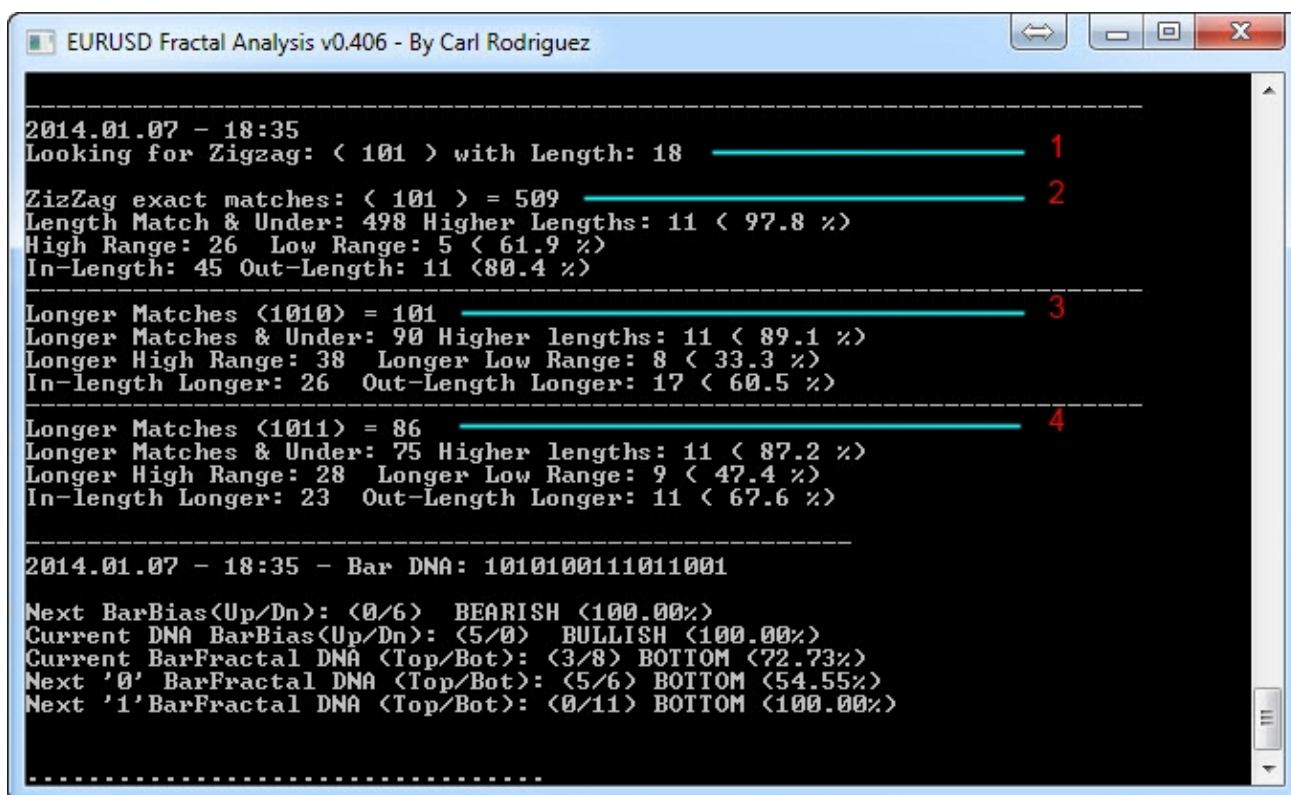


The Ultimate Pattern Machine *by Carl "crodzilla" Rodriguez*

Probabilities are the heart of the pattern matching routines. We want to find the higher probability outcomes to generate our signals. The following will describe, using my simple mind (and current state of my algorithm), my way of, "what will probably happen." There will **NOT** be any higher math associated with my way. I have a simple mind, although very logical. I will describe zigzag, length and "next bar" methods.

