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Using String Figures to Teach Math Skills

Part 5: Opening Theory

by
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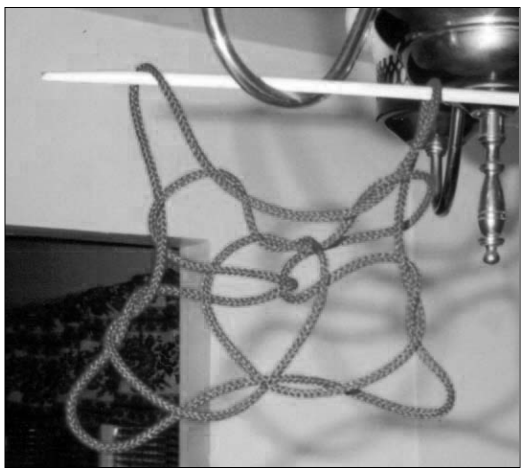


Photo of a 'Heart' string figure suspended on an old chopstick that hangs from the author's kitchen table lighting fixture."Almost no one notices it there until i tell them about it on their third or fourth visit to "Chez Murphy's Gourmet Cuisine". This pleasing design results from combining chiral moves.

ABSTRACT

String figures are excellent tools for helping students acquire spatial skills. They also promote analytical thinking when taught systematically. In this article the author presents yet another system he uses to teach math skills to students who do not respond to traditional methods of learning. Two spatial concepts, chirality and asymmetry, are explored through systematic variation of a simple string figure.

INTRODUCTION

There are many ways to approach string figures. In the literature which developed after anthropologists began recording various figures from around the world, emphasis was placed on particular methods of formation of different figures in a search for evidence concerning prehistoric contact between preliterate peoples. Until the appearance of the International String Figure Association, this tended to be the primary emphasis when string figures were subjected to scholarly analysis.

Under the aegis of the International String Figure Association other approaches have been developed and investigations that are more systematic have begun (Murphy 1997, 1998, 1999, 2000). This paper is a small consideration of the consequences of employing alternative or modified three-loop looms when weaving a figure that normally starts with Opening A. Specifically, i examine the effects of combining alternative three loop openings (Opening B, Left DNA, or Right DNA) with various chiral and asymmetric moves introduced early in the weaving sequence. For this reason i have named this article “Opening Theory”.

OPENING THEORY, PART I: CHIRALITY

We most often think of our environment as being three-dimensional, but actually we live in a four-dimensional universe: *chirality* or “handedness” is a constant companion. Our two hands can be matched as mirror images by placing their palms together, but they exhibit asymmetry when placed one on top of the other since the thumbs lie on opposite sides of the “pancake”.

We often think of Opening A string figures as being symmetrical, and in most cases the right half of a finished figure is indeed a reflection of the left half. But the opening itself is *chiral* (i.e., the left palmar string is taken up first, followed by the right palmar string). Granted, in most cases we get the same final design when Opening A is replaced with Opening B (right palmar string taken up first) or a three-loop DNA opening (Murphy 2000:218-219). But in some cases we do not. The following exercises explore this concept. i begin with a summary of common three loop looms and how they differ. This is followed by instructions for making a canonical figure or “test pattern” for exploring chirality issues. Loop rotations are also reviewed.

THREE-LOOP LOOMS

Opening A

The formation of Opening A has been amply described throughout the string figure literature. My procedural analysis would be as follows:

- Place both thumbs into the loop of string from below.
- Introduce the little fingers into the loop from below (this results in the formation of a palmar string). In the literature this stage in the formation of Opening A is called *Position 1*.
- The right hand reaches to the left palm and the right index picks up the left palmar string and returns to position.
- The left hand then reaches to the right palm, passes through the right index loop from above, picks up the right palmar string, and returns. The result is shown in fig. 1.

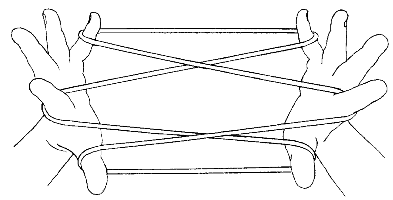


Fig. 1 - *Opening A*

Opening B

Opening B is formed in the same way except the left hand acts first, followed by the right hand. The result is shown in fig. 2.

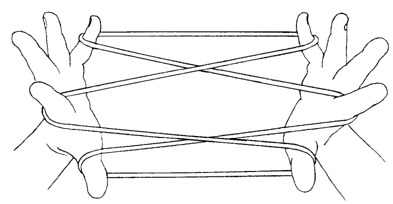


Fig. 2 - *Opening B*

Left DNA

The only difference between Opening A and a 3-loop DNA loom is the parity of one or more string crossings. Also different is the way the loom is built: rather than starting with Position 1, a DNA loom starts with a single loop on each little finger. i call it a DNA loom because of the way the strings form a spiral or double helix as loops are added to the hands. A Left DNA loom is formed by adding loops with the *left* thumb:

- Begin by placing the loop on each little finger so that the near and far strings are parallel and do not cross.
- Create a second loop as follows: Insert the left thumb, *from above*, into the little finger loop and return with the near little finger string (rotate the left thumb toward you and up); insert the right thumb, from below, into the left thumb loop and extend.
- On each hand transfer the thumb loop to the index finger.
- Now create a third loop: Insert the left thumb, *from above*, into the index loop and return with

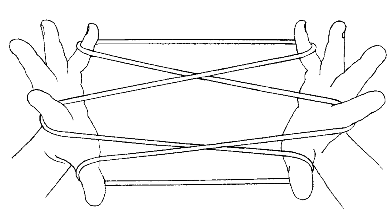


Fig. 3 - *Left DNA opening*

the near index string (rotate the left thumb toward you and up); insert the right thumb, from below, into the left thumb loop and extend (fig. 3). To confirm that the loom is correctly formed, rotate your left hand 90° so that the fingers of your left hand point away from you. If none of the strings touch the loom was formed correctly.

