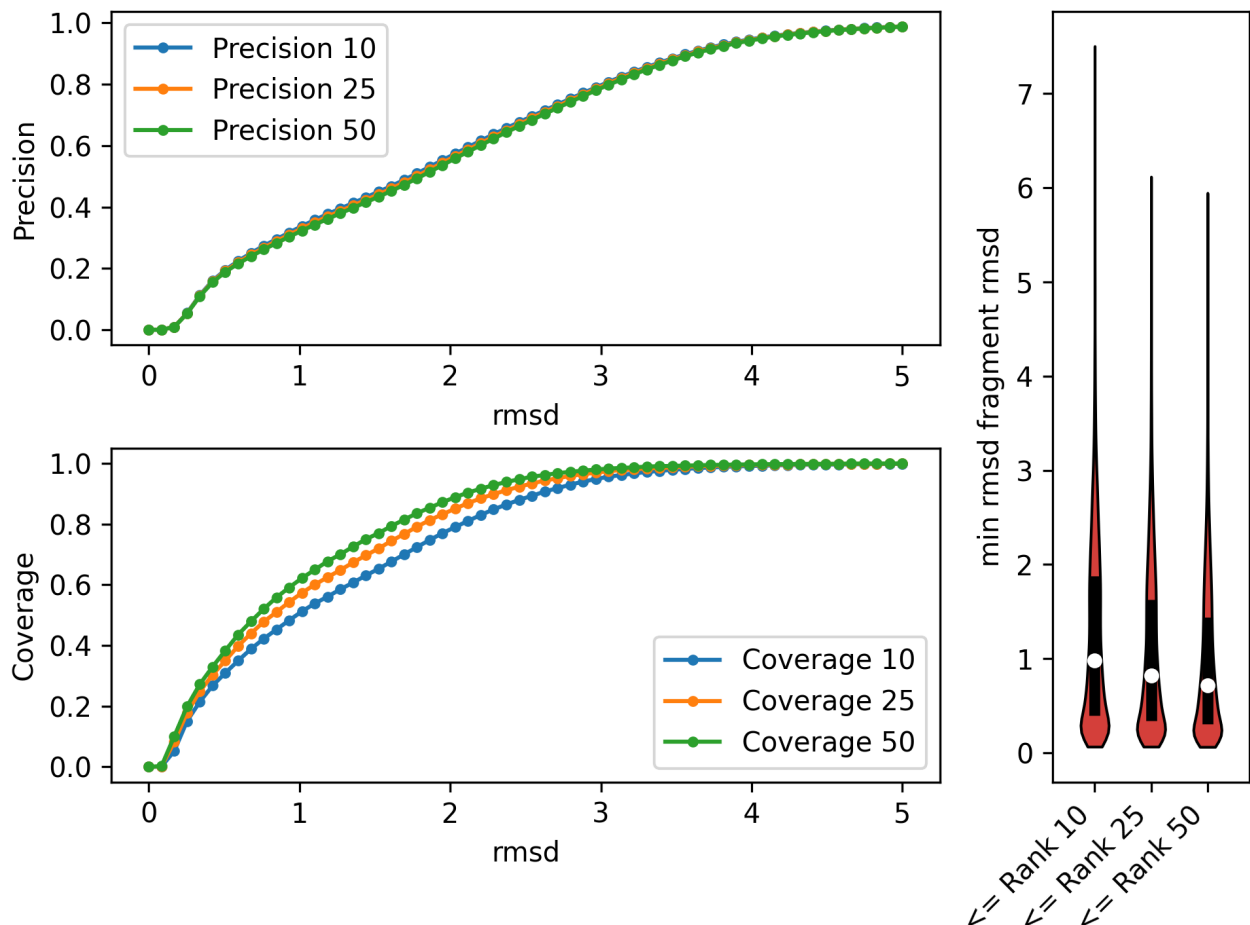


# Scientific test: make\_fragments

## FAILURES

None

## RESULTS



## AUTHOR AND DATE

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## PURPOSE OF THE TEST

This tests how fragments are made and the results of fragment picking

## What does the benchmark test and why?

This test benchmarks the whole 'make fragments' pipeline which includes:

- Running blast
- Running psipred
- Building the nr database
- running rosetta fragment picker

Why test the whole pipeline instead of just fragment\_picker?

- Most improvements to the pipeline (unpublished so far) have mainly been thanks to:
  - Improved databases
  - Improved SS prediction
  - Alternative methods of PSSM generation
  - Addition of additional outside information
- Database related questions often come up, this will give us a baseline to compare against
  - The NR database is unversioned -- This gives us, and the community a version to benchmark against
- The make-fragments pipeline relies on a lot of non-rosetta downloads, and therefore has a high barrier to entry

therefore we can come up a sort of pros and cons list for whole pipeline vs rosetta part only:

- Pros for whole pipeline:
  - Scientifically -- fragment picking is the sum of the whole, and testing only the rosetta part is not representative
  - Most community documentation is based on 'make\_fragments.pl' and it has a tendency to be outdated
  - Because most improvements have been database/outside input improvements, a full pipeline test is more representative
  - When someone inevitably updates the pipeline, they will be able to easily compare results
- Cons against the whole pipeline:
  - It takes a very long time to run
  - It is multithreaded (which is incompatible with CONDOR)
  - Because outside programs are run -- we are scientifically checking the sum of the whole

In the end, there is no right or wrong answer, however, due to a significant number of forum, and email questions relating to the install

of fragment picking to local machines + the hopes that someone will be able to easily update the 2 perl scripts to something more manageable

(like python) I have chosen to benchmark the whole pipeline.

