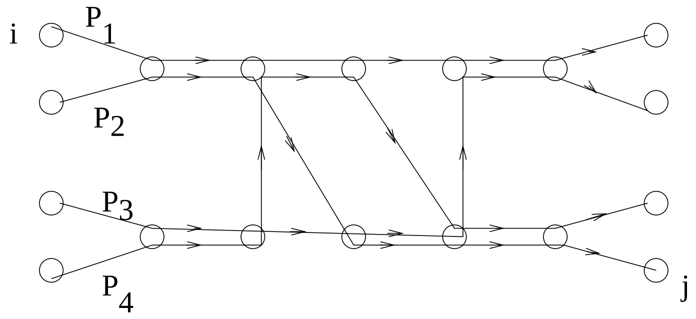

FIG. 2.1. *An example*

Proof. Let S be a blocking state for $(G,2)$. Thus there exist $i \in I$ and $j \in O$ such that both i,j are contained in at most 1 directed path of S, and any directed i-j-path contains an edge e with $S(e)=2$.

We shall construct a blocking state for $(G,1)$. For each vertex v of G, denote by $E^+(v)$ the outlinks of v, and by $E^-(v)$ the inlinks of v. Let $E(v)=E^+(v)\cup E^-(v)$. Let

$$s^+(v)=\sum_{e\in E^+(v)} S(e)=\sum_{P\in S}|P\cap E^+(v)|,$$

$$s^-(v)=\sum_{e\in E^-(v)} S(e)=\sum_{P\in S}|P\cap E^-(v)|$$

and

$$s(v)=s^+(v)+s^-(v)=\sum_{P\in S}|P\cap E(v)|.$$

Since each directed path $P\in S$ connects a vertex of I to a vertex of O, we conclude that for each vertex $v\notin I\cup O$, $|P\cap E^+(v)|=|P\cap E^-(v)|$. Hence $s^+(v)=s^-(v)$ and $s(v)=2s^+(v)$. Let $E_1=\{e\in E : S(e)=1\}$ and let $E_2=\{e\in E : S(e)=2\}$. Then $s(v)=|E_1\cap E(v)|+2|E_2\cap E(v)|$. If $v\notin(I\cup O)$, then $s(v)$ is even, and hence $|E_1\cap E(v)|$ is even. Let $G_1=(V,E_1)$ be the subgraph of G induced by the edge set E_1. As each vertex of $V-(I\cup O)$ has even degree in G_1, we can decompose G_1 into edge-disjoint union of (not necessarily directed) cycles and paths, say

$$E_1=(P_1\cup P_2\cup\cdots\cup P_l)\cup(C_1\cup C_2\cup\cdots\cup C_m),$$

where each path P_k connects two vertices of $I\cup O$. We color the edges of each P_k and C_l by two colors, a and b, as described below.

Given an undirected cycle (or a path), there are two choices for the *positive direction* of the cycle (or path). If the cycle is drawn on the plane, then either the clockwise direction, or the anticlockwise direction can be chosen as the positive direction. For a path with end vertices i and j, one can traverse the path from i to j, or from j to i. Once a positive direction is chosen, then those directed edges agree with the positive direction of the cycle (or path) are called *forward edges*, and those directed edges oppose the positive direction are called *backward edges*. Arbitrarily choose a positive direction of C_l (or P_k), and color the forward edges of C_l (or P_k) by color a, and backward edges by color b.

Let $E_a \subset E_1$ be the edges of color a and $E_b \subset E_1$ be the edges of color b. Let $B_1 = E_a \cup E_2$ and $B_2 = E_b \cup E_2$. Suppose $v \notin (I \cup O)$. Let $i_a(v)$ (respectively, $o_a(v)$) be the number of inlinks (respectively, outlinks) of v of color a, and let $i_b(v)$ (respectively, $o_b(v)$) be the number of inlinks (respectively, outlinks) of v of color b.