Right DNA

A Right DNA loom is formed in the same way, except the *right* thumb is used to create the second and third loops. The result is shown in fig. 4. To confirm that the loom is correctly formed, rotate your right hand 90° so that the fingers of your right hand point away from you. If none of the strings touch the loom was formed correctly.

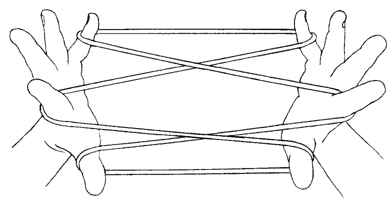


Fig. 4 - *Right DNA opening*

Another way to confirm that the looms are correctly formed is to drop the index loops. Openings A and B will dissolve, but the two DNA openings will produce a wrap (a pair of interlocking strings) near the center of the figure.

Forming the Canonical Figure

In my previous article (Murphy 2000:239-244) i introduced the concept of a canonical figure or "test pattern", a simple weaving sequence that can be used to study the effects of small, systematic changes such as loop rotations and other minor modifications.

The canonical figure i have chosen for this article is nothing more than the Klamath Net (Murphy 1999:169-172) with the *First Weave* (K-1) and *Second Weave* (K-2) eliminated. i used this same "reductionist" approach to create 'Vertical Net' from 'Inuit Net' (see Murphy 2000:226-235). All that remains is *Forming the Loom*, a modified *Shifting the Loops* sequence, *Fixing the Bottom* and *Cleaning the Top*. To make the test pattern more informative i have introduced a loop exchange between *Fixing the Bottom* and *Cleaning the Top*. The figure is formed as follows:

Forming the Loom

- Begin with a three-loop loom (Opening A, Opening B, Left DNA, or Right DNA).

Shifting the Loops

- Introduce the middle and ring fingers into the little finger loop from above and close them to the palm to secure the near little finger string.

- Withdraw the little finger from its loop and reintroduce it from the opposite side, closing it to the palm. The three lesser fingers now clutch the former little finger loop.

Fixing the Bottom

- Without withdrawing the middle finger from the lesser fingers loop, pass each middle finger toward you under the index loop and insert it, from above, into thumb loop; curl the middle finger around the far thumb string and draw it away from you through the lesser fingers loop; withdraw the ring-little fingers and close the middle finger to the palm; reinsert the ring-little fingers into the middle finger loop, closing the far middle finger string to the palm.
- Near each middle finger a loop surrounds the palmar string of each hand; the loop has an upper and a lower string (the latter being a transverse string); pass each middle finger toward you through this loop, then curl the middle finger around the lower string, drawing it away from you through the ring-little finger loop; drop the ring-little finger loop and reinsert these two fingers into the middle finger loop, closing the far middle finger string to the palm.

Exchanging the Index loops

- Transfer the right index loop to the top of the left index, inserting the left index from above; insert the right index from above and from the near side, into the left lower index loop, then lift this loop over the left upper index loop and off the left index, returning the right index to its original position.

Cleaning the Top

- Withdraw the middle finger from the lesser fingers loop and insert it, from below, into the index loop; pinch the near thumb string between the tips of the index and middle fingers, and draw this string through the index-middle finger loop by rotating the index-middle finger pair away from you and up, thus placing the retrieved string on the back of each index (the index-middle finger loop slips off as you return).
- Drop the thumb loop and extend to complete the figure.

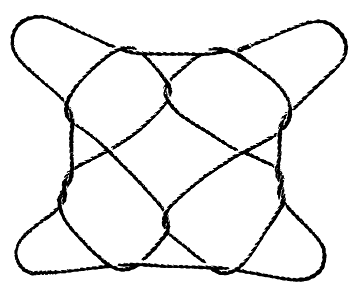


Fig. 5 - *Canonical figure*

If you started with Opening A, the resulting figure is shown in fig. 5. There should be upper and lower wraps in the center of the figure. These are a consequence of the loop exchange maneuver.

Loop Rotations

In a sense, loop rotations are also chiral since they can occur in two directions: either toward you or away from you. In some cases the resulting designs are vastly different. In my notational system, +1/2 indicates a half-turn rotation away from you whereas -1/2 indicates a half-turn rotation towards you. Likewise, +2/2 indicates a full rotation away from you whereas -2/2 indicates a full rotation towards you. 0 is used to indicate no rotation at all.

Full-turn rotations are easily accomplished by tracing out a circle with the tip of your finger, avoiding adjacent loops. Half-turn rotations are best accomplished using two transfers (a method i call “rolling”). For example, to accomplish a +1/2 rotation of the index loop, first transfer the index loop to the thumb, inserting the thumb *from below*, then retransfer this loop to the index, inserting the index *from above*. To accomplish a -1/2 rotation do the same, but reverse *from above* and *from below*. Rolling avoids the awkwardness of having to use the opposite hand to lift a loop off a finger, twist it, and reset it. Full rotations can also be accomplished by rolling (i.e., by using four transfers to combine two half-turn rotations).

A Matrix for Exploring Chirality

To tabulate the outcome of all five rotations (0, +1/2, -1/2, +2/2, -2/2) applied to each of the four looms, one needs a 4-by-5 matrix.

		Opening			
		A	**B**	**Left DNA**	**Right DNA**
Index loop rotation	**0**	fig. 6	fig. 7	fig. 8	fig. 9
	+1/2	fig. 10	fig. 11	fig. 12	fig. 13
	-1/2	fig. 14	fig. 15	fig. 16	fig. 17
	+2/2	fig. 18	fig. 19	fig. 20	fig. 21
	-2/2	fig. 22	fig. 23	fig. 24	fig. 25

All twenty figures are shown on the following page:

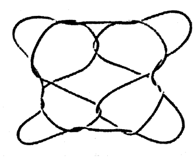


Fig. 6

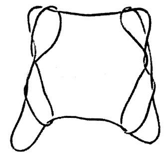


Fig. 7

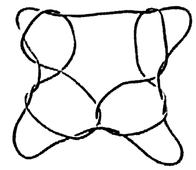


Fig. 8

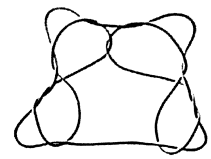


Fig. 9

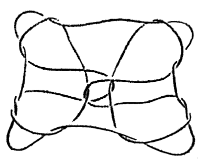


Fig. 10

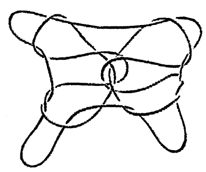


Fig. 11

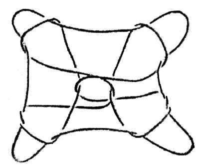


Fig. 12

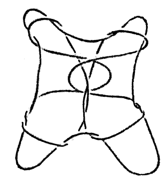


Fig. 13

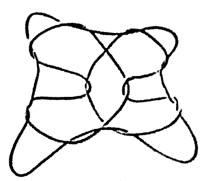


Fig. 14

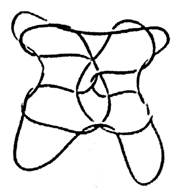


Fig. 15

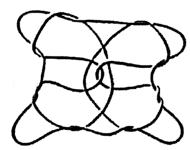


Fig. 16

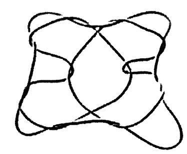


Fig. 17

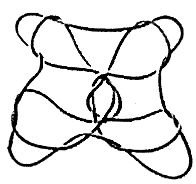


Fig. 18

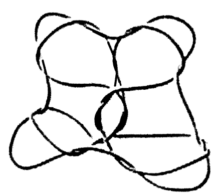


Fig. 19

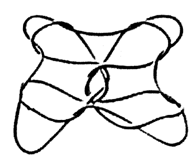


Fig. 20

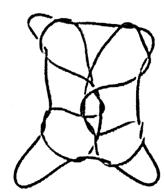


Fig. 21

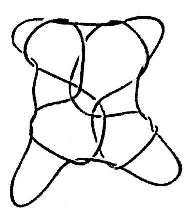


Fig. 22

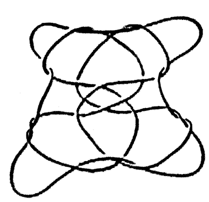


Fig. 23

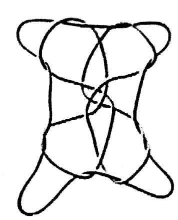


Fig. 24

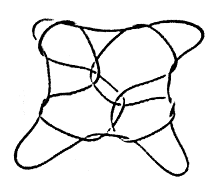


Fig. 25

Matrix Results: Observations

Each row of the matrix reveals a different trend:

First Row: *No index loop rotation*
When no index loop rotation is introduced, each opening gives a distinctly different result.

Second Row: *+1/2 index loop rotation*
When a +1/2 index loop rotation is introduced, the Opening A and Left DNA openings give similar figures. The Opening B and Right DNA figures are also similar.

Third Row: *-1/2 index loop rotation*
When a -1/2 index loop rotation is introduced, the Opening A and Right DNA openings give similar figures. The Opening B and Left DNA figures are also similar. In this case, similarities are determined by which hand acts first in the formation of the opening.

Fourth Row: *+2/2 index loop rotation*
All of these figures look basically the same.

Fifth Row: *-2/2 index loop rotation*
When a -2/2 index loop rotation is introduced, the Opening A and Right DNA openings give similar figures. The Opening B and Left DNA figures are also similar. This case resembles the outcome of a -1/2 index loop rotation.

In summary, we often think of Opening A, Opening B, Left DNA, and Right DNA as being functionally equivalent 3-loop openings. In fact, for the majority of traditional 3-loop figures this statement is true: the resulting designs look the same. Indeed, if no loop exchange is introduced between *Fixing the Bottom* and *Cleaning the Top* in our canonical figure, all four openings give the same design (except for trivial differences in string crossings). But if a loop exchange is introduced between the two moves, differences in the final design become apparent.

Why is this so? Because a loop exchange has *chirality*: either the right loop passes through the left loop or vice-versa. The four openings are likewise *chiral*: in forming Opening A or a Right DNA Opening, the right hand acts first, and with Opening B or a Left DNA Opening the left hand acts first. When more than one chiral event occurs in a weaving sequence, the resulting designs can differ depending on which chirality (right vs. left) was selected at each stage.

It is important to note that in the above experiment, the chirality of the loop exchange was fixed (always right loop passing through left loop). As a result, two wraps occur in the center of the “Opening A, no index loop rotation” design (fig. 6), and no wraps are seen in the center of the “Opening B, no index loop rotation” design (fig. 7). But if the chirality of the loop exchanged is reversed (i.e., left loop passing through right loop), then one obtains the opposite results: the “Opening B, no index loop rotation” figure has two wraps in the center, and the “Opening A, no index loop rotation” figure has no wraps. Likewise, all other matrix figures are similarly affected.

Experimenting with Matrix Figures

After completing the above matrix, i selected the “Left DNA, -1/2 index loop rotation” design (fig. 16) for further experimentation. Three novel figures resulted. Use a thick soft string for best results.

Left DNA Heart-1

- Left DNA opening
- Rotate each index loop -1/2.
- Fix the Bottom.
- With index fingers pointing away, release the index loops onto your lap. Pass the index fingers away from you through the central diamond, pick up the string segment that forms the upper side of the diamond (part of the near index string of the opposite hand), return hands to the upright position, and extend. The former index loops are absorbed in the process.

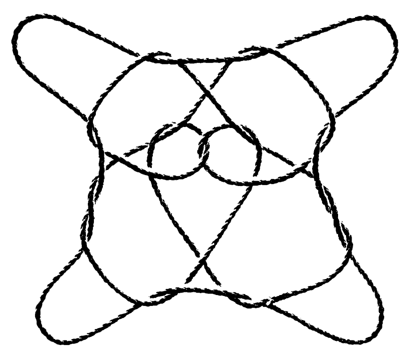


Fig. 26 - *Left DNA Heart*

- Exchange the index loops (right through left).
- Clean the top. Arrange the center to reveal a ‘Heart’ (fig. 26).