Zigzag

First, we must find the higher probability zigzag pattern. Example below:



```
EURUSD Fractal Analysis v0.406 - By Carl Rodriguez

-----
2014.01.07 - 18:35
Looking for Zigzag: < 101 > with Length: 18 ----- 1
ZizZag exact matches: < 101 > = 509 ----- 2
Length Match & Under: 498 Higher Lengths: 11 < 97.8 %>
High Range: 26 Low Range: 5 < 61.9 %>
In-Length: 45 Out-Length: 11 < 80.4 %>
-----
Longer Matches <1010> = 101 ----- 3
Longer Matches & Under: 90 Higher lengths: 11 < 89.1 %>
Longer High Range: 38 Longer Low Range: 8 < 33.3 %>
In-length Longer: 26 Out-Length Longer: 17 < 60.5 %>
-----
Longer Matches <1011> = 86 ----- 4
Longer Matches & Under: 75 Higher lengths: 11 < 87.2 %>
Longer High Range: 28 Longer Low Range: 9 < 47.4 %>
In-length Longer: 23 Out-Length Longer: 11 < 67.6 %>
-----
2014.01.07 - 18:35 - Bar DNA: 1010100111011001
Next BarBias<Up/Dn>: <0/6> BEARISH <100.00%>
Current DNA BarBias<Up/Dn>: <5/0> BULLISH <100.00%>
Current BarFractal DNA <Top/Bot>: <3/8> BOTTOM <72.73%>
Next '0' BarFractal DNA <Top/Bot>: <5/6> BOTTOM <54.55%>
Next '1' BarFractal DNA <Top/Bot>: <0/11> BOTTOM <100.00%>
-----
```

1. Our current (real-time) zigzag fractal pattern is: (101) with a total length of 18 bars.
2. A search of our historical database finds 509 exact match occurrences.
3. By adding (making the current zigzag pattern longer) we are trying to find out if there are more probable LONGER patterns. In this case, the (1010) pattern only occurred 101 times.
4. The (1011) pattern only occurred 86 times.

So, (101) occurs more often than the longer patterns. For now, that pattern is the most probable. Next we should look at the length probability.

Another example, as to the additional logic of longer patterns. Example below:

```

-----
01/07/2014 08:20
Looking for Zigzag: < 10 > with Length: 9 ----- 1
ZizZag exact matches: < 10 > = 340 ----- 2
Length Match & Under: 269 Higher Lengths: 71 < 79.1 %>
High Range: 18 Low Range: 3 < 40.0 %>
In-Length: 189 Out-Length: 89 < 68.0 %>
-----
Longer Matches <100> = 53 ----- 3
Longer Matches & Under: 13 Higher lengths: 40 < 24.5 %>
Longer High Range: 19 Longer Low Range: 7 < 16.7 %>
In-length Longer: 13 Out-Length Longer: 23 < 36.1 %>
Projected # bars until In-Length Longer > 50%: 15
-----
Longer Matches <101> = 599 ----- 4
Longer Matches & Under: 284 Higher lengths: 315 < 47.4 %>
Longer High Range: 22 Longer Low Range: 4 < 27.8 %>
In-length Longer: 269 Out-Length Longer: 300 < 47.3 %>
Projected # bars until In-Length Longer > 50%: 16 ----- 5
-----
08:20 - Bar DNA: 1010010101011100

Next BarBias<Up/Dn>: <9/0> BULLISH <100.00%>
Current DNA BarBias<Up/Dn>: <5/3> BULLISH <62.50%>
BarFractal DNA <Top/Bot>: <9/2> TOP <-81.82%>
BarFractal DNA <Top/Bot>: <8/3> TOP <-72.73%>
BarFractal DNA <Top/Bot>: <5/6> BOTTOM <54.55%>
.....

```

1. Zigzag fractal pattern of (10) with a length of 9 bars.
2. This pattern has exact matches in the database 340 times.
3. The longer pattern (100) has 53 pattern matches in the database.
4. The longer pattern (101) has 599 pattern matches in the database. This pattern is the more probable pattern than the (10) pattern.
5. This pattern is also longer, projected 16 bars, which is also important. If this pattern length was the same or shorter than the (10) pattern, then we would use the original length.

