`braidlab`: a software package for braids and loops

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release 2.1

Abstract

`braidlab` is a Matlab package for analyzing data using braids. It was designed to be fast, so it can be used on relatively large problems. It uses the object-oriented features of Matlab to provide a class for braids on punctured disks and a class for equivalence classes of simple closed loops. The growth of loops under iterated action by braids is used to compute the topological entropy of braids, as well as for determining the equality of braids. This guide is a survey of the main capabilities of `braidlab`, with many examples; the help messages of the various commands provide more details. Some of the examples contain novel observations, such as the existence of cycles of the linear effective action for arbitrary braids.

Contents

1 A tour of `braidlab`

You will need access to a recent version of Matlab to use `braidlab`. See Appendix A for instructions on how to install `braidlab` on your machine.

1.1 The `braid` class

1.1.1 Constructor and elementary operations

`braidlab` defines a number of classes, most importantly `braid` and `loop`. The braid $\sigma_1\sigma_2^{-1}$ is constructed with

```
>> a = braid([1 -2])    % defaults to 3 strings

a = < 1 -2 >
```

which defaults to the minimum required strings, 3. The same braid on 4 strings is constructed with

```
> a4 = braid([1 -2],4)    % force 4 strings

a4 = < 1 -2 >
```

Two braids can be multiplied:

```
>> a = braid([1 -2]); b = braid([1 2]);
>> a*b, b*a

ans = < 1 -2  1  2 >

ans = < 1  2  1 -2 >
```

Powers can also be taken, including the inverse:

```
>> a^5, inv(a), a*a^-1

ans = < 1 -2  1 -2  1 -2  1 -2  1 -2 >

ans = < 2 -1 >

ans = < 1 -2  2 -1 >
```

Note that this last expression is the identity braid, but is not simplified. The method `compact` attempts to simplify the braid:

```
>> compact(a*a^-1)

ans = < e >
```

The method `compact` is based on the heuristic algorithm of Bangert *et al.* (2002), since finding the braid of minimum length in the standard generators is in general

difficult (Paterson & Razborov, 1991). Hence, there is no guarantee that in general `compact` will find the identity braid, even though it do so here. To really test if a braid is the identity (trivial braid), use the method `istrivial`:

```
>> istrivial(a*a^-1)

ans = 1
```

The number of strings is

```
>> a.n

ans = 3
```

Note that

```
>> help braid
```

describes the class `braid`. To get more information on the `braid` constructor, invoke

```
>> help braid.braid
```

which refers to the method `braid` within the class `braid`. (Use `methods(braid)` to list all the methods in the class.) There are other ways to construct a `braid`, such as using random generators, here a braid with 5 strings and 10 random generators:

```
>> braid('random',5,10)

ans = < 1  4 -4  2  4 -1 -2  4  4  4 >
```

The constructor can also build some standard braids:

```
>> braid('halftwist',5)

ans = < 4  3  2  1  4  3  2  4  3  4 >

>> braid('8_21')  % braid for 8-crossing knot #21

ans = < 4  3  2  1  4  3  2  4  3  4 >
```

In Section 1.2 we will show how to construct a braid from a trajectory data set.

The `braid` class handles equality of braids:

```
>> a = braid([1 -2]); b = braid([1 -2 2 1 2 -1 -2 -1]);
>> a == b
```

```
ans = 1
```

These are the same braid, even though they appear different from their generator sequence (Birman, 1975). Equality is determined efficiently by acting on loop coordinates (Dynnikov, 2002), as described by Dehornoy (2008). See Sections 1.3–1.4 for more details. If for some reason lexicographic (generator-per-generator) equality of braids is needed, use the method `lexeq(b1,b2)`.

We can extract a subbraid by choosing specific strings: for example, if we take the 4-string braid $\sigma_1\sigma_2\sigma_3^{-1}$ and discard the third string, we obtain $\sigma_1\sigma_2^{-1}$:

```
>> a = braid([1 2 -3]);
>> subbraid(a,[1 2 4])   % subbraid using strings 1,2,4

ans = < 1 -2 >
```

The opposite of subbraid is the *tensor product*, the larger braid obtained by laying two braids side-by-side (Kassel & Turaev, 2008):

```
>> a = braid([1 2 -3]); b = braid([1 -2]);
>> tensor(a,b)

ans = < 1  2 -3  5 -6 >
```

Here, the tensor product of a 4-braid and a 3-braid has 7 strings. The generators $\sigma_1\sigma_2^{-1}$ of `b` became $\sigma_5\sigma_6^{-1}$ after re-indexing so they appear to the right of `a`.

1.1.2 Topological entropy and complexity

There are a few methods that exploit the connection between braids and homeomorphisms of the punctured disk. Braids label *isotopy classes* of homeomorphisms, so we can assign a topological entropy to a braid:

```
>> entropy(braid([1 2 -3]))

ans = 0.8314
```

The entropy is computed by iterated action on a loop (Moussafir, 2006). This can fail if the braid is finite-order or has very low entropy:

```
>> entropy(braid([1 2]))
Warning: Failed to converge to requested tolerance; braid is
   likely finite-order or has low entropy.  Returning zero
   entropy.
```

```
ans = 0
```

To force the entropy to be computed using the Bestvina–Handel train track algorithm (Bestvina & Handel, 1995), we add an optional `'method'` parameter:

```
>> entropy(braid([1 2]),'method','trains')

ans = 0
```

Note that for large braids the Bestvina–Handel algorithm is impractical. But when applicable it can also determine the Thurston–Nielsen type of the braid (Fathi *et al.*, 1979; Thurston, 1988; Casson & Bleiler, 1988; Boyland, 1994):

```
>> tntype(braid([1 2 -3]))

ans = pseudo-Anosov
>> tntype(braid([1 2]))

ans = finite-order
>> tntype(braid([1 2],4))  % reducing curve around 1,2,3

ans = reducible
```

`braidlab` uses Toby Hall's implementation of the Bestvina–Handel algorithm (Hall, 2012).

The topological entropy is a measure of braid complexity that relies on iterating the braid. It gives the maximum growth rate of a 'rubber band' anchored on the braid, as the rubber band slides up many repeated copies of the braid. For finite-order braids, this will converge to zero. The *geometric complexity* of a braid (Dynnikov & Wiest, 2007), is defined in terms of the $\log_2$ of the number of intersections of a set of curves with the real axis, after one application of the braid:

```
>> complexity(braid([1 -2]))

ans = 2
>> complexity(braid([1 2]))

ans = 1.5850
```

See Section 1.3 or '`help braid.complexity`' for details on how the geometric complexity is computed.

1.1.3 Representation and invariants

There are a few remaining methods in the braid class, which we describe briefly. The reduced Burau matrix representation (Burau, 1936; Birman, 1975) of a braid is obtained with the method `burau`:

```
>> burau(braid([1 -2]),-1)

ans = 1     -1
     -1      2
```

where the last argument (-1) is the value of the parameter t in the Laurent polynomials that appear in the entries of the Burau matrices. With access to Matlab's wavelet toolbox, we can use actual Laurent polynomials as the entries:

```
>> B = burau(braid([1 -2]),laurpoly(1,1))

     | - z^(+1)          z^(+1)      |
     |                               |
 B = |                               |
     |                               |
     |   - 1         + 1 - z^(-1)    |
```

but the matrix is now given as a cell array[1] , each entry containing a `laurpoly` object:

```
>> B{2,2}

ans(z) = + 1 - z^(-1)
```

Another option is to use Matlab's symbolic toolbox:

```
>> B = burau(braid([1 -2]),sym('t'))

B = [ -t,        t]
    [ -1, 1 - 1/t]
```

where now `B` is a matrix of `sym` objects:

```
>> B(2,2)

ans = 1 - 1/t
```

[1] A Matlab cell array is similar to a numeric array, except that its entries can hold any data, not just numeric. The entries are indexed as `a{1,2}` rather than `a(1,2)`, and matrix operations like multiplication are not defined.