Chopstick Heart

This is the figure seen in the photo on the first page of this article. After i invented the figure i suspended it from a chopstick and hung it from a light fixture in my kitchen. It has been there ever since.

- Opening B
- Rotate each index loop -1/2.
- Fix the Bottom.
- Transfer the right index loop to the top of the left index, inserting the left

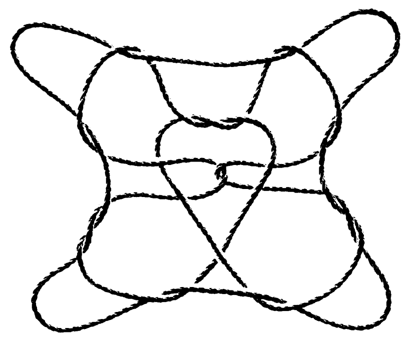


Fig. 27 - *Chopstick Heart*

index from above; insert the right index from the far side and from below into the upper left index loop; pick up the left upper far index string but do not return; pass the right index tip toward you over the left upper near index string, then insert the right index, from above and from the near side, into the left lower index loop. With the right index tip lift the left lower index loop over the left upper index loop and off the left index; Navaho the right index loops (lift the lower loop over the upper loop and release it). Extend and arrange. The near index strings should interlock. The far index strings coil around each other before entering the center of the design (these strings will form the top of the heart).

- Clean the top. Arrange the center to reveal a 'Heart' (fig. 27).

If a Left DNA opening is used instead of Opening B, a very similar design results. However, the resulting figure has radically different properties when tension is applied. See the appendix for a complete discussion.

Left DNA Mickey

- Left DNA opening
- Rotate each index loop -1/2.
- Do the First Inuit Weave: Pass each thumb away from you over the near index string and under the far index string, then pick up the near little fingers string and return; pass each middle finger toward you over both index strings and down through the upper thumb loop, then pick up the lower far thumb string and return; drop both thumb loops and extend.
- Do a modified Second Inuit Weave: Pass each thumb away from you under the near index string, pick up the far index string, and return; pass each thumb away from you over the near index string and under all other strings (the former far index string will slip off in the process); pick up the far little finger string and return, drawing it through the loop hooked down by each thumb.
- Release each little finger loop and extend.
- On each hand transfer the middle finger loop to the little finger, inserting the little finger from above.
- Fix the Bottom.
- Exchange the index loops (right through left).
- Clean the Top. Arrange the center to reveal a 'Mouse Face' (fig. 28).

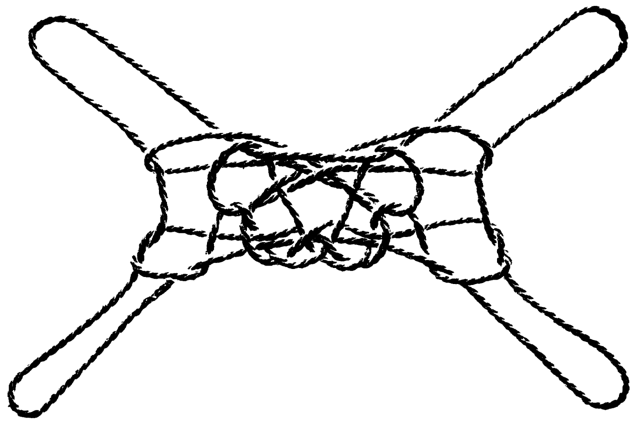


Fig. 28 - *Left DNA Mickey*

OPENING THEORY, PART 2: ASYMMETRY

In the manufacture of most traditional string figures both hands act in unison. But in the following section i explore the consequences of asymmetric moves (i.e., the right hand doing something different from the left hand). For purposes of illustration we will work with the Opening A version of our canonical figure. At least two moves in the canonical weaving sequence can be accomplished asymmetrically:

> (1) The index loop rotations (i.e., the right and left index loops can be rotated a half turn (or full turn!) in the same direction or in opposite directions)
>
> (2) The retrieval of right palmar string during the loom formation (i.e., through the right index loop or outside of it)

Methods for accomplishing each are given below.

Asymmetric index loop rotations

In Part 1 of this article, index loop rotations were introduced *after* the loom was formed. But in this section (Part 2), they are introduced *as* the loom is formed (i.e., during the palmar string retrievals). First, begin Opening A in the standard way by establishing Position 1:

- Place both thumbs into the loop of string from below.
- Introduce the little fingers into the loop from below (this results in the formation of a palmar string).

Next, the right hand reaches to the left palm, and retrieves the left palmar string in one of the following ways:

0 rotation: The right index retrieves the left palmar string *from below* and returns to position.

+1/2 rotation: The right index retrieves the left palmar string *from above,* then rotates a *half turn toward* the body so that the finger is upright, and returns to position.

-1/2 rotation: The right index retrieves the left palmar string *from above,* then rotates a *half turn away* from the body so that the finger is upright, and returns to position.

+2/2 rotation: The right index retrieves the left palmar string *from below,* then rotates a *full turn away* from the body (avoiding other strings), and returns to position.

-2/2 rotation: The right index retrieves the left palmar string *from below,* then rotates a *full turn toward* the body (avoiding other strings), and returns to position.

Once the left palmar string taken up, the retrieval of the right palmar string is likewise achieved using any of the five options listed above.

Asymmetric right palmar string retrievals

In Opening A, once the left palmar string taken up, the right palmar string is usually retrieved *symmetrically* by first passing the left index down through the right index loop. But it can also be retrieved asymmetrically by passing the left index to the near side or far side of the right index loop rather than through it. These three options are defined as follows:

Center retrieval: The left hand reaches to the right palm, passes through the right index loop from above, retrieves the right palmar string (from above or from below, with or without rotation), and returns.

Near side retrieval: The left hand reaches to the right palm, passes to the thumb side (the near side) of the right index loop, retrieves the right palmar string (from above or from below, with or without rotation), and returns.