Another example, as to the additional logic of longer patterns. Example below:

```

01/07/2014 08:23
Looking for Zigzag: < 0101 > with Length: 12 ----- 1
ZizZag exact matches: < 0101 > = 77 ----- 2
Length Match & Under: 32 Higher Lengths: 45 < 41.6 %>
High Range: 27 Low Range: 8 < 21.1 %>
In-Length: 28 Out-Length: 30 < 48.3 %>
Projected # bars until In-Length > 50%: 27 ----- 3
-----
Longer Matches <01010> = 138 ----- 4
Longer Matches & Under: 19 Higher lengths: 119 < 13.8 %>
Longer High Range: 28 Longer Low Range: 8 < 20.0 %>
In-length Longer: 18 Out-Length Longer: 65 < 21.7 %>
Projected # bars until In-Length Longer > 50%: 23 ----- 5
-----
Longer Matches <01011> = 8
Longer Matches & Under: 1 Higher lengths: 7 < 12.5 %>
Longer High Range: 19 Longer Low Range: 11 < 12.5 %>
In-length Longer: 1 Out-Length Longer: 2 < 33.3 %>
Projected # bars until In-Length Longer > 50%: 19
-----
Next BarBias(Up/Dn): <9/0> BULLISH <100.00%>
Current DNA BarBias(Up/Dn): <5/3> BULLISH <62.50%>
BarFractal DNA <Top/Bot>: <9/2> TOP <-81.82%>
BarFractal DNA <Top/Bot>: <8/3> TOP <-72.73%>
BarFractal DNA <Top/Bot>: <5/6> BOTTOM <54.55%>
.....

```

1. The current (real-time) zigzag pattern of (0101) is 12 bars in length.
2. Our database shows this pattern has occurred 77 times.
3. Our projected length for this pattern is 27 bars.
4. The longer pattern of (01010) shows an occurrence of 138 times, which is the higher probable pattern.
5. However, the projected length of 23 bars, shorter than the exact pattern, means that this pattern is invalid. We would expect a longer pattern to have a longer length. Use original pattern and length.

Length

To find the highest probable length of a specific pattern, we use a quasi-Gaussian distribution method. We put all pattern matches into a set of lengths. And when a higher percentage of these lengths have been exceeded by the current length, we can move to the "next bar" calculation.

Example:

We have a current fractal pattern of (1010) which occurs 10 times in our database. These are 10 pattern lengths associated with this fractal pattern are put into the following set: (10, 10, 11, 11, 12, 13, 13, 13, 14, 15).

We will group this set into 2 additional sets, "-3 to 0" and "0 to +3" based on the real-time pattern length.

So, if our **current (real-time) length is 10**, lets see what the other 2 sets look like: The "-3 to 0" means this group should contain lengths of 7 to 10. There are 2 lengths in the main set out of 10 that are in this group.

The "0 to +3" set means this group should contain lengths of 10 to 13. There are 8 lengths in the main set out of 10 that are in this group.

We want the "-3 to 0" set to qualify our length requirement. Lets say we want over 50% of this group to contain our pattern lengths (simulate Gaussian statistic).

In the above example, we have 2 "in-length" out of 10, or **20%**. The real-time length of 10 does not pass us into the "next bar" probability.

Now, lets skip to a **current (real-time) length of 12:**

The "-3 to 0" set should contain lengths of 9 to 12. There are 5 lengths in this set. The "0 to +3" set should contain lengths of 12 to 15. There are 6 lengths in this set.

The "in-length" calculation is 5 out of 11 or **45%**. So, the real-time length of 12 does not pass us into the "next bar" probability.

Now, lets say our **current (real-time) length is 13:**

The "-3 to 0" set should contain lengths of 10 to 13. There are 8 lengths in this set. The "0 to +3" set should contain lengths of 13 to 16. There are 5 lengths in this set.

