Targeting and sequencing algorithms for the Hectospec's optical fiber robotic positioner

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ABSTRACT

The Hectospec is a moderate dispersion spectrograph fed by 300 optical fibers. Hectospec's pair of five-axis robots will position fibers at the 1° diameter f/5 focus of the converted MMT, allowing efficient multi-object spectroscopy. We discuss algorithms that we have developed to match the optical fibers to celestial objects and then to compute the appropriate sequence of robotic positioner moves to reconfigure the fibers between successive observations. Both algorithms require essentially no user interaction, consume only modest computer resources and allow effective deployment of the Hectospec's 300 fibers. The target-to-fiber matching algorithm is a recursive procedure which allows simultaneous optimization of the multiple observations that are required to complete a large survey. The robotic motion sequence algorithm allows the two Hectospec robots to work together efficiently to move fibers directly between observing configurations.

Keywords: MMT, Optical, Spectroscopy

1. INTRODUCTION

Hectospec will be the first instrument to use the wide field f/5 focus of the converted MMT. A pair of five-axis robots will position 300 optical fibers on a curved focal plate. The fibers feed a moderate dispersion spectrograph[1,2] or an echelle spectrograph[3] located in a adjacent instrument room. The targeting and sequencing software determine where the fibers will be placed in the focal surface and how the positioner robots will move them.

Observing targets must be carefully allocated to the fibers to fully use the capabilities of the instrument. This process is called target-to-fiber matching. The goal of the targeting program is to match a minimum of 270 targets in each field. Any remaining unmatched (~10%) fibers are distributed on the focal plate to sample the sky background.

The placement of fibers on the focal plate is mechanically constrained. The fibers are allowed to rotate ±2° about their radial position. The fibers may extend past the center of the focal plate by 2 mm and they may never cross other fibers. These constraints are illustrated in Figure 1, surprisingly, they do not hinder efficient use of the instrument.

The robot fiber positioners are constructed to be fast and accurate, each capable of picking up and placing a fiber in its new location in two seconds. The two positioning robots working together will reconfigure the field of fibers in just over five minutes. The sequencing software constructs a series of robot positioner motions which allows each robot to move its share of the fibers while not interfering with the other robot.

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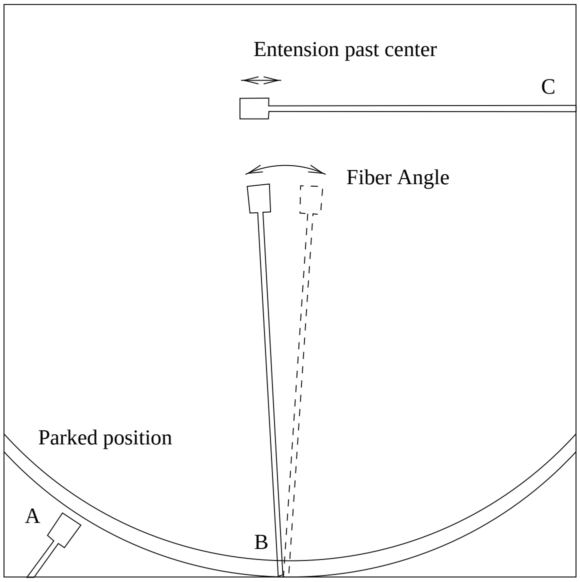

Figure 1. Fiber A is in the parked position. Fiber B is shown at its maximum fiber angles of ±2° about the strictly radial position. Fiber C is shown at its maximum extension past the center of the focal plate.

2. TARGET TO FIBER MATCHING

Each Hectospec observation will require a configuration file specifying the focal plane positions of the 300 fiber probes. The targeting software automates the matching of targets to fibers for single field observations and for large multi-field surveys. We have attempted to make the program as simple as possible to run. The only required input is the user catalog in an ASCII tab delimited format. All conversion and adjustments from FK5 J2000 standard coordinates to focal plate positions are handled by the program.

The targeting procedure has been generalized to allow assignments to multiple Hectospec observations. These multiple observations may have different field centers or instrument rotation angles. The fibers in all observations to be optimized are concatenated together into a single list. The remote swap procedure works on multiple observation configurations simultaneously.