Far side retrieval: The left hand reaches to the right palm, passes to the little finger side (the far side) of the right index loop, retrieves the right palmar string (from above or from below, with or without rotation), and returns.

MATRICES FOR EXPLORING ASYMMETRY

Since asymmetric loop rotations and right palmar string retrievals can occur in the same canonical weaving sequence, three 5-by-5 matrices are required to explore all combinations. All 75 figures are shown on the following pages.

First retrieval (right index)

Second retrieval (left index)	**0**	**+1/2**	**-1/2**	**+2/2**	**-2/2**
0	fig. 29	fig. 30	fig. 31	fig. 32	fig. 33
+1/2	fig. 34	fig. 35	fig. 36	fig. 37	fig. 38
-1/2	fig. 39	fig. 40	fig. 41	fig. 42	fig. 43
+2/2	fig. 44	fig. 45	fig. 46	fig. 47	fig. 48
-2/2	fig. 49	fig. 50	fig. 51	fig. 52	fig. 53

CENTER RETRIEVAL MATRIX

First retrieval (right index)

Second retrieval (left index)	**0**	**+1/2**	**-1/2**	**+2/2**	**-2/2**
0	fig. 54	fig. 55	fig. 56	fig. 57	fig. 58
+1/2	fig. 59	fig. 60	fig. 61	fig. 62	fig. 63
-1/2	fig. 64	fig. 65	fig. 66	fig. 67	fig. 68
+2/2	fig. 69	fig. 70	fig. 71	fig. 72	fig. 73
-2/2	fig. 74	fig. 75	fig. 76	fig. 77	fig. 78

NEAR SIDE RETRIEVAL MATRIX

First retrieval (right index)

Second retrieval (left index)	**0**	**+1/2**	**-1/2**	**+2/2**	**-2/2**
0	fig. 79	fig. 80	fig. 81	fig. 82	fig. 83
+1/2	fig. 84	fig. 85	fig. 86	fig. 87	fig. 88
-1/2	fig. 89	fig. 90	fig. 91	fig. 92	fig. 93
+2/2	fig. 94	fig. 95	fig. 96	fig. 97	fig. 98
-2/2	fig. 99	fig. 100	fig. 101	fig. 102	fig. 103

FAR SIDE RETRIEVAL MATRIX

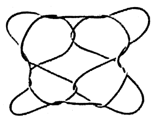


Fig. 29

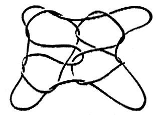


Fig. 30

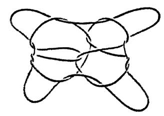


Fig. 31

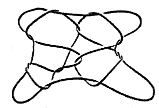


Fig. 32

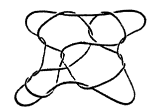


Fig. 33

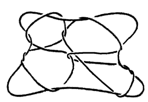


Fig. 34

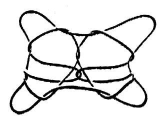


Fig. 35

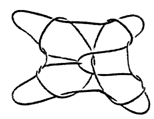


Fig. 36

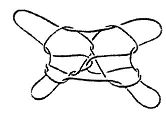


Fig. 37

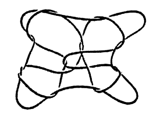


Fig. 38

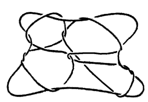


Fig. 39

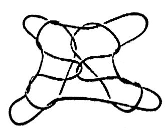


Fig. 40

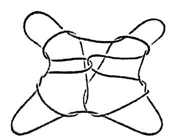


Fig. 41

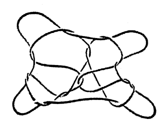


Fig. 42

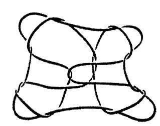


Fig. 43

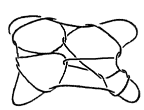


Fig. 44

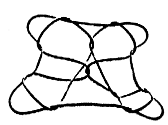


Fig. 45

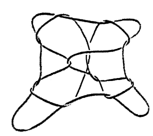


Fig. 46

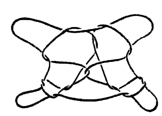


Fig. 47

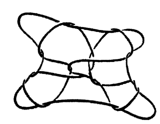


Fig. 48

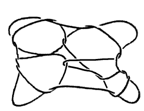


Fig. 49

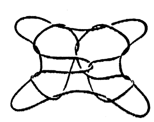


Fig. 50

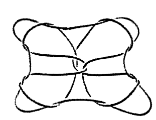


Fig. 51

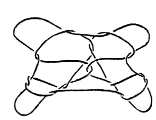
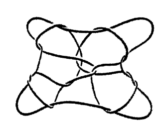


Fig. 52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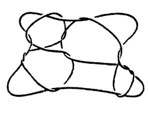
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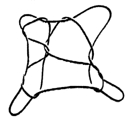
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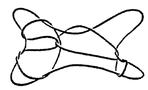
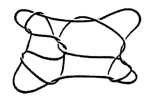


Fig. 56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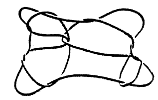
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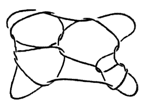
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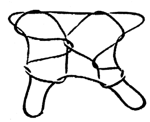


Fig. 60

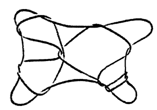


Fig. 61

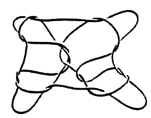


Fig. 62

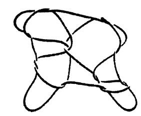
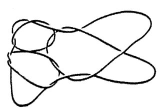


Fig. 63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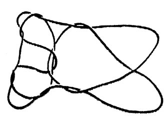
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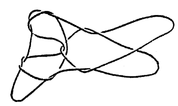
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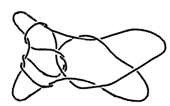