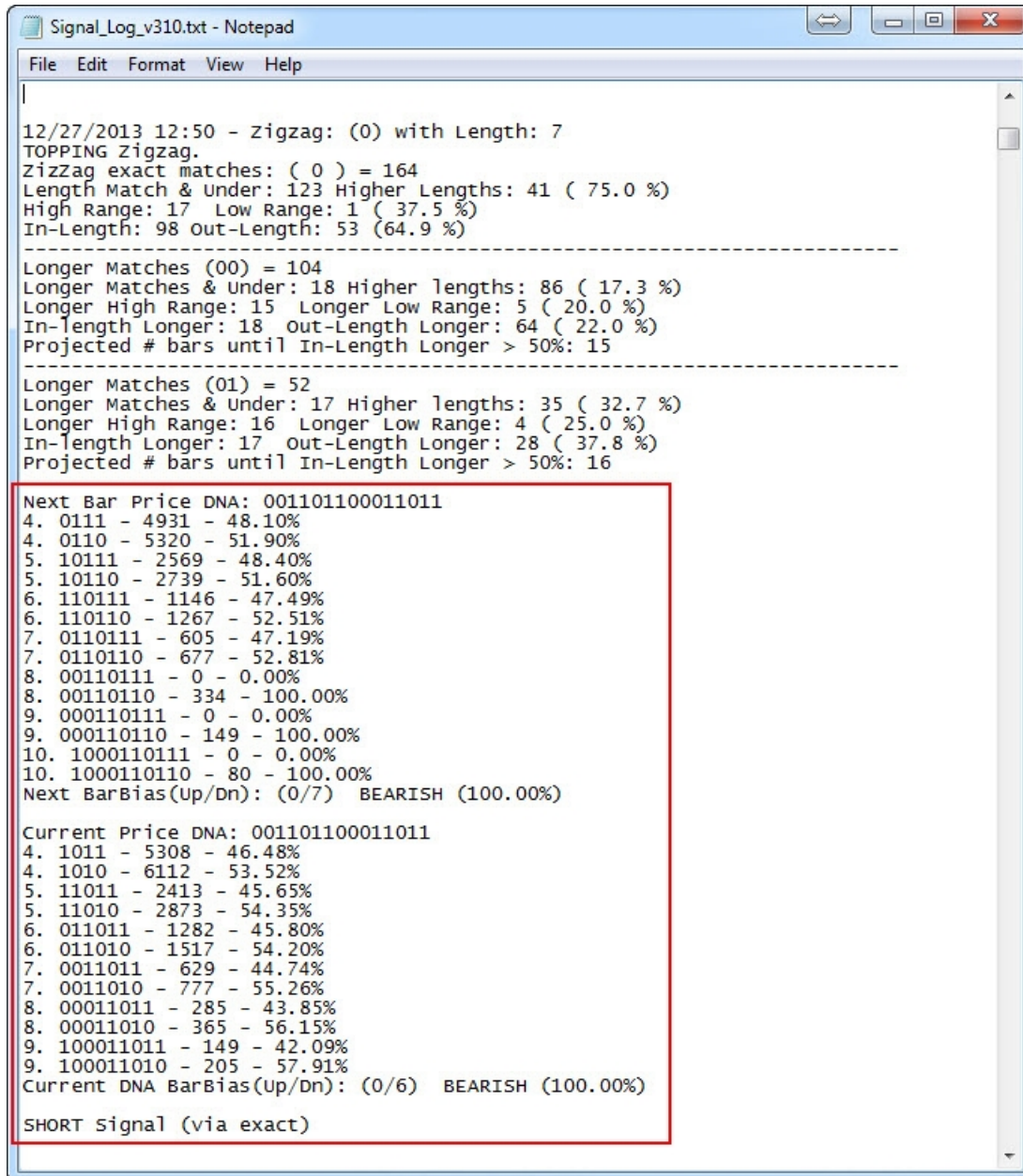
The "in-length" calculation is 8 out of 13 or **62%**. We would now go to our "next bar" calculation.

Side Note: The reason for the above limited-set quasi-Gaussian distribution method can accommodate large sets of lengths. For example, if you have a set of lengths as follows: (10,11,11,12,12,12,12,12,13,13,14,15,16,17,18,19,20,20,20,20,20,21,21,21,21)

You can visually see that lengths 12 and 20 will probably produce a high probability hit-rate. Fractal patterns will cluster certain lengths at different cycles as history repeats itself. So, our method will give you a high probability at these differing lengths, commensurate with history.