The reduced Burau matrix of a braid can be used to compute the *Alexander–Conway polynomial* (or Alexander polynomial for short) of its closure. For instance, the trefoil knot is given by the closure of the braid σ_1^3 (Weisstein, 2013), which gives a Laurent polynomial

```
>> alexpoly(braid([1 1 1]))  % can also use braid('trefoil')

ans(z) = + z^(+2) - z^(+1) + 1
```

The figure-eight knot is the closure of $(\sigma_1\sigma_2^{-1})^2$:

```
>> alexpoly(braid([1 -2 1 -2]))  % or braid('figure-8')

ans(z) = - 1 + 3*z^(-1) - z^(-2)
```

This can be 'centered' so that it satisfies $p(z) = \pm p(1/z)$:

```
>> alexpoly(braid([1 -2 1 -2]),'centered')

ans(z) = - z^(+1) + 3 - z^(-1)
```

The centered Alexander polynomial is a knot invariant, so it can be used to determine when two knots are not the same. For knots, the centered polynomial is guaranteed to have integral powers. For links, such as the Hopf link consisting of two singly-linked loops, it might not:

```
>> alexpoly(braid([1 1]),'centered')  % the Hopf link

Error using braidlab.braid/alexpoly
Polynomial with fractional powers.  Remove 'centered' option
   or use the symbolic toolbox.
```

Fractional powers cannot be represented with a `laurpoly` object. In that case we can drop the 'centered' option, which yields the uncentered polynomial $1 - z$. Alternatively, we can switch to using a variable from the symbolic toolbox:

```
>> alexpoly(braid([1 1]),sym('x'),'centered')

ans = 1/x^(1/2) - x^(1/2)
```

which can represent fractional powers. This polynomial satisfies $p(x) = -p(1/x)$.

The method `perm` gives the permutation of strings corresponding to a braid:

```
>> perm(braid([1 2 -3]))
```

```
ans = 2  3  4  1
```

If the strings are unpermuted, then the braid is *pure*, which can also be tested with the method `ispure`.

Finally, the *writhe* of a braid is the sum of the powers of its generators. The writhe of $\sigma_1^{+1}\sigma_2^{+1}\sigma_3^{-1}$ is $+1+1-1=1$:

```
>> writhe(braid([1 2 -3]))

ans = 1
```

The writhe is a braid invariant.

1.2 Constructing a braid from data

1.2.1 An example

One of the main purposes of `braidlab` is to analyze two-dimensional trajectory data using braids. We can assign a braid to trajectory data by looking for *crossings* along a projection line (Thiffeault, 2005, 2010). The `braid` constructor allows us to do this easily.

The folder `testsuite` contains a dataset of trajectories, from laboratory data for granular media (Puckett *et al.*, 2012). From the `testsuite` folder, we load the data:

```
>> clear; load testdata
>> whos
  Name          Size                Bytes  Class     Attributes

  XY         9740x2x4            623360  double
  ti            1x9740             77920  double
```

Here `ti` is the vector of times, and `XY` is a three-dimensional array: its first component specifies the timestep, its second specifies the X or Y coordinate, and its third specifies one of the 4 particles. Figure 1(a) shows the X and Y coordinates of these four trajectories, with time plotted vertically. Figure 1(b) shows the same data, but projected along the X direction. To construct a braid from this data, we simply execute

```
>> b = braid(XY);
>> b.length

ans = 894
```

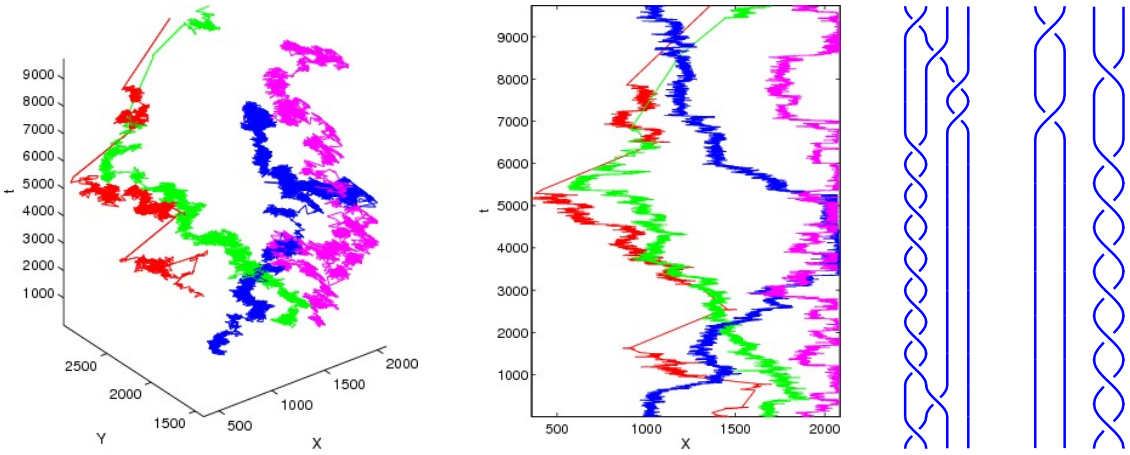


Figure 1: (a) A dataset of four trajectories, (b) projected along the X axis. (c) The compacted braid $\sigma_1^{-1}\sigma_2^{-1}\sigma_1^{-8}\sigma_3^2\sigma_2\sigma_1$ corresponding to the X projection in (b). (d) The compacted braid $\sigma_3^{-7}\sigma_1\sigma_3^{-1}\sigma_1$ corresponding to the Y projection, with closure enforced. The braids in (c) and (d) are conjugate.

This is a very long braid! But Figure 1(b) suggests that this is misleading: many of the crossings are 'wiggles' that cancel each other out. Indeed, if we attempt to shorten the braid:

```
>> b = compact(b)

b = < -1 -2 -1 -1 -1 -1 -1 -1 -1 -1  3  3  2  1 >
>> b.length

ans = 14
```

we find the number of generators (the length) has dropped to 14! We can then plot this shortened braid as a braid diagram using `plot(b)` to produce Figure 1(c). The braid diagram allows us to see some topological information clearly, such as the fact that the second and third particles undergo a large number of twists around each other; we can check this by creating a subbraid with only those two strings:

```
>> subbraid(bX,[2 3])

ans = < -1 -1 -1 -1 -1 -1 -1 -1 >
```

which shows that the winding number between these two strings is -4.