Fig. 67

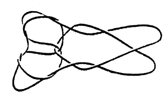


Fig. 68

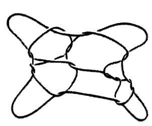


Fig. 69

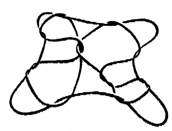


Fig. 70

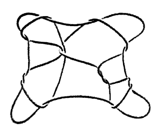


Fig. 71

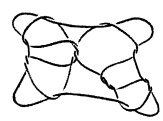


Fig. 72

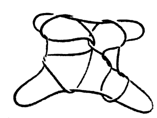


Fig. 73

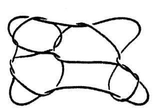


Fig. 74

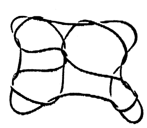


Fig. 75

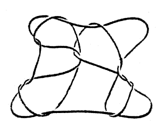


Fig. 76

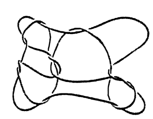


Fig. 77

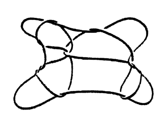


Fig. 78

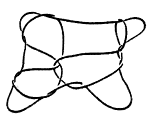


Fig. 79

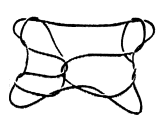


Fig. 80

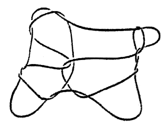


Fig. 81

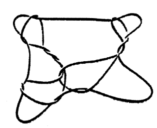


Fig. 82

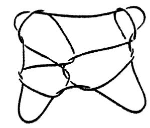


Fig. 83

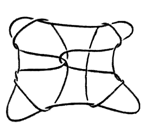


Fig. 84

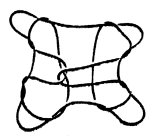


Fig. 85

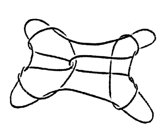


Fig. 86

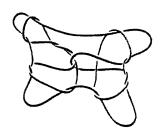


Fig. 87

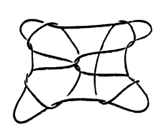
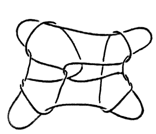


Fig. 88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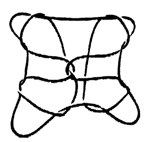
Fig. 90

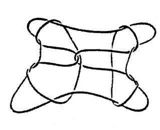
Fig. 91

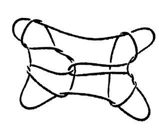
Fig. 92

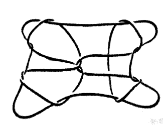
Fig. 93

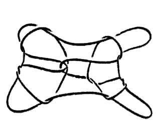
Fig. 94

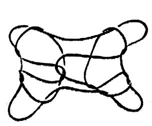
Fig. 95

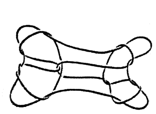
Fig. 96

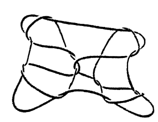
Fig. 97

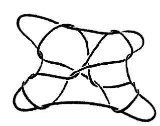
Fig. 98

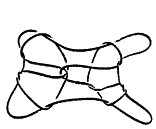
Fig. 99

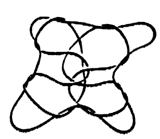
Fig. 100

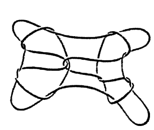
Fig. 101

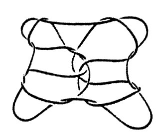
Fig. 102

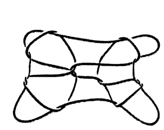
Fig. 103

On the preceding pages i arranged the drawings to match the matrix. Note that in nearly every case, only the left half of the design changes as one proceeds across a row (the right half is constant), suggesting that the first retrieval is responsible for the observed differences. The right half of the design changes as one proceeds down a column (the left half is constant), suggesting that the second retrieval is responsible for these differences.

Experimenting with Matrix Figures

After completing the above three matrices, i selected the "-1/2, -1/2" design (fig. 41) from the center retrieval matrix for further experimentation. It amused me to consider whether i could improve the figure. The figure intrigued me because the two vertical strings on the far side of the design interlock just like the two horizontal strings on the near side. Could i find a way to make the two vertical strings *not* interlock? The proposed design would be a pleasant figure (fig. 104). Could i accomplish this using the canonical method with a modified three-loop loom? i set to work.

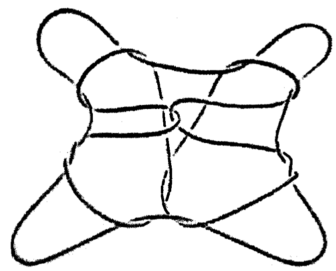

Fig. 41

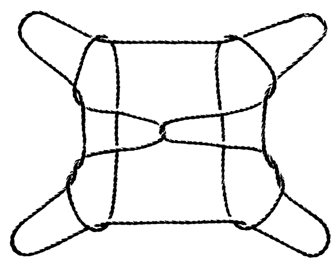

Fig. 104 - *Target figure*

After some fiddling, i learned that i could create the target figure by forming a Left DNA opening and swapping the near and far transverse strings using loop passage or "braiding" techniques (Murphy 2000:235-244). But i also learned that there are four ways to swap the two strings, and only one way produces the desired figure.