## BENCHMARK DATASET

### How many proteins are in the set?

From casp12: 51 proteins

From casp13: 14 proteins

Total: 65 proteins

**What dataset are you using? Is it published? If yes, please add a citation.**

casp12 and casp13

**What are the input files? How were they created?**

They are pulled pdbs from the casp website and manually renamed by me (Daniel Farrell). The set has the format:

```
{
  "casp_12": {
    "target_id": {
      "pdb_text": "pdb_text...",
      "target_sequence": "MYSEQUENCE..."
    }
  }
  ...
}
```

## PROTOCOL

**State and briefly describe the protocol.**

The input file is a sequence, we take the sequence and run 'make\\_fragments.pl' on it. This tests how the most general/public facing fragment picking protocol works. The perl script runs and we get 3mers and 9mers from it. The 9mers are used for testing purposes and are compared against the native pdb if a full 9 residue match exists. those results are curated and plotted.

make\\_fragments.pl works briefly by:

- run `psiblast` for pssm generation
- run `psipred` for ss-prediction
- run `psiblast` for homolog detection
- run sparksX for phi psi and solvent accessibility predictions
- run `fragment\_picker` to finally pick fragments

The protocol isn't ideal (multiple psiblast runs), however this is what most people use to pick fragments (if not robetta). The main differences between this and robetta are alternative methods of ss-prediction, and robetta has integrated the hhsuite into their fragment picking methods.

I unfortunately am unaware of the accuracy of the picker without sparksX or psiblast etc. This will simply be a baseline due to the fact that this is essentially a snapshot of the protocol from 5-7 years ago, and most of the people that built it have moved on.

## Is there a publication that describes the protocol?

Gront, D., Kulp, D. W., Vernon, R. M., Strauss, C. E. M. & Baker, D. Generalized Fragment Picking in Rosetta : Design , Protocols and Applications. 6, (2011).

## How many CPU hours does this benchmark take approximately?

First the nr database has to be built (~20 cores x 1-2 days). Then each total amount of running `make\\_fragments.pl` takes about 1 (or 2-3) cores 3-10 hrs. For a total of ~2000 hrs. Different

`psiblast` calls can take up to 3 cores (for unknown reasons) but this should work.

## PERFORMANCE METRICS

### What are the performance metrics used and why were they chosen?

I plotted `coverage` and `precision` based on many fragment picking papers such as:

de Oliveira SH, Shi J, Deane CM. Building a better fragment library for de novo protein structure prediction.

`precision` is defined as proportion of good fragments in the library (at various cutoff to define 'good')

`coverage` is defined as the percentage of target residues represented by at least one good fragment in the library

```
coverages = []
for every rmsd_cutoff in 0->5 (60 bins):
    total = 0
    cov_count = 0
    For every residue ( aka fragment set ):
        for every fragment_cutoff in [10, 25, 50]:
            total += 1
            if the minimum rmsd in the fragments from 0->cutoff is less than the rmsd of the residue:
                cov_count += 1
    covered.append(cov_count/total)
```

I also plotted violin plots to show overall distributions of all plotted fragments at different cutoffs (most rosetta protocols use the top 25 fragments, but we pick 200).

### How do you define a pass/fail for this test?

We can set a pass/fail based on the median and quartile ranges of the top 25 fragments + looking at the deviations from run to run. With an identical database the files that we make are deterministic so we can use this test to determine the changes in all aspects of fragment-picking.

## **How were any cutoffs defined?**

By the current results.

## **KEY RESULTS**

### **What is the baseline to compare things to - experimental data or a previous Rosetta protocol?**

The baseline is the solved crystal/nmr structures from casp

### **Describe outliers in the dataset.**

There are no outliers.

## **DEFINITIONS AND COMMENTS**

### **State anything you think is important for someone else to replicate your results.**

- Ask Sergey Lyskov to the stored `nr` database. We pegged it to `May 25 2019`. the n
- There are some executables (sparksX, psiblast, psipred) that we should probably host o
- Most of the improvements in fragment picking over the last few years have been datab

## **LIMITATIONS**

### **What are the limitations of the benchmark? Consider dataset, quality measures, protocol etc.**

This benchmark is specifically crafted to test our capabilities at getting near-rmsd fragments. For some protocols having near-native fragments may not be enough (ie abinitio). Additionally we are limited to the older version of make fragments as the new one has been integrated into robetta and is not yet ready for public release.

### **How could the benchmark be improved?**

- Newer fragment picker pipeline from robetta
- multithreaded fragment\\_picker
- A non-casp dataset
- less blast/psiblast runs

### **What goals should be hit to make this a "good" benchmark?**