1.2.2 Changing the projection line and enforcing closure

The braid in the previous section was constructed from the data by assuming a projection along the X axis (the default). We can choose a different projection by specifying an optional angle for the projection line; for instance, to project along the Y axis we invoke

```
>> b = braid(XY,pi/2);    % project onto Y axis
>> b.length

ans = 673
>> b.compact

ans = < -3 -3 -3 -3 -3 -3 -3  1 -3 >
```

In general, a change of projection line only changes the braid by conjugation (Boyland, 1994; Thiffeault, 2010). We can test for conjugacy:

```
>> bX = compact(braid(XY,0)); bY = compact(braid(XY,pi/2));
>> conjtest(bX,bY)    % test for conjugacy of braids

ans = 0
```

The braids are not conjugate. This is because our trajectories do not form a 'true' braid: the final points do not correspond exactly with the initial points, as a set. If we truly want a rotationally-conjugate braid out of our data, we need to enforce a closure method:

```
>> XY = closure(XY);    % close braid and avoid new crossings
>> bX = compact(braid(XY,0)), bY = compact(braid(XY,pi/2))

bX = < -1 -2 -1 -1 -1 -1 -1 -1 -1 -1  3  3  2  1 >

bY = < -3 -3 -3 -3 -3 -3 -3  1 -3  1 >
```

This default closure simply draws line segments from the final points to the initial points in such a way that no new crossings are created in the X projection. Hence, the X-projected braid `bX` is unchanged by the closure, but here the Y-projected braid `bY` is longer by one generator (`bY` is plotted in Figure 1(d)). This is enough to make the braids conjugate:

```
>> [~,c] = conjtest(bX,bY)  % ~ means discard first return arg

c = < 3  2 >
```

where the optional second argument `c` is the conjugating braid, as we can verify:

```
>> bX == c*bY*c^-1

ans = 1
```

There are other ways to enforce closure of a braid (see `help closure`), in particular `closure(XY,'mindist')`, which minimizes the total distance between the initial and final points.

Note that `conjtest` uses the library *CBraid* (Cha, 2011) to first convert the braids to Garside canonical form (Birman & Brendle, 2005), then to determine conjugacy. This is very inefficient, so is impractical for large braids.

1.2.3 The `databraid` subclass

In some instances when dealing with data it is important to know the *crossing times*, that is, the times at which two particles exchanged position along the projection line. A braid object does not keep this information, but there is an object that does: a `databraid`. Its constructor takes an optional vector of times as an argument, and it has a data member `tcross` that retains the crossing times. Using the same data `XY` from before, sampled at times `ti`, we have

```
>> b = databraid(XY,ti);
>> b.tcross(1:3)

ans = 870.9010
      872.1758
      887.0089
```

There are always exactly as many crossing times as generators in the braid. Many operations that can be done to a `braid` also work on a `databraid`, with a few differences:

- `compact` works a bit differently. It is less effective than `braid.compact` since it must preserve the order of generators in order to maintain the ordering of the crossing times.

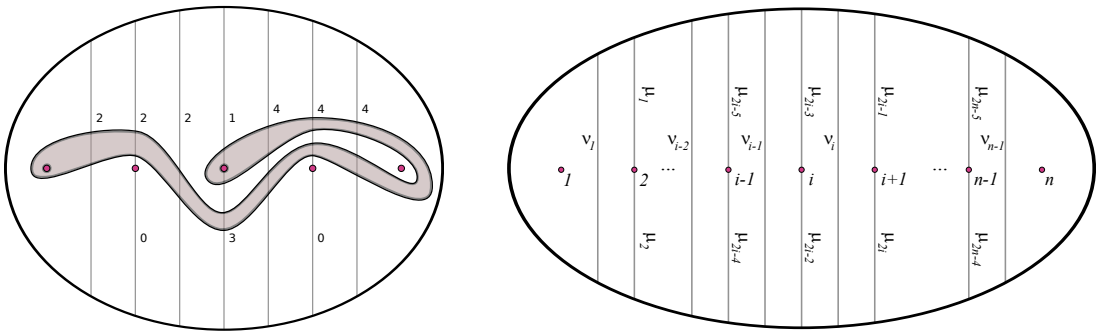


Figure 2: (a) A simple close loop in a disk with $n = 5$ punctures. (b) Definition of intersection numbers μ_i and ν_i. [From Thiffeault (2010).]

- Equality testing checks if two `databraid`s are lexicographically equal (i.e., generator-by-generator) and that their crossing times all agree. This is very restrictive. To check if the underlying braids are equal, first convert the `databraid`s to `braid`s by using the method `databraid.braid`.
- Multiplication of two `databraid`s is only defined if the crossing times of the first braid are all earlier than the second.
- Powers and inverses of `databraid`s are not defined.
- Entropy of `databraid`s is an ambiguously defined concept. While entropy of certain braids can be computed non-iteratively, e.g., in Hall & Yurttaş (2009), in general, it is only estimated by an iterative process. This relies on self-multiplication of the braid, which is ill-defined for `databraid`s. While functions `entropy` and `complexity` can still be used, the appropriate concept for `databraid`s is `databraid.dilatation` which takes into the account the time over which the `databraid` is recorded.

1.3 The `loop` class

1.3.1 Loop coordinates

A simple closed loop on a disk with 5 punctures is shown in Figure 2(a). We consider equivalence classes of such loops under homotopies relative to the punctures. In

particular, the loops are *essential*, meaning that they are not null-homotopic or homotopic to the boundary or a puncture. The *intersection numbers* are also shown in Figure 2(a): these count the minimum number of intersections of an equivalence class of loops with the fixed vertical lines shown. For n punctures, we define the intersection numbers μ_i and ν_i in Figure 2(b).

Any given loop will lead to a unique set of intersection numbers, but a general collection of intersection numbers do not typically correspond to a loop. It is therefore more convenient to define

$$a_i = \tfrac{1}{2}\left(\mu_{2i} - \mu_{2i-1}\right), \qquad b_i = \tfrac{1}{2}\left(\nu_i - \nu_{i+1}\right), \qquad i = 1, \ldots, n-2. \tag{1}$$

We then combine these in a vector of length $(2n-4)$,

$$\boldsymbol{u} = (a_1, \ldots, a_{n-2}, b_1, \ldots, b_{n-2}), \tag{2}$$

which gives the *loop coordinates* (or *Dynnikov coordinates*) for the loop. (Some authors such as Dehornoy (2008) give the coordinates as $(a_1, b_1, \ldots, a_{n-2}, b_{n-2})$.) There is now a bijection between $\mathbb{Z}^{2n-4}$ and essential simple closed loops (Dynnikov, 2002; Moussafir, 2006; Hall & Yurttaş, 2009; Thiffeault, 2010). Actually, *multiloops*: loop coordinates can describe unions of disjoint loops (see Section 1.4).[2]

Let's create the loop in Figure 2(a) as a `loop` object:

```
>> l = loop([-1 1 -2 0 -1 0])

l = (( -1 1 -2 0 -1 0 ))
```

Figure 3(a) shows the output of the `plot(l)` command. We can convert from loop coordinates to intersection numbers with

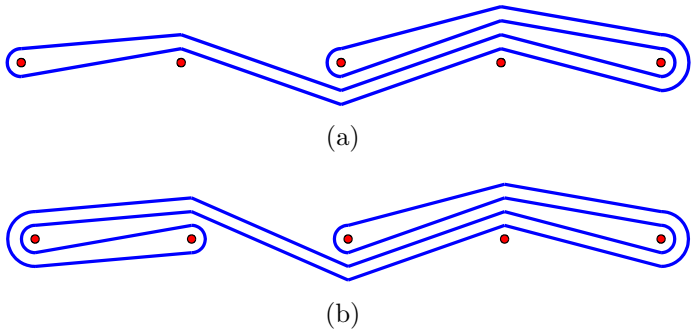
```
>> intersec(l)

ans = 2 0 1 3 4 0 2 2 4 4    % [mu1 ... mu6 nu1 ... nu4]
```

which returns $\mu_1 \ldots \mu_{2n-4}$ followed by $\nu_1 \ldots \mu_{n-1}$, as defined in Figure 2(b).