When a fiber is assigned to a target its position is tested against other fibers within its configuration to see that it is legal. This feature allows several Hectospec observations with complete or partial overlapping area to be optimized simultaneously and results in a significant increase in the number of targets that can be matched with fibers.

The target to fiber matching proceeds in several steps: (1) preparation, (2) constrained remote swap, (3) full remote swap and (4) sky fiber allocation. These steps will be described in more detail in sections 2.1 through 2.3.

2.1. Preparation

The first step before matching can begin is to prepare all of the input coordinates and match targets with fibers satisfying the mechanical constraints to reach them. To simplify program use for the user, astronomical coordinates are input as FK5 J2000 standard coordinates. These coordinates are converted to focal surface coordinates at a particular RA and Dec field center. The observing date and time must be known to compute the refraction correction, if they are not given as inputs, likely values are computed and

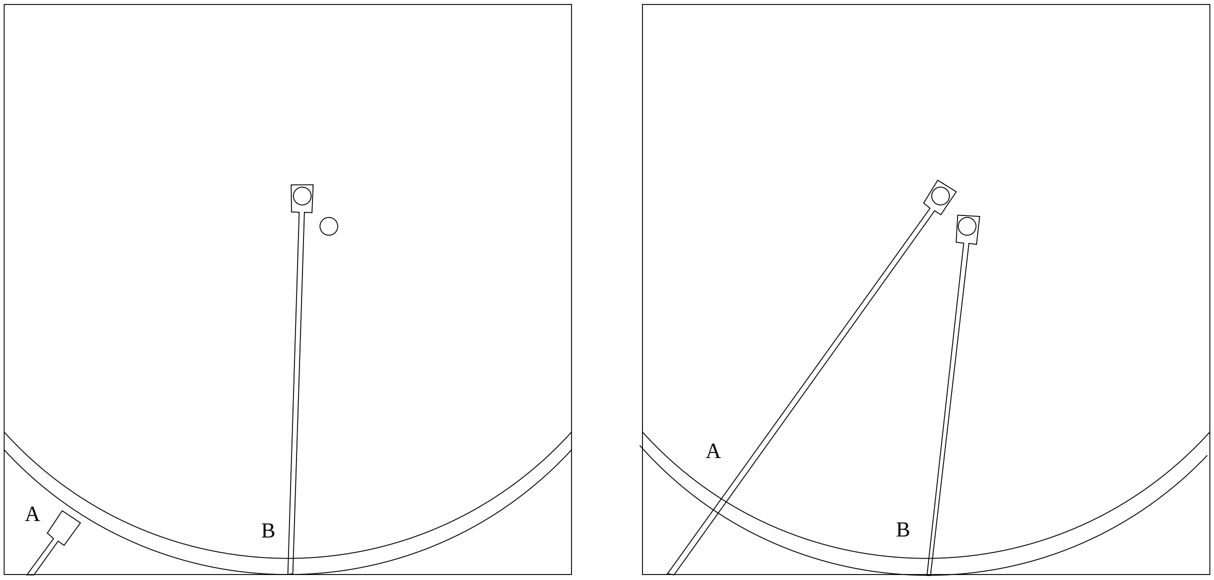

Figure 2. Before a swap: Fiber A blocks access to an unassigned target. After a swap: Fiber B has been swapped to the unassigned target, fiber A reaches the newly freed target.

used. If more than one field center is indicated, the focal surface coordinates at each pointing are computed for the target. A list of fibers that can reach each target and a list of targets that can be reached by each fiber is composed. The data structure built in this step enables the program to quickly pair targets with the fibers that reach it.

2.2. Remote Swap

The targets are matched to fibers by a procedure called the remote swap. The remote swap is a generalization and merger of earlier procedures due to Dave Becker[4] that were called radial fit and local swap. The swap depth parameter is the only user parameter of the procedure. It determines the number of recursive attempts that will be allowed before the procedure fails to match a target.

