MATCHING WITH MAD9:

Matching is efficient (at least as in MAD8), but is very slow compared to MAD8.

Some reasons that we found and tested with a simple matching job:

• Each time that you make an iteration in the matching, MAD9 recalculates the twiss parameters or whatever for all the elements in the sequence, instead to recalculates only for the elements constrained as MAD8 made. To test this we use a simple FODO with two parameters QF and QD and we try to match the μ_x and μ_y . We repite the test with 10*FODO and 20*FODO, matching for these cases the phase advance per cell. We found that the CPU time spent in matching:

FODO: 0.19 s

10*FODO: 0.61 s

20*FODO:1.11 s

matching of 20*FODO is 5.8 times slower than a simple FODO, with the same number of calls.

 The speed of matching is sensible to the syntax of the constraints. Testing the simple FODO in a matching we found that CPU time spent when you use:

```
constraint, twfodo @ m1 ->
mux == 0.27 ,wgt = 1;
    constraint, twfodo @ m1 ->
muy == 1/6,wgt = 1;
instead

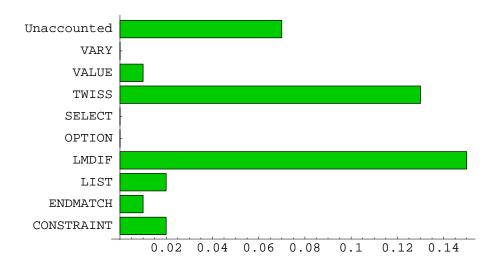
constraint,row(twfodo,m1,{MUX,MUY})
=={0.27,1/6},wgt={1,1};}
is 0.20 and 0.19 respectively. More visible in complex situations as LHC.
```

• If you need to calculate some initial conditions for your matching, the speed of matching is ameliorated when you use static twiss or twisstrack tables. The default is dynamic this means that in each iteration you recalculates all.

For more information and matching examples:

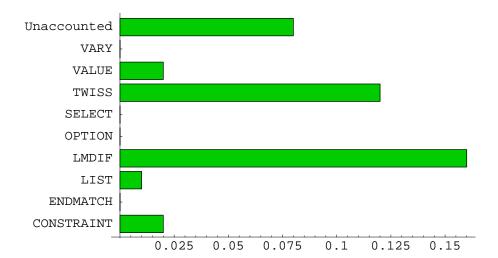
/afs/cern.ch/user/a/afaus/public/mad9/matching/

fodo9-1.nb

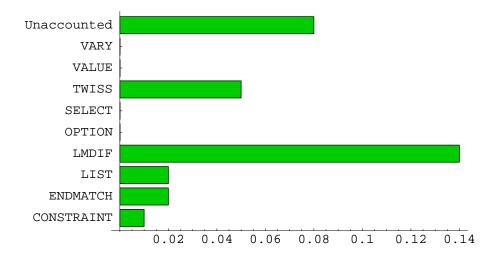




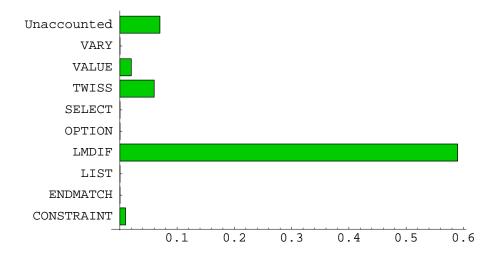
fodo9-2.nb



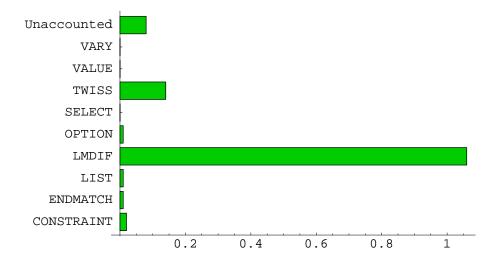
fodo9-3.nb



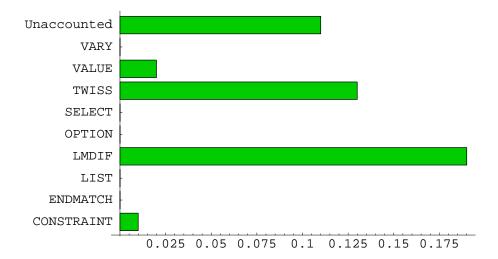
fodo9-4.nb



fodo9-5.nb



fodo9-6.nb



fodo9-7.nb