We can also extract the loop coordinates from a `loop` object using the methods `a`, `b`, and `ab`:

```
>> l = loop ([-1 1 -2 0 -1 0]);
>> l.a
```

[2]Here we use multiloop as a convenient mnemonic. The technical term is *integral lamination*: a set of disjoint non-homotopic simple closed curves (Moussafir, 2006).



(a)

(b)

Figure 3: (a) The loop `((-1 1 -2 0 -1 0))`. (b) The braid generator σ_1^{-1} applied to the loop in (a).

```
ans = -1      1     -2
>> l.b

ans =  0     -1      0
>> [a,b] = l.ab

a = -1      1     -2
b =  0     -1      0
```

As for braids, `l.n` returns the number of punctures (or strings).

1.3.2 Acting on loops with braids

Now we can act on this loop with braids. For example, we define the braid `b` to be σ_1^{-1} with 5 strings, corresponding to the 5 punctures, and then act on the loop `l` by using the multiplication operator:

```
>> b = braid([-1],5);    % one generator with 5 strings
>> b*l                   % act on a loop with a braid

ans = (( -1  1 -2  1 -1  0 ))
```

Figure 3(b) shows `plot(b*l)`. The first and second punctures were interchanged counterclockwise (the action of σ_1^{-1}), dragging the loop along.

The minimum length of an equivalence class of loops is determined by assuming the punctures are one unit of length apart and have zero size. After pulling tight the

loop on the punctures, it is then made up of unit-length segments. The minimum length is thus an integer. For the loop in Figure 3(a),

```
>> minlength(l)

ans = 12
```

Another useful measure of a loop's complexity is its minimum intersection number with the real axis (Moussafir, 2006; Hall & Yurttaş, 2009; Thiffeault, 2010), which for this loop is the same as its minimum length:

```
>> intaxis(l)

ans = 12
```

The `intaxis` method is used to measure a braid's geometric complexity, as defined by Dynnikov & Wiest (2007).

Sometimes we wish to study a large set of different loops. The loop constructor vectorizes:

```
>> ll = loop([-1 1 -2 0; 1 -2 3 4])

ll = (( -1  1 -2  0 ))
     ((  1 -2  3  4 ))
```

We can then, for instance, compute the length of every loop:

```
>> minlength(ll)

ans = 14
      34
```

or even act on all the loops with the same braid:

```
>> b = braid([1 -2]);
>> b*ll

ans = (( 2   1  -2   1 ))
      (( 5  -2  -3  11 ))
```

Some commands, such as `plot`, do not vectorize. Different loops can then be accessed by indexing, such as `plot(ll(2))`.

The `entropy` method of the `braid` class (Section 1.1) computes the topological entropy of a braid by repeatedly acting on a loop, and monitoring the growth rate

of the loop. For example, let us compare the entropy obtained by acting 100 times on an initial loop, compared with the `entropy` method:

```
>> b = braid([1 2 3 -4]);
% apply braid 100 times to l, then compute growth of length
>> log(minlength(b^100*l)/minlength(l)) / 100

ans = 0.7637
>> entropy(b)

ans = 0.7672
```

The entropy value returned by `entropy(b)` is more precise, since that method monitors convergence and adjusts the number of iterations accordingly.

1.4 Loop coordinates for a braid

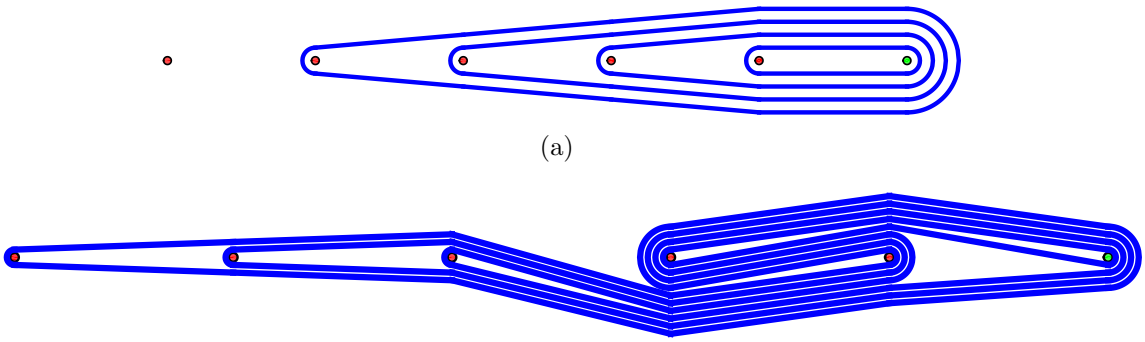
The command `loop(n,'basepoint')` returns a *canonical set of loops* for n punctures:

```
>> l = loop(5,'bp')    % 'bp' is short for 'basepoint'

ans = (( 0  0  0  0 -1 -1 -1 -1 ))*
```

This multiloop is depicted in Figure 4(a), with basepoint puncture shown in green. The `*` indicates that this loop has a basepoint. Note that the multiloop returned by `loop(5,'bp')` actually has 6 punctures! The rightmost puncture is meant to represent the boundary of a disk, or a base point for the fundamental group on a sphere with n punctures. The loops form a (nonoriented) generating set for the fundamental group of the disk with n punctures. The extra puncture thus plays no role dynamically, and `l.n` returns 5. If you want the true total number of punctures, including the base point, use `l.totaln`.

The canonical set of loops allows us to define loop coordinates for a braid, which is a unique normal form. The canonical loop coordinates for braids exploit the fact that two braids are equal if and only if they act the same way on the fundamental group of the disk (Dehornoy, 2008). Hence, if we take a braid and act on `loop(5,'bp')`,

```
>> b = braid([1 2 3 -4]);
>> b*loop(5,'bp')

ans = (( 0  0  3 -1 -1 -1 -4  3 ))*
```



(a)

(b)

Figure 4: (a) The multiloop created by `loop(5,'bp')`, with basepoint puncture in green. (b) The multiloop `b*loop(5,'bp')`, where `b` is the braid $\sigma_1\sigma_2\sigma_3\sigma_4^{-1}$.

then the set of numbers `(( 0 0 3 -1 -1 -1 -4 3 ))*` can be thought of as *uniquely* characterizing the braid. It is this property that is used to rapidly determine equality of braids. (The loop `b*loop(5,'bp')` is plotted in Figure 4(b).) The same loop coordinates for the braid can be obtained without creating an intermediate loop with

```
>> loopcoords(b)

ans = (( 0  0  3 -1 -1 -1 -4  3 ))*
```

2 The effective linear action and its cycles

2.1 Effective linear action

In Section 1.3.2 we introduced the action of a braid γ on a loop $\boldsymbol{u}$. Here $\boldsymbol{u} = (a_1, \ldots, a_{n-2}, b_1, \ldots, b_{n-2})$ is a vector of coordinates for the loop, defined in Section 1.3.1. We write $\boldsymbol{u}' = \gamma \cdot \boldsymbol{u}$ for the new, updated coordinates after the action. These updated coordinates are given by composing the action of individual generators.