The remote swap procedure itself works as follows: for each remaining unassigned target, each of the unused fibers which can reach the target are tried in turn until a fiber that reaches the target without crossing other fibers is found. This fiber is then assigned to the target and the next target is examined. If no unassigned fiber is found for that target, and the depth parameter is greater than zero, a swap is attempted. In the swap, each assigned fiber that reaches the target is tried until a fiber that reaches without crossing another fiber is found. The fiber is temporarily assigned to the target. The original target of the swapped fiber is temporarily unassigned, and the algorithm is called recursively decrementing the depth parameter. A successful swap is illustrated in Figure 2.

To complete the optimization the remote swap routine is called three times. The first two calls are made with the swapping depth set to 0, the extension past the center of the focal plate set to 0 and the fiber angle limit constrained to 0.5 and 1.0 degrees, respectively. These steps are meant to match the easiest targets to fibers with small angles as quickly as possible. Since no swapping occurs, a target either is matched to a fiber or it is skipped, quickly moving on to try the next target. This is an important feature. Matching targets at small fiber angles before they are matched at larger angles keeps fibers from blocking their neighbors.

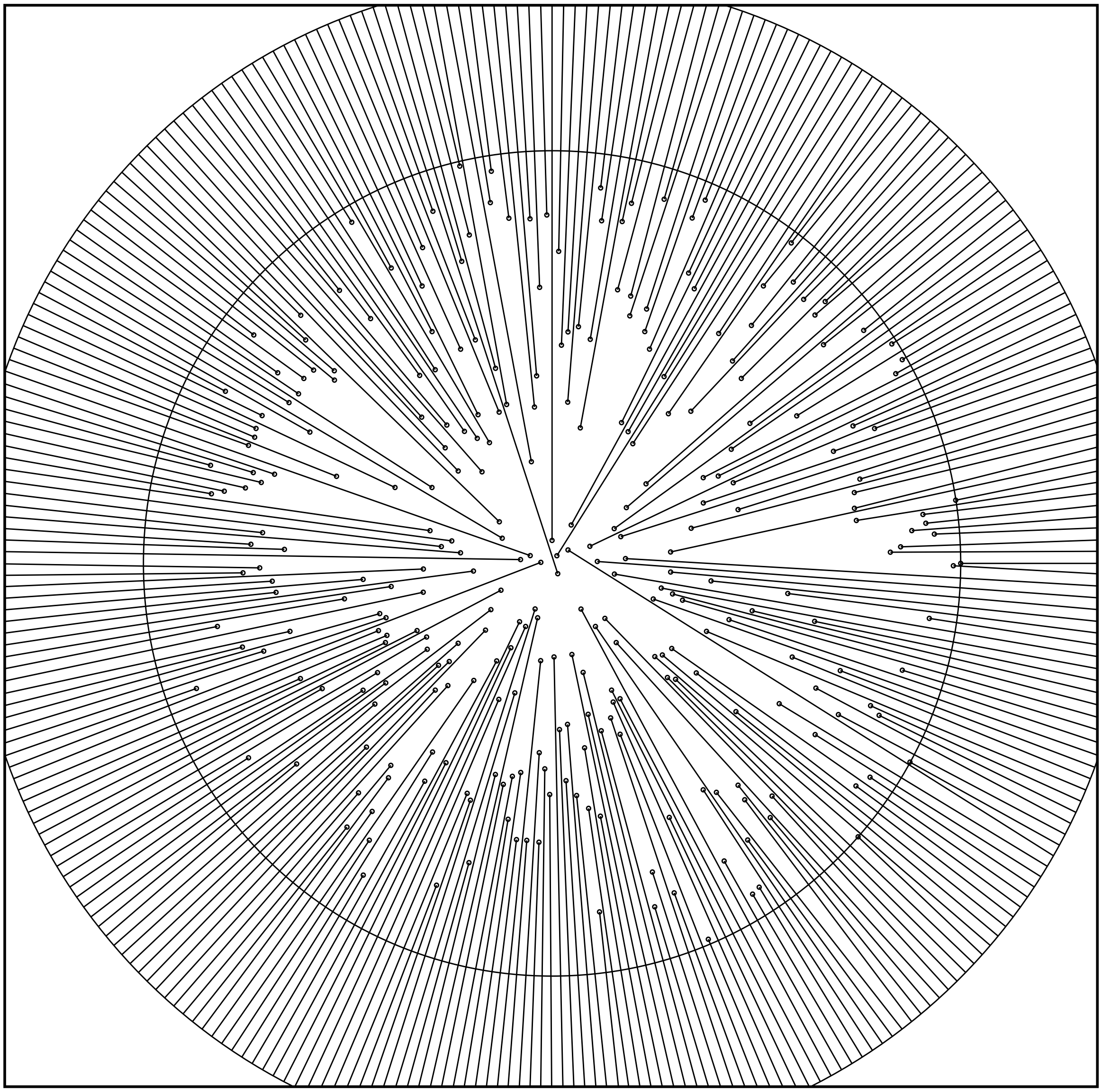

Figure 3. Simple one field configuration on test field 50.cat.

The third call allows the full swapping depth, fiber angle and extension past the focal surface center. This step is more time consuming, swapping the assigned fibers that reach an unassigned target in an attempt to get an unassigned fiber to match with an assigned neighbor target. Most of the matching during a this call to remote swap takes place in the first few levels. Depths greater than about 7 or 8 yield little further improvement.

2.3. Sky Fiber Allocation

The remaining unmatched fibers are available for background sky allocation. These fibers are automatically distributed on the focal plate as the last step in the matching process, to allow uniform radial sampling of the focal surface.

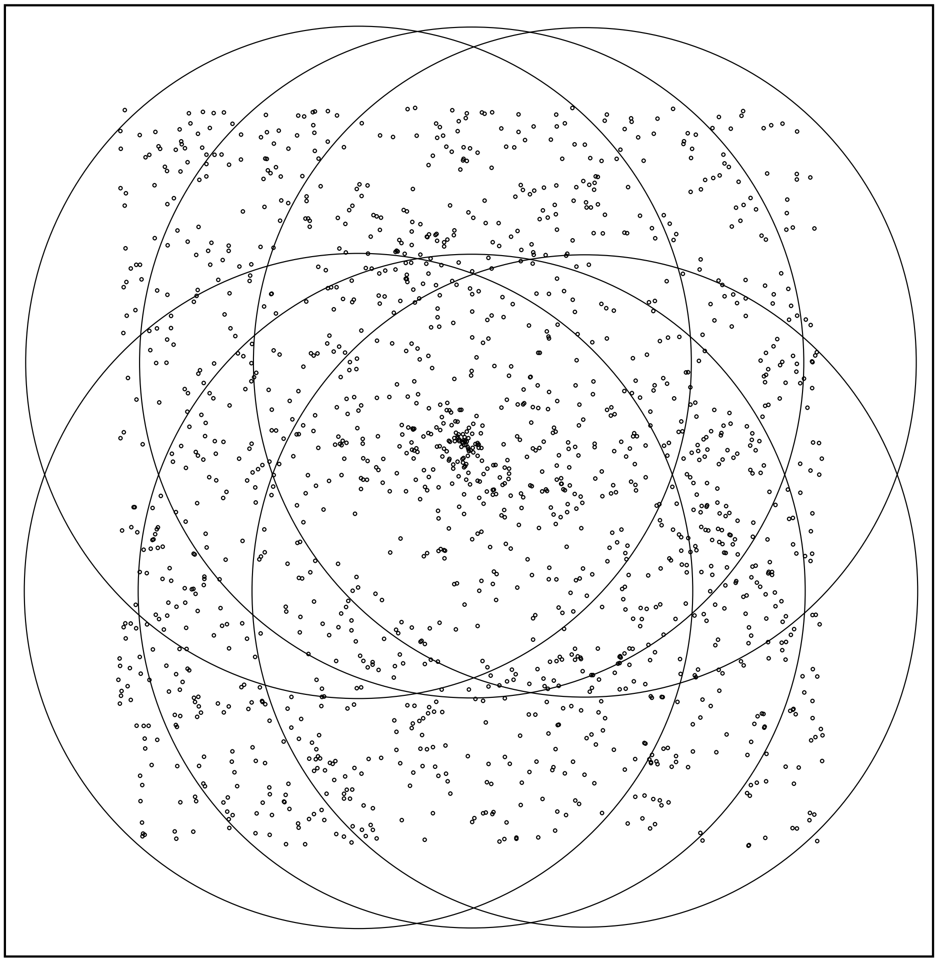

Figure 4. Six observations of a2141 on a regular grid.