If P_k (or C_l) contains v, then either P_k (or C_l) contains two inlinks or two outlinks of v which are colored by distinct colors, or one outlink and one inlink of v which are colored by the same color. Therefore

$$i_a(v) + o_b(v) = o_a(v) + i_b(v).$$

Let $i_2(v) = |E_2 \cap E^-(v)|$ and $o_2(v) = |E_2 \cap E^+(v)|$. Then

$$s^-(v) = i_a(v) + i_b(v) + 2i_2(v)$$

and

$$s^+(v) = o_a(v) + o_b(v) + 2o_2(v).$$

As $s^+(v) = s^-(v)$, we conclude that $i_a(v) + i_2(v) = o_a(v) + o_2(v)$ and $i_b(v) + i_2(v) = o_b(v) + o_2(v)$.

Let H_1 be the directed subgraph of G induced by the edge set $E_a \cup E_2$ and H_2 the directed subgraph of G induced by the edge set $E_b \cup E_2$. Then for each vertex $v \notin (I \cup O)$, the number of inlinks of v in H_1 is $i_a(v) + i_2(v)$ and the number of outlinks of v in H_1 is $o_a(v) + o_2(v)$. So the number of inlinks of v is equal to the number of outlinks of v. As G is acyclic, H_1 is acyclic. Therefore H_1, and similarly H_2, can be decomposed into directed paths joining vertices of I to vertices of O. For $k = 1, 2$, denote by S_k the collection of directed paths which form a decomposition of H_k. For each edge e of G, $0 \le S_k(e) \le 1$ and $S(e) = S_1(e) + S_2(e)$. Moreover, both i and j are not contained in any directed paths of S_2. As any directed i-j-path of G contains an edge e with $S(e) = 2$, and hence $S_2(e) = 1$. Therefore S_2 is a blocking state of $(G, 1)$. $\square$

4. Strictly nonblocking for $(G, 1)$ implies the same for (G, f). In this section, we prove that the strict nonblocking of the classical model implies the strict nonblocking of the 1-rate(f) model for any $f \ge 1$. Our proof needs a result concerning integer flows of graphs.

Let G be a directed graph. An *integer flow* of G is a mapping $\phi : E \to Z$ which assigns to each edge $e \in E$ an integer $\phi(e)$ such that for each vertex v of G,

$$\sum_{e \in E^+(v)} \phi(e) = \sum_{e \in E^-(v)} \phi(e).$$

An integer flow ϕ is called a *non-negative* k-flow if for each edge e, $0 \le \phi(e) \le k - 1$. Lemma 4.1 below is due to Little, Tutte and Younger [9].

LEMMA 4.1. *For each nonnegative k-flow f of G, there exist $k-1$ nonnegative 2-flows ϕ_t $(t = 1, 2, \cdots, k-1)$ such that $\phi = \sum_{t=1}^{k-1} \phi_t$.*

LEMMA 4.2. *Suppose G is acyclic. If S is a state of (G, f), then there are f states $S_1, S_2, \cdots, S_f$ of $(G, 1)$ such that for each edge e of G, $S(e) = \sum_{i=1}^{f} S_i(e)$.*

Proof. Let S be a state of (G, f). Let G' be the directed graph obtained from G by identifying all the inputs and outputs, i.e., identifying all the vertices of $I \cup O$ into a single vertex v^*. We view S as a weight assignment to the edges of G'. It is easy to see that for each vertex v of G',

$$\sum_{e\in E^+(v)} S(e) = \sum_{e\in E^-(v)} S(e),$$

and for each edge of G',

$$0 \leq S(e) \leq f.$$

Therefore S is a nonnegative $(f+1)$-flow of G'. By Lemma 4.1, G' has f nonnegative 2-flows S_t $(t = 1, 2, \cdots, f)$ such that $S = \sum_{t=1}^{k-1} S_t$. Each nonnegative 2-flows S_t corresponds to a directed cycle, say C_t, of G'. As G is acyclic, each C_t contains the vertex v^*. In other words, Each C_t corresponds to a directed path of G joining a vertex of I to a vertex of O. Thus each S_t is indeed a state of $(G, 1)$. □

THEOREM 4.3. *If* $(G, 1)$ *is strictly nonblocking then* (G, f) *is strictly nonblocking for any* $f \geq 1$.