For $1 < i < n-1$, we can express the update rules for the braid group generator σ_i

acting on $\boldsymbol{u}$ as

$$a'_{i-1} = a_{i-1} - b^+_{i-1} - \left(b^+_i + c_{i-1}\right)^+ , \tag{3a}$$
$$b'_{i-1} = b_i + c^-_{i-1} , \tag{3b}$$
$$a'_i = a_i - b^-_i - \left(b^-_{i-1} - c_{i-1}\right)^- , \tag{3c}$$
$$b'_i = b_{i-1} - c^-_{i-1} , \tag{3d}$$

where

$$c_{i-1} = a_{i-1} - a_i - b^+_i + b^-_{i-1} . \tag{4}$$

Coordinates not listed (i.e., a_k and b_k for $k \neq i$ or $i-1$) are unchanged. The superscripts $^{+/-}$ are defined as

$$f^+ \coloneqq \max(f, 0), \qquad f^- \coloneqq \min(f, 0). \tag{5}$$

(See Thiffeault (2010) for the update rules for the generators σ_1, σ_{n-1}, and the inverse generators. The update rules are in several other papers but use different conventions.)

Notice that the action (3) is *piecewise-linear* in the loop coordinates: once the $^{+/-}$ operators are resolved, what is left is a linear operation on the vector $\boldsymbol{u}$. We can thus write

$$\boldsymbol{u}' = M(\gamma, \boldsymbol{u}) \cdot \boldsymbol{u}, \qquad M(\gamma, \boldsymbol{u}) \in \mathrm{SL}_{2n-4}(\mathbb{Z}), \tag{6}$$

where the dot now denotes the standard matrix product. Here $M(\gamma, \boldsymbol{u})$ is the *effective linear action* of the braid γ on the loop $\boldsymbol{u}$.

Let's show an example using `braidlab`. We take the braid $\sigma_1\sigma_2^{-1}$ and the loop with coordinates $a_1 = 0$, $b_1 = -1$. The action is

```
>> b = braid([1 -2]); l = loop([0 -1]);
>> lp = b*l

lp = (( 1 -1 ))
```

The effective linear action can be obtained by requesting a second output argument from the result of `*`:

```
>> [lp,M] = b*l; full(M)

ans = 1 -1
      0  1
```

Note that the effective linear action `M` is by default returned as a sparse matrix, which it often is when dealing with many strands. We use `full` to convert it back into a regular full matrix. We can then verify that the matrix product of `M` and the column vector of coordinates `l.coords'` is the same as the action `lp = b*l`:

```
>> M*l.coords'

ans = 1
      -1
>> lp.coords'

ans = 1
      -1
```

The difference is that `M` may only be applied *to this specific loop* (or a loop that happens to share the same effective linear action).

A common thing to do is to find the effective linear action on the canonical set `loop(b.n,'bp')` (see Section 1.4):

```
>> [~,M] = b*loop(b.n,'bp'); full(M)

ans = 0      0     -1      0
      0      1      0      1
      0      1      1      1
      1     -1     -1      0
```

The canonical set assumes an extra puncture, so the matrix dimension is larger by 2.

The effective linear action doesn't seem to offer much at this point. Its real advantage will become apparent in Section 2.2, when we find that it can achieve periodic limit cycles.

2.2 Limit cycles of the effective linear action

The effective linear action has a very interesting behavior when a braid is iterated on some initial loop. Consider the following example:

```
>> b = braid([1 -2]); l = loop([1 1]);
>> [l,M] = b*l; l, full(M)

l = (( 3 -1 ))

M = 2   1
```

```
   -1    0
```

Now repeat this last command:

```
>> [l,M] = b*l; l, full(M)

l = (( 7 -4 ))

M = 2  -1
   -1   1
```

And again:

```
>> b = braid([1 -2]); l = loop([1 1]);
>> [l,M] = b*l; l, full(M)

l = (( 18 -11 ))

M = 2  -1
   -1   1
```

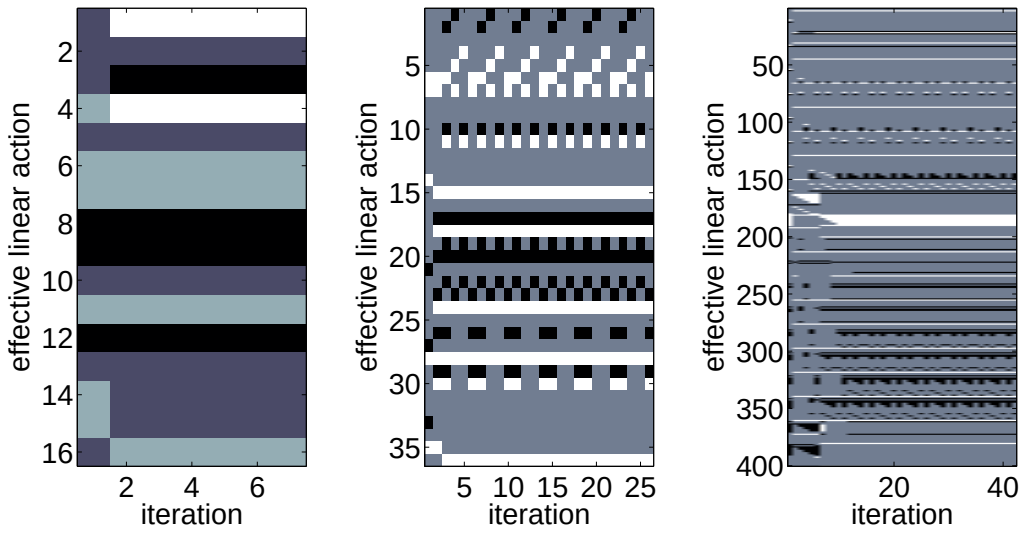
The effective linear action `M` has not changed. In fact it has achieved a fixed point: running the same command again will change the loop, but the linear action will remain the same forever. `braidlab` can automate the iteration with the method `cycle`. Figure 5(a) shows the output of

```
>> b = braid([1 -2]); M = cycle(b,'plot');
```

The member function `cycle` iterates the braid on an initial loop, taken to be the canonical set `loop(b.n,'bp')`. The vertical axis in Fig. 5(a) shows the elements of the effective linear action as a function of iterates of the braid. The matrix of the action is flattened into a vector of length 4^2, where 4 is the dimension the initial loop `loop(b.n,'bp')`. It is evident that the fixed point is reached rapidly, since the 'stripes' stop changing.

Such fixed points of the effective linear action are ubiquitous for braids corresponding to a pseudo-Anosov isotopy class, such as $\sigma_1\sigma_2^{-1}$. In general, instead of a fixed point we may find a *limit cycle* of some period. Yurttaş (2014) discussed these limit cycles for pseudo-Anosov braids: they occur when the unstable foliation falls on the boundary of the linear regions of the update rules. We can reproduce her example with the following:[3]

[3]To get exactly the same matrices, we use the braid $\sigma_1^{-1}\sigma_2^{-1}\sigma_3^{-1}\sigma_4$ rather than her $\sigma_1\sigma_2\sigma_3\sigma_4^{-1}$, since her generators rotate the punctures counterclockwise.