2.4. Results

A typical fiber configuration is shown in Figure 3. The goal of the target matching is to match at least 270 of 500 input targets with one Hectospec exposure (300 available fibers). The effectiveness of target matching has been developed sufficiently to allow more convenient but more restrictive mechanical constraints on fiber placement.

Table 1 shows typical results for test fields used in developing the software. The inputs 50.cat and 31.cat are two simulated fields of 500 galaxies with a realistic galaxy-galaxy correlation function. These are matched to single Hectospec fields. The a2141.cat, a1746.cat and j384.cat are extracted from the POSS-II survey[5] plates.

A2141.cat is a catalog for a dense cluster of galaxies. This catalog has been matched to four observations centered on the cluster and also to six observations in a regular grid covering 1 square degree as shown in Figure 4. A1746 is a field of smaller dense clumps, it has been matched against 7 configurations arrayed in a hex pattern. The large survey catalog j384.cat is a 4° x 4° area and is matched to 64 observations on a regular grid. The targeting algorithm can optimize these 64 observations distributed over 4 square degrees in 15 minutes of Sun UltraSPARC 1 CPU time.

Table 1. Typical results from target to fiber matching runs.

Input File	No. of Configurations Fit	No. of targets	No. of Targets Matched
50.cat	1	500	271
31.cat	1	500	278
a2141.cat	4	1144	1057
a2141.cat	6	1603	1533
a1746.cat	7	1998	1798
j384.cat	64	16450	14529

3. POSITION OPTIMIZATION

When more than a few observations are to be made near the same position, the positions of the field centers can be adjusted to allow matching more targets. This optimization matches the density of targets in the field to the density of available fibers in overlapping Hectospec observations. The optimization may be started from a rectangular or hexagonal grid pattern of observations. In addition, a simple heuristic approach has been developed to create an initial guess for the field centers based on the target distribution of the catalog. The position optimization procedure produces a file of field centers that is provided to the targeting program as an auxiliary input.

The packing density of the fibers is a complex function of the input target positions and density, the fiber angle and length constraints, button size and the target matching procedure itself. This function has been empirically determined by matching the fibers against artificial test inputs. To perform the optimization, the input targets are binned in $30''$ bins to form the target density array. The fiber density array is created by summing the fiber density function at each of the field centers. The difference between the target density and the fiber density is minimized by adjusting the field centers using the simplex search technique.[6]

3.1. Results

The results of target matching on optimized field center inputs in table 2 can be compared with the gridded inputs shown in table 1. The optimization provides only a small increase in the number of matched targets for the a2141 and a1746 inputs. In general, only a modest improvement is found for small catalogs with at most a single cluster of targets. For the larger, less uniform, j384 field the optimization allows 907 more targets to be matched with 2 fewer observations. Although the procedure is robust, it is not as automatic as the target matching or sequencing. It requires the manual adjustment of a “normalization” parameter which controls how tightly observations are grouped about dense clusters of targets in a large field.

4. FIBER SEQUENCING

The Hectospec has two robot positioners. To minimize the instrument reconfiguration time the two robots must be carefully coordinated. For safety, the two robots move synchronously. When one robot makes an XY axis or Z axis move the other robot must make the same type of move or remain stationary. The determination of the order in which to move the fibers is called fiber sequencing. The two main sequencing issues encountered are that the robots must share the space in the center of the focal surface and that some of the fibers must be moved before others to avoid tangling. The sequencing procedure successfully moves

Table 2. Typical results from target matching on optimized fields.