Proof. Assume (G, f) is not strictly nonblocking and S is a blocking state of (G, f). Then there exist $i \in I$ and $j \in O$ such that both i and j are contained in fewer than f directed paths in S, and every directed i-j-path of G contains an edge e with $S(e) = f$. By Lemma 4.2, there exists f states, $S_1, S_2, \cdots, S_f$, of $(G, 1)$ such that for every edge e,

$$S(e) = \sum_{k=1}^{f} S_k(e).$$

As both i and j are contained in fewer than f directed paths in S, there exists $1 \leq a, b \leq f$ such that i is not contained in any path of S_a, and j is not contained in any path of S_b. If $a = b$, then S_a is a blocking state of $(S, 1)$. Assume $a \neq b$. Then $S_a \cup S_b$ is a blocking state of $(G, 2)$. By Theorem 3.1, $(G, 1)$ has a blocking state. □

COROLLARY 4.4. *Suppose* $G = (V, E, O, I)$ *is an acyclic network. Then for any positive integers* f, f', (G, f) *is strictly nonblocking is and only if* (G, f') *is strictly nonblocking.*

Proof. The strictly nonblocking of (G, f) is equivalent to strictly nonblocking of $(G, 1)$, for any integer f. Hence strictly nonblocking of (G, f) is equivalent to strictly nonblocking of (G, f'). □

5. Some concluding remarks. Some other implications between the classical model and the multirate model are available from the literature. These involve some other notions of nonblockingness. A network is *wide-sense nonblocking* if every request can be routed provided all routing follows a given algorithm. A network is *rearrangeably nonblocking* if all requests can be routed if they are given at once (instead of the usual "sequential" model).

Let $C(n_1, r_1, m, n_2, r_2)$ denote the 3-stage clos network whose nodes are partitioned into three stages (parts):

the first stage consists of r_1 nodes each with n_1 inlinks and m outlinks,
the second stage consists of m nodes each with r_1 inlinks and r_2 outlinks,
the third stage consists of r_2 nodes each with m inlinks and n_2 outlinks ,

such that there exists a link from each stage-i node to each stage-$(i+1)$ node, but no other links between two nodes.

Clos [4] proved

LEMMA 5.1. *$C(n_1,r_1,m,n_2,r_2)$ is strictly nonblocking under the classical model if and only if*

$$m \geq \min\{n_1+n_2-1, n_1r_1, n_2r_2\}.$$

Hwang and Yeh, as reported in [6], proved a similar result under a model slightly more general than the 1-rate(f) model, suppose each input has capacity f_0, each output has capacity $f_0^{'}$, each link between stage 1 and stage 2 has capacity f_1, and each link between stage 2 and stage 3 has capacity f_2.

LEMMA 5.2. *$C(n_1,r_1,m,n_2,r_2;f_0,f_0^{'},f_1,f_2)$ is strictly nonblocking if and only if*

$$m \geq \lfloor \frac{\min\{n_1f_1, n_2r_2f_2\}-1}{f_0} \rfloor + \lfloor \frac{\min\{n_1r_1f_1, n_2r_2\}-1}{f_0} \rfloor + 1.$$

By setting $f_0 = f_0^{'} = f_1 = f_2 = f$, we obtain

COROLLARY 5.3. *$C(n_1,r_1,m,n_2,r_2)$ is strictly nonblocking under the 1-rate(f) model if and only if*

$$m \geq \min\{n_1+n_2-1, n_1r_1, n_2r_2\}.$$

Note that the conditions in Lemmas 5.1 and Corollary 5.3 are the same. Hence

THEOREM 5.4. *For $C(n_1,r_1,m,n_2,r_2)$, strictly nonblocking under the classical model implies the same for the 1-rate(f) model, and vice versa.*

Benes [1] proved

LEMMA 5.5. *$C(n,2,m,n,2)$ is wide-sense nonblocking under the classical model if and only if $m \geq \lfloor \frac{3n}{2} \rfloor$.*