(a) (b) (c)

Figure 5: The plot produced by `cycle(b,'plot')` for (a) `b = braid([1 -2])`; (b) `b = braid([1 2 3])`; (c) `b = braid('psi',11)`.

```
>> b = braid([-1 -2 -3 4]);
>> M = b.cycle(loop(b.n),'iter')

M = [6x6 double]    [6x6 double]
```

The option `'iter'` tells `cycle` to compute an individual matrix for each iterate of the cycle, rather than the net product of all the matrices in the cycle. The output is a cell array of two 6 by 6 matrices, corresponding to the period-2 cycle:

```
>> full(M{1}), full(M{2})

ans =  -1     1     0     0     0     0
        0     0     0     1     1     0
        0     0     2    -1    -1     1
        0     0     0     0     1     0
       -1     0     1    -1    -1     1
        0     0     1     0     0     1

ans =   0     0     0     1     0     0
```

```
     0     0     0     1     1     0
     0     0     2    -1    -1     1
    -1     1     0    -1     1     0
     0    -1     1     0    -1     1
     0     0     1     0     0     1
```

as given by Yurttaş (2014). Note that we use an initial loop for n punctures (`loop(b.n)`) without base point, rather than the default, to reproduce her example exactly. For the pseudo-Anosov case, any initial loop will give the same matrices.

What is more surprising is that these limit cycles occur for finite-order braids as well. Figure 5(b) is produced by

```
>> b = braid([1 2 3]); [~,period] = cycle(b,'plot')

period = 4
```

Indeed, staring at the pattern in Fig. 5(b) it is easy to see that the effective action does achieve a limit cycle of period 4. This braid is definitely not pseudo-Anosov: it is finite-order. However, we do not expect such limit cycles to be unique in the non-pseudo-Anosov case.

Pseudo-Anosov braids can achieve longer cycles, which `braidlab` can find: Figure 5(c) is the plot produced by

```
>> b = braid('psi',11); [M,period] = cycle(b,'plot');
```

The period here is 5, and the matrix M is 20 by 20. The braid `braid('psi',11)` is the braid ψ_{11} in the notation of Venzke (2008). It is a pseudo-Anosov braid with low dilatation (Hironaka & Kin, 2006; Thiffeault & Finn, 2006), conjectured to be the lowest possible for 11 strings.[4] The braids ψ_n are known to have to lowest dilatation for n string for $n \leq 8$ (Lanneau & Thiffeault, 2011).

The largest eigenvalue of the matrix `M` gives us the dilatation of the braid, which in itself is not a real improvement over our earlier entropy iterative algorithm (Section 1.1.2). However, with the matrix in hand we can find the characteristic polynomial:[5]

```
>> b = braid('psi',7); [M,period] = cycle(b);
>> factor(poly2sym(charpoly(M)))  % convert to symbolic form

ans = (x^2 + 1)*(x^3 - x^2 - 1)*(x^3 + x - 1)*(x - 1)^2*(x +
   1)^2
```

[4]The dilatation of a braid is the exponential of its entropy.

[5]Matlab's symbolic toolbox is needed for `poly2sym` and `factor`.

Compare this to the known polynomial that gives the dilation:

```
>> factor(poly2sym(psiroots(7,'poly')))

ans = (x + 1)*(x^3 - x^2 - 1)*(x^3 + x - 1)
```

(The function `psiroots` returns the roots and characteristic polynomial of a ψ braid; this is useful for testing purposes.) Note that the factor whose largest root is the dilatation, `x^3 - x^2 - 1`, appears in both polynomials. This is not always the case, though the dilatation has to be a root of both polynomials.

To our knowledge, the existence of these limit cycles has not been fully explained (except in the pseudo-Anosov case by Yurttaş (2014)). They seem to occur for *any* braid, regardless of its isotopy class. In that sense they could provide an alternative to the the Bestvina–Handel train track algorithm (Bestvina & Handel, 1995), which is used to compute the isotopy class of a braid. `braidlab` has some experimental support for this in the form of the method `reducing`:

```
>> b = braid([-3  1 -4  2 -3 -1 -2  3 -2  4  3  4]);
>> l = b.reducing
Warning: This function is experimental!  Use with caution!

ans = (( 0 -1  0  0  0  0 ))

>> b*l   % check that it is indeed a reducing curve

ans = (( 0 -1  0  0  0  0 ))
```

`reducing` found a reducing curve for the braid and returned it as a set of loop coordinates. However, note that at this point `reducing` can return too many curves, or none even when one exists.

3 An example: Taffy pullers

Taffy pullers are a class of devices designed to stretch and fold soft candy repeatedly (Finn & Thiffeault, 2011). The goal is to aerate the taffy. Since many folds are required, the process has been mechanized using fixed and moving rods. The two most typical designs are shown in Figure 6: the one in Figure 6(a) has a single fixed rod (gray) and two moving rods, each rotating on a different axis. The design in Figure 6(a) has four moving rods, sharing two axes of rotation. (There are several videos of taffy pullers on YouTube.)

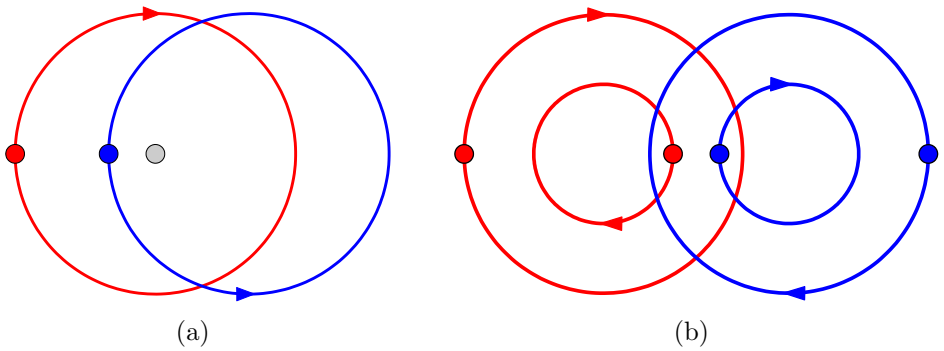


Figure 6: (a) Three-rod taffy puller. (b) Four-rod taffy puller.

Let's use `braidlab` to analyze the rod motion. From the folder `doc/examples`, run the command

```
>> b = taffy('3rods')

b = < -2   1   1 -2 >
```

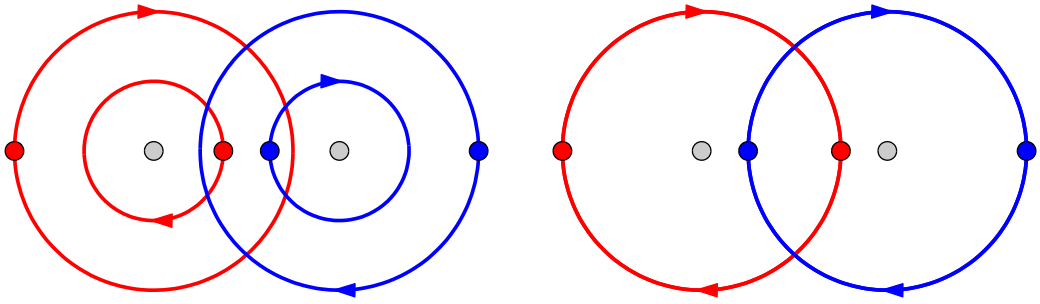
which also produces Figure 6(a). The Thurston–Nielsen type and topological entropy of this braid are

```
>> [t,entr] = tntype(b)

t = pseudo-Anosov

entr = 1.7627
```

One would expect a competent taffy puller to be pseudo-Anosov, as this one is. It implies that there is no 'bad' initial condition where a piece of taffy never gets stretched, or stretches slowly. A reducible or finite-order braid would indicate poor design. The entropy is a measure of the taffy puller's effectiveness: it gives the rate of growth of curves anchored on the rods. Thus, the length of the taffy is multiplied (asymptotically) by $e^{1.7627} \simeq 5.828$ for each full period of rod motion. Needless to say, this leads to extremely rapid growth, since after 10 periods the taffy length has been multiplied by roughly 10^7.