Input File	No. of Configurations Fit	No. of targets	No. of Targets Matched
a2141.cat	4	1144	1064
a1746.cat	7	1998	1808
j384.cat	62	16450	15436

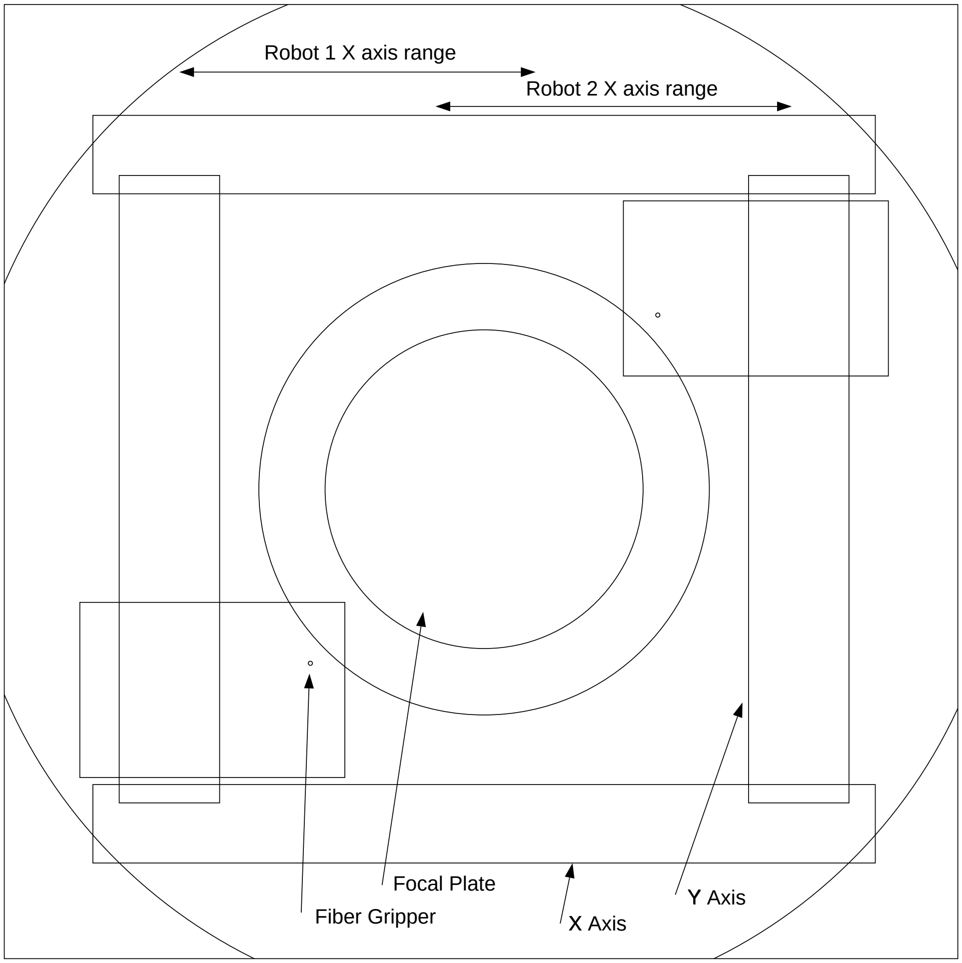

Figure 5. Schematic of robot positioners in their home positions.

the fibers directly from one observing configuration to the next (parking the minimum number of fibers) and effectively coordinates the two positioner robots. Figure 5 is a schematic layout of the robots over the Hectospec focal plane. The two robots share their X axis travel rails and most be kept from colliding during an instrument reconfiguration.

For the purposes of moving fibers a "move" is considered to be a complete pick and place operation. The pick and place consists of moving from the current robot position, picking up a fiber, moving to the