On the other hand, Fishburn et al. [5] proved

LEMMA 5.6. *$C(n,2,m,n,2)$ is wide-sense nonblocking under the 1-rate(f) model if and only if $m \geq \lceil \frac{3n}{2} \rceil$.*

By comparing Lemmas 5.5 and 5.6, we obtain

THEOREM 5.7. *For $C(n,2,m,n,2)$, wide-sense nonblocking under the classical model does not imply the same for the 1-rate model.*

Finally, Chung and Ross [3] proved

LEMMA 5.8. *Rearrangeably nonblocking under the classical model implies the same for the 1-rate(f) model.*

For the other direction, only special cases have been proved. Slepian (see [1]) proved the following result (he ignored the terms n_1r_1 and n_2r_2 which reflect the boundary effects):

LEMMA 5.9. *$C(n_1,r_1,m,n_2,r_2)$ is rearrangeably nonblocking under the classical model if and only if $m \geq \max\{\min\{n_1,n_2r_2\}, \min\{n_1r_1,n_2\}\}$.*

On the other hand, Hwang and Yeh, as reported in [6], proved

LEMMA 5.10. *$C(n_1,r_1,m,n_2,r_2;f_0,f_0^{'},f_1,f_2)$ is rearrangeably nonblocking if and only if*

$$m \geq \max\{\frac{\min\{n_1f_1, n_2r_2f_2\}}{f_0}, \frac{\min\{n_1r_1f_1, n_2f_2\}}{f_0^{'}}\}.$$

By setting $f_0 = f_0^{'} = f_1 = f_2$, we obtain

COROLLARY 5.11. *$C(n_1, r_1, m, n_2, r_2)$ is rearrangeably nonblocking under the 1-rate(f) model if and only if* $m \geq \max\{\min\{n_1, n_2r_2\}, \min\{n_1r_1, n_2\}\}$.

By comparing Lemma 5.9 and Corollary 5.11, we obtain

THEOREM 5.12. *For the 3-stage Clos network, rearrangeably nonblocking under the 1-rate(f) model implies the same for the classical model.*

Note that all these results deal with the very special 3-stage Clos networks. Chung and Ross, and us, are the only exceptions to attack the much harder general networks.

To Summarize, we have

	classical		1-rate(f)	remark
strict		$\Longrightarrow$		proved
		$\Longleftarrow$		proved
wide sense		$\Longrightarrow$		not true
		$\Longleftarrow$		possible
rearrangeable		$\Longrightarrow$		proved
		$\Longleftarrow$		possible

REFERENCES

[1] V. E. Benes, Mathematical theory of connecting networks and telephone traffic, in *Academic Press.*, New York. (1965).

[2] J. A. Bondy and U. S. Murty, Graph theory with applications, *Macmillian, London*, 1976.

[3] S. P. Chung, K. W. Ross, On nonblocking interconnection networks. *SIAM J. Comput.* 20(1991) 726-736.

[4] C. Clos, A study of nonblocking switching networks, *Bell Syst. Tech. J.* 32(1953) 406-424.

[5] P. C. Fishburn, F. K. Hwang, D. Z. Du, B. Gao. On 1-rate wide-sense nonblocking for 3-stage Clos networks. *Disc. Appl. Math.* 78(1997) 75-87.

[6] F. K. Hwang, The mathematical theory of nonblocking switching network, *World Scientific, Singapore*, (1998).

[7] A. Jajszczyk, On nonblocking switching networks composed of digital symmetrical matrices, *IEEE Trans. Commun.,* 31(1983) 2-9.

[8] S.-Y. R. Li, Algebraic Switching Theory and Broadband Applications, *Academic, New York*, 2000.

[9] C. H. C. Little, W. T. Tutte and D. H. Younger, A theorem on integer flows, *Ars, Combin.,* 26A(1988), 109-112.

[10] P. Odlyzko and S. Das, Nonblocking rearrangeable networks with distributed control, *Proc. ICC'84,* vol.1, May 1984, pp.294-298.

[11] C. Q. Zhang, Integer flows and cycle double covers of graphs, *Marcel Dekker, Inc.* 1997.