The design in Figure 6(b) can be plotted and analyzed with

```
>> b = taffy('4rods')
```



(a) (b)

Figure 7: (a) A six-rod taffy puller based on Figure 6(b), with two added fixed rods (gray). This is a poor design, since it leads to a reducible braid. (b) Same as (a), but with the same radius of motion for all the rods. The braid is in this case pseudo-Anosov, with larger entropy than the 4-rod design.

```
b = < 1  3  2  2  1  3 >
```

When we apply `tntype` to this braid we find the braid is pseudo-Anosov with exactly the same entropy as the 3-rod taffy puller, 1.7627. There is thus no obvious advantage to using more rods in this case.

A simple modification of the 4-rod design in Figure 6(b) is shown in Figure 7(a). The only change is to extend the rotation axles into two extra fixed rods (shown in gray). The resulting braid is

```
>> b = taffy('6rods-bad')

b = < 2  1  2  4  5  4  3  3  2  1  2  4  5  4 >
```

with Thurston–Nielsen type

```
>> tntype(b)

ans = reducible
```

There are reducing curves in this design: simply wrap a loop around the left gray rod and the inner red rod, and it will rotate without stretching. To avoid this, we extend the radius of motion of the inner rods to equal that of the outer ones, and obtain the design shown in Figure 6(b). The corresponding braid is

```
>> b = taffy('6rods')
```

```
b = < 3  2  1  2  4  5  4  3  3  2  1  2  5  4  5  3 >
```

with Thurston–Nielsen type and entropy

```
>> [t,entr] = tntype(b)

t = pseudo-Anosov

entr = 2.6339
```

The fixed rods have increased the entropy by 50%! This sounds like a fairly small change, but what it means is that this 6-rod design achieves growth of 10^7 in about 6 iterations rather than 10. Alexander Flanagan constructed this six-rod device while an undergraduate student at the University of Wisconsin – Madison, but as far as we know this new design has not yet been used in commercial applications.

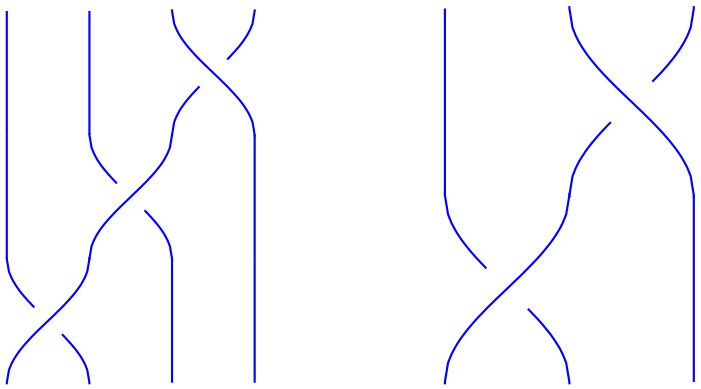
The symmetric design of the taffy pullers illustrates one pitfall when constructing braids. If we give an optional projection angle of $\pi/2$ to `taffy`:

```
>> taffy('4rods',pi/2)
Error using colorbraiding
Coincident projection coordinate; change projection angle
   (type help braid.braid).
```

This corresponds to using the y (vertical) axis to compute the braid, but as we can see from Figure 6(b) this is a bad choice, since all the rods are initially perfectly aligned along that axis. The braid obtained would depend sensitively on numerical roundoff when comparing the rod projections. Instead of attempting to construct the braid, `braidlab` returns an error and asks the user to modify the projection axis. A tiny change in the projection line is sufficient to break the symmetry:

```
>> taffy('4rods',pi/2 + .01)

ans = < -2  2  1  3  2 -3 -1  3  1  2  1  3 >
>> compact(ans)

ans = < 3  1  2  2  3  1 >
```

which is actually equal to the braid formed from projecting on the x axis, though it need only be conjugate (see Section 1.2).



(a) (b)

Figure 8: Removing the third string from the braid (a) $\sigma_1\sigma_2\sigma_3^{-1}$ yields the braid (b) $\sigma_1\sigma_2^{-1}$.

4 Side note: On filling-in punctures

Recall the command `subbraid` from Section 1.1. We took the 4-string braid $\sigma_1\sigma_2\sigma_3^{-1}$ and discarded the third string, to obtain $\sigma_1\sigma_2^{-1}$:

```
>> a = braid([1 2 -3]);
>> b = subbraid(a,[1 2 4])    % discard string 3, keep 1,2,4

b = < 1 -2 >
```

The braids `a` and `b` are shown in Fig. 8; their entropy is

```
>> a.entropy, b.entropy

ans = 0.8314
ans = 0.9624
```

Note that the entropy of the subbraid `b` is *higher* than the original braid. This is counter-intuitive: shouldn't removing strings cause loops to shorten, therefore lowering their growth?[6]

[6]In fact, the entropy obtained by the removal of a string is constrained by the minimum possible entropy for the remaining number of strings (Song *et al.*, 2002; Hironaka & Kin, 2006; Thiffeault & Finn, 2006; Ham & Song, 2007; Venzke, 2008; Lanneau & Thiffeault, 2011). So here the entropy of the 3-braid could only be zero or ≥ 0.9624.

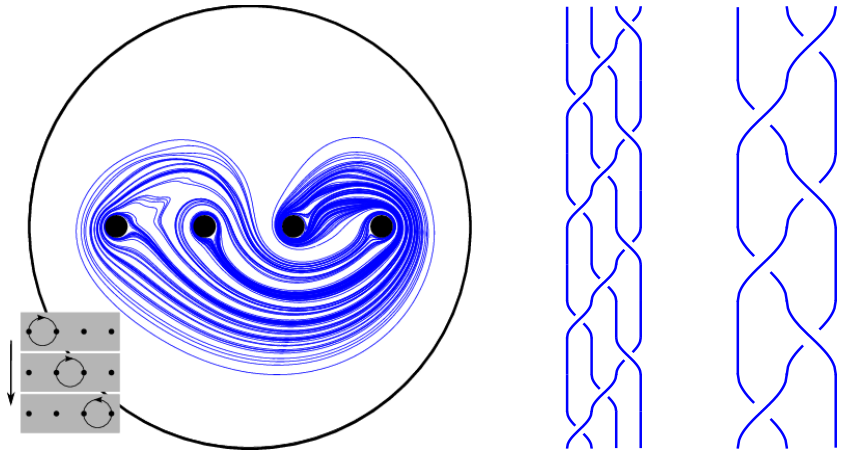


Figure 9: (a) The mixing protocol specified by the braid $\sigma_1\sigma_2\sigma_3^{-1}$ (Thiffeault *et al.*, 2008). The inset shows how the rods are moved. (b) The pure braid $(\sigma_1\sigma_2\sigma_3^{-1})^4$. (c) The braid $(\sigma_1\sigma_2^{-1})^2\sigma_1\sigma_2$, obtained by removing the third string from (b).

In some sense this must be true: consider the rod-stirring device shown in Fig. 9(a), where the rods move according the to braid $\sigma_1\sigma_2\sigma_3^{-1}$. Removing the third string can be regarded as *filling-in* the third puncture (rod); clearly then the material line can be shortened, leading to a decrease in entropy.