Next Bar

The last part of our method is the "next bar" method. I think my method is rather crude. But it makes sense to my simple mind.



```
Signal_Log_v310.txt - Notepad
File Edit Format View Help

12/27/2013 12:50 - Zigzag: (0) with Length: 7
TOPPING Zigzag.
Zigzag exact matches: ( 0 ) = 164
Length Match & Under: 123 Higher Lengths: 41 ( 75.0 %)
High Range: 17 Low Range: 1 ( 37.5 %)
In-Length: 98 Out-Length: 53 (64.9 %)

-----
Longer Matches (00) = 104
Longer Matches & Under: 18 Higher lengths: 86 ( 17.3 %)
Longer High Range: 15 Longer Low Range: 5 ( 20.0 %)
In-length Longer: 18 Out-Length Longer: 64 ( 22.0 %)
Projected # bars until In-Length Longer > 50%: 15

-----
Longer Matches (01) = 52
Longer Matches & Under: 17 Higher lengths: 35 ( 32.7 %)
Longer High Range: 16 Longer Low Range: 4 ( 25.0 %)
In-length Longer: 17 Out-Length Longer: 28 ( 37.8 %)
Projected # bars until In-Length Longer > 50%: 16

Next Bar Price DNA: 001101100011011
4. 0111 - 4931 - 48.10%
4. 0110 - 5320 - 51.90%
5. 10111 - 2569 - 48.40%
5. 10110 - 2739 - 51.60%
6. 110111 - 1146 - 47.49%
6. 110110 - 1267 - 52.51%
7. 0110111 - 605 - 47.19%
7. 0110110 - 677 - 52.81%
8. 00110111 - 0 - 0.00%
8. 00110110 - 334 - 100.00%
9. 000110111 - 0 - 0.00%
9. 000110110 - 149 - 100.00%
10. 1000110111 - 0 - 0.00%
10. 1000110110 - 80 - 100.00%
Next BarBias(Up/Dn): (0/7) BEARISH (100.00%)

Current Price DNA: 001101100011011
4. 1011 - 5308 - 46.48%
4. 1010 - 6112 - 53.52%
5. 11011 - 2413 - 45.65%
5. 11010 - 2873 - 54.35%
6. 011011 - 1282 - 45.80%
6. 011010 - 1517 - 54.20%
7. 0011011 - 629 - 44.74%
7. 0011010 - 777 - 55.26%
8. 00011011 - 285 - 43.85%
8. 00011010 - 365 - 56.15%
9. 100011011 - 149 - 42.09%
9. 100011010 - 205 - 57.91%
Current DNA BarBias(Up/Dn): (0/6) BEARISH (100.00%)

SHORT signal (via exact)
```