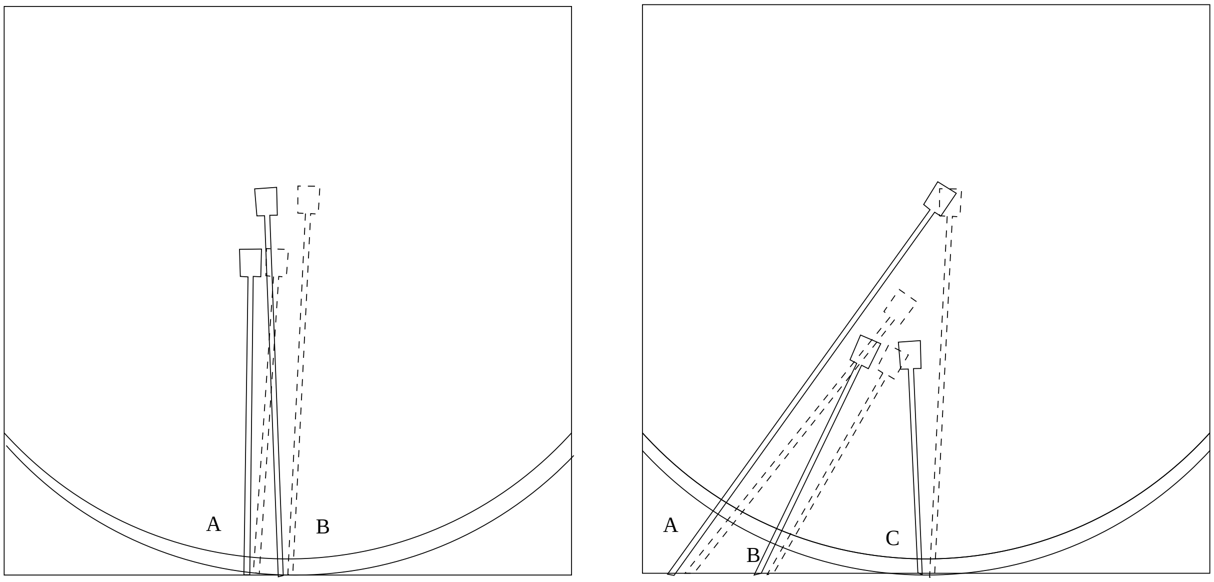

Figure 6. The initial configuration is indicated with solid outlines, the final configuration with dashed lines. Left: Two fibers in a simple conflict. Fiber A cannot be moved before fiber B. Right: A more complex case, A cannot move before B, B cannot move before C, C cannot move before A. One of the fibers must be placed in its parked position.

fiber's final location and placing the fiber on the focal plate. Two other types of moves are allowed. A move to the "idle" position is made when no safe move can be found for one of the robots. The idle move positions a robot in the center of Y axis travel a safe distance from the other robot. A move to the "home" position is made when a robot has completed moving its share of the fibers.

The main consideration in determining if a move is safe is whether it may be paired with the move that will be executed by the other robot. Each of the two moves to be paired (one for each robot) is divided into pick and place halves. The moves can be paired if the start and end of both halves are separated by a minimum safe distance on the X axis. The idle and home moves may always be paired with any move of the other robot.

Some of the positions of fibers in the final configuration will conflict with the positions of fibers in the initial configuration and these fibers must be moved out of the way first. A fiber may not be moved until all of the fibers with which it conflicts with have been moved. Rings of conflicts can arise involving three or more fibers. In this case, One of the fibers will have to be parked. Examples of these relationships are shown in Figure 6.

4.1. Creating A Sequence

First, a list of the fibers whose positions have changed is created. This list is then split between the two robots. Fibers whose start and end position are within reach of both robots will appear on the list of both robots. Some fibers on the lists are unavailable because other fibers must be moved first.

The choice of which fiber each robot will move is made by sorting the available fibers by a weighting function. The function preferentially selects fibers that: (1) that are closest to the center, (2) that have conflicts with other fibers or (3) that are near the current robot position. The best pair of fiber moves that can be safely executed simultaneously is chosen. If there are no moves that can be safely paired, the most desirable move of either robot is paired with an idle move for the other robot. This procedure is repeated until no fibers are left to move and the robots are moved to their home positions.

4.2. Results

The fiber sequencing software benefits from the simple geometry allowed for fiber placement. Since fibers cannot cross, there is no complex layering state to track and untangle each time the instrument is reconfigured. In addition, the ±2° fiber angle constraint results in fewer inter-fiber conflicts than would occur if larger angles were allowed.

Reconfiguration sequences were computed from input catalogs representing fields of stars, fields of galaxies and clusters of galaxies. Computing the sequence takes less than 10 seconds on an UltraSparc class machine. The average reconfiguration takes 160 pick and place steps, with a minimum of 150 steps and a maximum of 175 steps. The maximum number of steps corresponds to observations of clusters of galaxies centered in the focal plane. At two seconds per pick and place, Hectospec reconfigurations should take an average of 320 seconds.

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