The flaw in the argument is that even though we can remove any string, we cannot fill in a puncture that is permuted, since the resulting braid does not define a homeomorphism on the filled-in surface. To remedy this, let us take enough powers of the braid $\sigma_1\sigma_2\sigma_3^{-1}$ to ensure that the third puncture returns to its original position, using the method `perm` to find the permutation induced by the braid:

```
>> perm(a)

ans = 2     3     4     1
```

The permutation is cyclic (it can be constructed with exactly one cycle), so the fourth power should do it:

```
>> perm(a^4)

ans = 1     2     3     4
```

This is now a pure braid: all the strings return to their original position (Fig. 9(b)). Now here's the surprise: the subbraid obtained by removing the third string from `a^4` is

```
>> b2 = subbraid(a^4,[1 2 4])

b2 = < 1 -2  1 -2  1  2 >
```

which is *not* `b^4` (Fig. 9(c))! However, now there is no paradox in the entropies:[7]

```
>> entropy(a^4), entropy(b2)

ans = 3.3258

Warning: Failed to converge to requested tolerance; braid is
   likely finite-order or has low entropy.  Returning zero
   entropy.

ans = 0
```

`braidlab` has trouble computing the entropy because the braid `b2` appears to be finite-order. Indeed, the braid `b2` is conjugate to σ_1^2:

```
>> c = braid([2 -1],3);
>> compact(c*b2*c^-1)

ans = < 1  1 >
```

showing that its entropy is indeed zero.

The moral is: when filling-in punctures, make sure that the strings being removed are permuted only among themselves. For very long, random braids, we still expect that removing a string will decrease the entropy, since the string being removed will have returned to its initial position many times.

Acknowledgments

The development of `braidlab` was supported by the US National Science Foundation, under grants DMS-0806821 and CMMI-1233935. The author thanks Michael Allshouse, Marko Budišić, and Margaux Filippi for extensive testing and comments.

[7] Song (2005) showed that the entropy of a pure braid is greater than $\log(2+\sqrt{5}) \simeq 1.4436$, if it is nonzero.

Michael Allshouse and Marko Budišić also contributed some of the code. James Puckett and Karen Daniels provided the test data from their granular medium experiments (Puckett *et al.*, 2012). `braidlab` uses Toby Hall's *Train* (Hall, 2012); Jae Choon Cha's *CBraid* (Cha, 2011); Juan González-Meneses's *Braiding* (González-Meneses, 2011); John D'Errico's *Variable Precision Integer Arithmetic* (D'Errico, 2013); Markus Buehren's *assignmentoptimal* (Buerhen, 2011); Jakob Progsch's *ThreadPool* (Progsch, 2012); and John R. Gilbert's function for computing the Smith Normal Form of a matrix (Gilbert, 1993).

A Installing `braidlab`

`braidlab` consists of Matlab files together with C and C++ auxiliary files, so-called MEX files. The MEX files are used to greatly speed up calculations. Many commands will work even if the MEX files are unavailable, but much more slowly. (A few commands won't work at all.) However, MEX files need to be first compiled with Matlab's `mex` compiler.

A.1 Precompiled packages

Some zip and tar files of the precompiled latest released version are available at `http://github.com/jeanluct/braidlab/releases`. If one of those suits your system, then download and untar/unzip (it might still work even if the system doesn't match perfectly).

A.2 Cloning the repository

If you prefer to have the latest (possibly unstable) development version, and know how to compile Matlab MEX files on your system, then you can clone the GitHub source repository with the terminal command

```
$ git clone git@github.com:jeanluct/braidlab.git
```

assuming Git is installed on your system. If you prefer to use Mercurial, make sure you have the `hg-git` extension enabled and type

```
$ hg clone git+ssh://git@github.com/jeanluct/braidlab.git
```

Either way, after the cloning finishes type

```
$ cd braidlab; make
```

to compile the MEX files. Note that you can still use `braidlab` even if you're unable to compile the MEX files, but some commands will be unavailable or run (much) more slowly.

If you receive error messages because GMP (the GNU MultiPrecision library) is not installed on your system, instead of the above use

```
$ cd braidlab; make BRAIDLAB_USE_GMP=0
```

This will slow down some functions, in particular testing for equality of large braids.

A.3 Setting Matlab's path

The package `braidlab` is defined inside a Matlab namespace, which are specified as subfolders beginning with a '`+`' character. The Matlab path must contain the folder that contains the subfolder `+braidlab`, and not the `+braidlab` folder itself:

```
>> addpath 'path to folder containing +braidlab'
```

To execute a `braidlab` *function*, either call it using the syntax `braidlab.`*function*, or import the whole namespace:

```
>> import braidlab.*
```

This allows invoking *function* by itself, without the `braidlab` prefix. For the remainder of this document, we assume this has been done and omit the `braidlab` prefix. The `addpath` and `import` commands can be added to `startup.m` to ensure they are executed at the start of every Matlab session.

A.4 Testing your installation

To check that everything is working, `braidlab` includes a testsuite. From Matlab, change to the `testsuite` folder, and run

```
>> test_braidlab
```

making sure the path is set properly (Section A.3). Note that running the testsuite requires Matlab version 2013a or later.

A.5 Troubleshooting

Here are some common problems that can occur when installing braidlab.

A.5.1 Unsupported compiler

Linux distributions often use very recent C/C++ compilers that are not yet supported by Matlab. If you get such an error from MEX, it will tell you which version of GCC it wants. For example, if it claims it needs GCC 4.7 or earlier, you can try

```
$ which gcc-4.7
```

to see if a path to the command exists. If it does, you have an earlier compiler installed and you can proceed to build `braidlab` as described in Section A.2 above, replacing the `make` command with

```
$ make CC=gcc-4.7 CXX=g++-4.7
```

Note that this only works with Matlab R2014a or later. Earlier versions of Matlab also require editing of a file called `mexopts.sh`.

If the `which` command above didn't return anything, you can try to install an older version of GCC:

```
$ sudo apt-get install gcc-4.7 g++4.7
```

This last line is for Ubuntu and Debian Linux distributions. Note that this will *not* overwrite the default compiler.

If your Linux distribution doesn't allow you to easily install the required compiler, you could always compile and install it from scratch! That's fairly tedious, though.

A.5.2 Polish LaTeX gets in the way

This is a strange one. If on compilation you see an error like this:

```
mex: unrecognized option '-largeArrayDims'
mex: unrecognized option '-O'
mex: unrecognized option '-DBRAIDLAB_USE_GMP'
This is pdfTeX, Version 3.1415926-2.5-1.40.14 (TeX Live 2013)
 restricted \write18 enabled.
entering extended mode
! I can't find file '"CFLAGS=-O -DMATLAB_MEX_FILE"'.
```

This is due to the command `mex` — part of the Polish LaTeX package — shadowing Matlab's `mex` compiler. A simple solution, if you don't use the Polish language often, is to simply remove the package:

```
$ sudo apt-get remove texlive-lang-polish
```

This last line is for Ubuntu and Debian Linux distributions. You can also manually rename the Polish `mex` command to something like `mex.polish`, and then make sure Matlab's `mex` is in your path.

Another solution is to make sure that the Matlab executable directory appears early in bash's path variable. On Mac OSX this reads

```
>> export PATH=/Applications/MATLAB_R2014a.app/bin:$PATH
```

for Matlab R2014a.

A.5.3 `largeArraydims` warning

You might get this warning:

```
Warning: Legacy MEX infrastructure is provided for
   compatibility; it will be removed in a future version of
   MATLAB.
```

This can be safely ignored. Matlab is transitioning from a shorter to a longer type of internal array indexing. Eventually the `-largeArraydims` flag will be removed from `braidlab`.

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