First swap method

In this method, the thumb loop is rotated -1/2, passed under the index loop, up through the little finger loop, and placed on the little finger. At the same time, the little finger loop is rotated +1/2, passed under the index index loop, and placed on the thumb. These moves can be visualized using *circle notation* (Murphy 2000:244-247), as shown in Chart 1. Here's how to accomplish the swap without having to use the opposite hand to braid the loops:

- Pass each middle finger down through the little finger loop, then toward you under the index loop, then down into the thumb loop; catch the far thumb string and return the middle finger to the upright position by rotating it away from you and up, thus drawing the far thumb string up

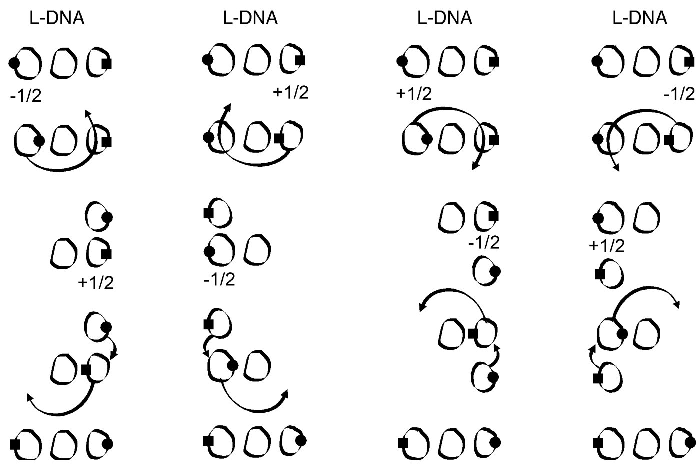

Chart 1 **Chart 2** **Chart 3** **Chart 4**

Circle notation showing four ways of swapping the transverse strings of a three loop loom. A black circle marks the near thumb string; a black square marks the far little finger string. At the end of the sequence, these two strings have swapped positions.

through the little finger loop. Release the thumb loop. The former near thumb string (a transverse string) becomes a far middle finger string as a result of this move.

- Pass each thumb away from you under all strings, pick up the far little finger string, and return. Release the little finger loop. The former far little finger string (a transverse string) becomes a near thumb string as a result of this move.
- Finally, transfer the middle finger loop to the little finger, inserting the little finger from below. You now have a Left DNA loom with the transverse strings swapped.

So the first figure i tried was:

- Left DNA opening
- Exchange transverse strings using the **First Swap Method**.
- Fix the Bottom.
- Exchange the index loops (right through left).
- Clean the top (fig. 105).

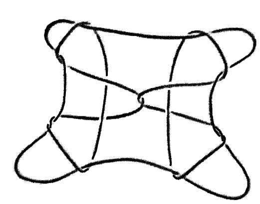

Fig. 105

The figure is a close approximation of the target design: the vertical strings no longer interlock. But you will notice that the vertical strings are captured by the interlocking horizontal strings. The front and back layers of string are not independent. This flaw encouraged me to try a second method of swapping the transverse strings.

Second swap method
In this method, the little finger loop is rotated +1/2, passed under the index loop, up through the thumb loop, and placed on the thumb. At the same time, the thumb loop is rotated -1/2, passed under the index index loop, and placed on the little finger. The swap is accomplished as follows:

- Pass each middle finger down through the thumb loop, then away from you under the index loop, then down into the little finger loop; catch the near little finger string and return the middle finger to the upright position by rotating it toward you and up, thus drawing the near little finger string up through the thumb loop. Release the little finger loop. The former far little finger string (a transverse string) becomes a near middle finger string as a result of this move.
- Pass each little finger toward you under all strings, pick up the near thumb string, and return. Release the thumb loop. The former near thumb string (a transverse string) becomes a far little finger string as a result of this move.
- Finally, transfer the middle finger loop to the thumb, inserting the thumb from below. You now have a Left DNA loom with the transverse strings swapped.

So the second figure i tried was:

- Left DNA opening
- Exchange transverse strings using the **Second Swap Method**.
- Fix the Bottom.
- Exchange the index loops (right through left).
- Clean the top (fig. 106).

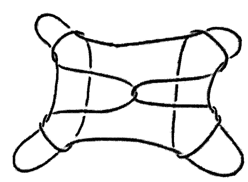

Fig. 106

Appropriately enough, this method produced the target figure (fig. 104). The vertical strings now travel across the far side of the figure without being trapped by the interlocking horizontal strings.

To finish the series, i asked what would happen if a swapped the near and far transverse strings using a third or fourth method.

Third swap method
In this method, the thumb loop is rotated +1/2, passed over the index loop, down through the little finger loop, and placed on the little finger. At the same time, the little finger loop is rotated -1/2, passed over the index loop, and placed on the thumb. It is accomplished as follows:

- Pass each little finger toward you over the index loop, then transfer the thumb loop to the little finger, inserting the little finger from above. The former near thumb string (a transverse string) is now an upper far little finger string.
- With the opposite hand grasp the lower little finger loop, lift it off the little finger (over the upper loop), rotate it a half turn toward you (-1/2 rotation), and place it on the thumb. the former lower far little finger string (a transverse string) is now a near thumb string. You now have a Left DNA loom with the transverse strings swapped.

When i made the canonical figure with this modified loom, i did not get the target figure unless i first “rolled” the figure on my hands so i could work the underside. Rolling, as described in my previous article (Murphy 2000:221) is accomplished as follows:

- Transfer the thumb loop to the middle finger, inserting the middle finger from above.
- Pass each thumb away from you under all the strings, pick up the far little finger string and return with it, then drop the little finger loop.
- Transfer the middle finger loop to the little finger, inserting the little finger from below.
- Transfer the index loop to the thumb, inserting the thumb from below, then retransfer this loop to the index, inserting the index from above. The entire figure has now been rotated a half turn away from you.

So the third figure i tried was:

- Left DNA opening
- Exchange transverse strings using the **Third Swap Method**.
- Roll the entire figure +1/2 turn away.
- Fix the Bottom.
- Exchange the index loops (right through left).
- Clean the top (fig. 107).

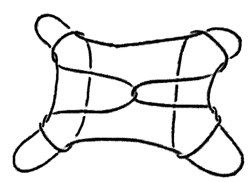

Fig. 107

To round out the investigation, i tried swapping the transverse strings using a fourth method.

Fourth swap method

In this method, the little finger loop is rotated -1/2, passed over the index loop, down through the thumb loop, and placed on the thumb. At the same time, the thumb loop is rotated +1/2, passed over the index index loop, and placed on the little finger. It is accomplished as follows:

- Pass each thumb away from you over the index loop, then transfer the little finger loop to the thumb, inserting the thumb from above. The former far little finger string (a transverse string) is now an upper near thumb string.
- With the opposite hand grasp the lower thumb loop, lift it off the thumb (over the upper loop), rotate it a half turn away from you (+1/2 rotation), and place it on the little finger. The former lower thumb string (a transverse string) is now a far little finger string. You now have a Left DNA loom with the transverse strings swapped.