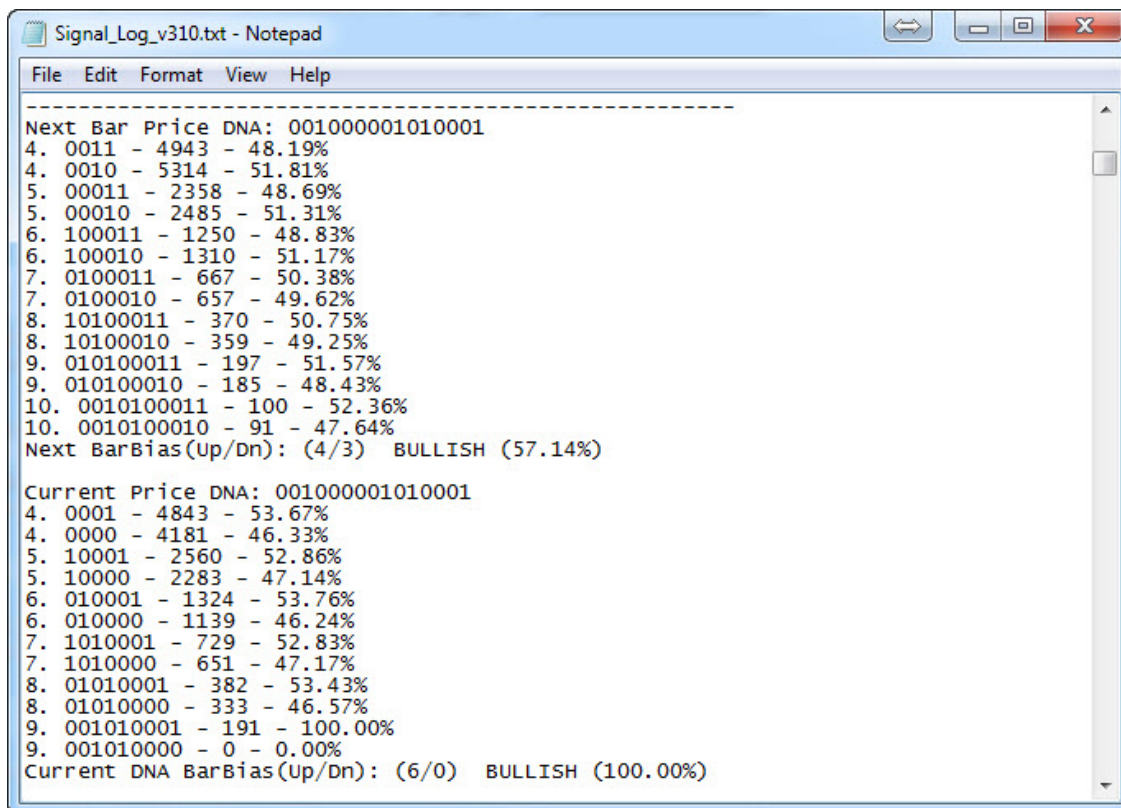
I search the database for 2 different sets of probabilities. The "next bar" set contains the current (real-time) bars plus the addition of '0' and '1'. We want to find out if the next bar is going to be bullish or bearish. If each pattern that exists in the database says the next bar is going to be bearish, then that is what we should expect. I use the "more than" (higher-math) theorem.

If there are more bullish bars than bearish bars, the bullish bars win that level. In the above example (next bar), levels 11, 12 and 13 do not exist in my database. I don't count them... they don't exist. And the current bar section does not include 10,11,12 or 13 levels.

I always use the 100% probability. I want all levels of patterns (4-13 in length) to be in consensus.

I also check the status of the "current bar." I use the current bar information and "flip" the last digit to its opposite and check to see if there is "momentum" to the opposite direction (of the zigzag), for the current bar too. It does not matter if consensus actually matches the current bar.

Example of "next bar" with unqualified probability (next bar at 57%):



```
Signal_Log_v310.txt - Notepad
File Edit Format View Help
-----
Next Bar Price DNA: 001000001010001
4. 0011 - 4943 - 48.19%
4. 0010 - 5314 - 51.81%
5. 00011 - 2358 - 48.69%
5. 00010 - 2485 - 51.31%
6. 100011 - 1250 - 48.83%
6. 100010 - 1310 - 51.17%
7. 0100011 - 667 - 50.38%
7. 0100010 - 657 - 49.62%
8. 10100011 - 370 - 50.75%
8. 10100010 - 359 - 49.25%
9. 010100011 - 197 - 51.57%
9. 010100010 - 185 - 48.43%
10. 0010100011 - 100 - 52.36%
10. 0010100010 - 91 - 47.64%
Next Bar Bias(up/Dn): (4/3) BULLISH (57.14%)

Current Price DNA: 001000001010001
4. 0001 - 4843 - 53.67%
4. 0000 - 4181 - 46.33%
5. 10001 - 2560 - 52.86%
5. 10000 - 2283 - 47.14%
6. 010001 - 1324 - 53.76%
6. 010000 - 1139 - 46.24%
7. 1010001 - 729 - 52.83%
7. 1010000 - 651 - 47.17%
8. 01010001 - 382 - 53.43%
8. 01010000 - 333 - 46.57%
9. 001010001 - 191 - 100.00%
9. 001010000 - 0 - 0.00%
Current DNA Bar Bias(up/Dn): (6/0) BULLISH (100.00%)
```

Thanks to GG53 for his kindness, by trying to teach all of us this interesting method. I hope this document simplifies and helps in utilizing this method.

Carl

References:

<http://www.forexfactory.com/showthread.php?t=440372> - The Ultimate Truth
<http://www.forexfactory.com/showthread.php?t=464948> - Fractals, ZZ & the Pissing Dog

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