So the fourth figure i tried was:

- Left DNA opening
- Exchange transverse strings using the **Fourth Swap Method**.
- Roll the entire figure +1/2 turn away.
- Fix the Bottom.
- Exchange the index loops (right through left).
- Clean the top (fig. 108).

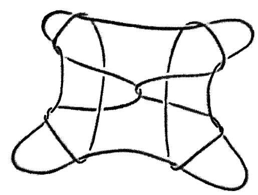

Fig. 108

As expected, i got the same result as **First Swap Method** with no rolling (the vertical strings are trapped within the interlocking horizontal loops).

When my swap/rolling methods were applied to a Right DNA opening i got an entirely different set of four figures:

- Right DNA opening
- Exchange transverse strings using the **First Swap Method**.
- Fix the Bottom.
- Exchange the index loops (right through left).
- Clean the top (fig. 109).

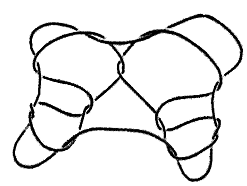

Fig. 109

- Right DNA opening
- Exchange transverse strings using the **Second Swap Method**.
- Fix the Bottom.
- Exchange the index loops (right through left).
- Clean the top (fig. 110).

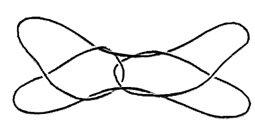

Fig. 110

- Right DNA opening
- Exchange transverse strings using the **Third Swap Method**.

- Roll the entire figure +1/2 turn away.
- Fix the Bottom.
- Exchange the index loops (right through left).
- Clean the top (fig. 111).

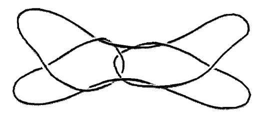

Fig. 111

- Right DNA opening
- Exchange transverse strings using the **Fourth Swap Method**.
- Roll the entire figure +1/2 turn away.
- Fix the Bottom.
- Exchange the index loops (right through left).
- Clean the top (fig. 112).

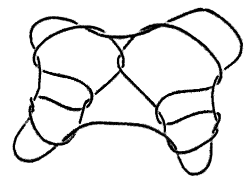

Fig. 112

CONCLUSION

Chirality (right vs. left hand acting first) and *asymmetry* (right and left doing different moves) are two aspects of string figure making that have not yet been explored in a systematic fashion. In this article i chose to do this using a canonical or “test” pattern that allows one to quickly evaluate the effects of chiral and asymmetric openings, largely because the canonical algorithm includes a second chiral move (a loop exchange) that magnifies loom differences. i also showed how rather simple matrix output figures can be used as starting points for engineering more complex designs.

i encourage readers to try other three-loop looms whenever they encounter an Opening A figure that includes a chiral move (a loop exchange, a katilluik move, a loop rotation). The results may surprise you!

* * *

As always, i close with a poem:

i love when a student asks
a hard question
one i don't know

right away i begin to think
to worry through the route to the answer

my father taught
the smartest man doesn't know
the answer
he only knows the path
to the answer

so i answer best
when i know the least

in public i think aloud
i teach

murphy twisting his hands meaningfully

inoli

LITERATURE CITED

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APPENDIX

Chopstick Heart Revisited

On page 220 i mentioned that my Chopstick Heart (fig. 27) can also be made from a Left DNA Opening, but that the final design has different properties. If the Opening B version is fully extended so that the strings are taut the heart merely shrinks (fig. 113), but if the Left DNA version is drawn tight the heart "flips" and assumes a new conformation that is not at all heart-like (fig. 114). Ten years ago Joseph Ornstein published an article on this phenomenon (*Bulletin of String Figures Association* 18:26-33). Ornstein called this duality of structure *intensionality*, the potential for strings to arrange themselves (or be arranged) differently, depending on how much tension is applied.

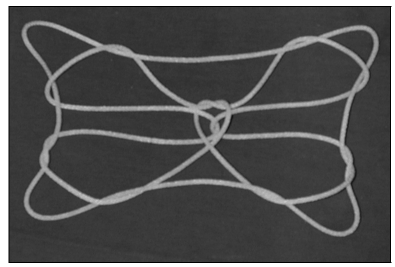

Fig. 113

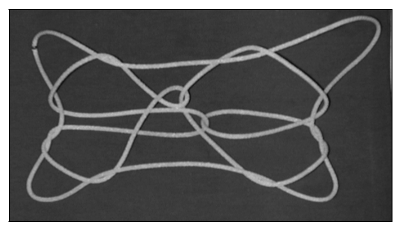

Fig. 114

If one examines both Chopstick Hearts carefully, one finds that only one string crossing differs (indicated by a * in fig. 115). This crossing is located at the base of the heart, far from the wrap that forms the top of the heart. Yet it is able to affect the conformation of the wrap as the figure is drawn tight. Can you explain why this is so?

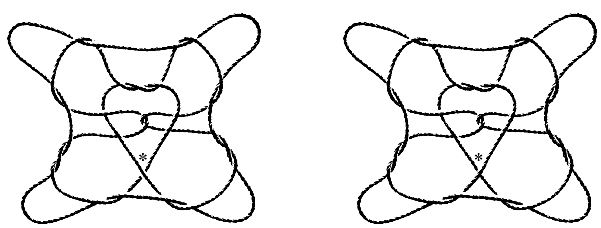

Fig. 115 - *Opening B vs. Left DNA Chopstick Heart*

In fig. 115 the left side of each heart is trapped between a pair of horizontal strings, whereas the right side of each heart is not. Can you devise a method for making a Chopstick Heart in which both sides (or neither side) is trapped? The task is similar to that presented on pages 227-232, in which methods were devised to trap or untrap the vertical strings that pass through the interlocking horizontal loops. If the target figures are truly impossible to form, can you devise a simple way to demonstrate this?