

4.0 DETERMINE THE AREA AND MEAN TRAVEL LENGTH FOR EACH HRAP CELL IN A SUBWATERSHED

4.1 INTERSECT PROCESSED DIGITAL ELEVATION MODEL WITH THE COVERAGE OF HRAP CELLS

Once the HRAP cell mesh is generated for the region of interest, the mesh is merged with the digital elevation model of the watershed produced in [Chapter 2](#) to generate parameters for each HRAP cell. Specifically, what is determined here is the average flow distance of each HRAP cell to a watershed outlet. The program `hrap_int.aml` in the Appendix intersects a vector coverage of HRAP polygons (`tk3geoccalb`) with a vector coverage of watershed boundaries (`tksubshedsc`), computes Flowlength statistics for each resulting sector based on the values in `flmerge_grid`, and writes selected statistics to an output file. The input requirements are a watershed coverage, a coverage of HRAP polygons, a value (Flowlength) grid, and a watershed grid. The names of the inputs and an output file name are passed as arguments at the command line. For example,

```
Arc: &r <aml_name> <wshed_cov> <hrap_cov> <value_grid> <wshed_grid> <out_file>
```

```
Arc: &r hrap_int tksubshedsc tk3geoccalb flmerge_grid tksubsheds tk3file.out
```

Use of the Arc Intersect command, the Grid Polygrid function, the Grid Zonalstats function, a Tables Relate, and the Tables Unload command are key lines in `hrap_int.aml`.

```
(1) INTERSECT <in_cover> <intersect_cover> <out_cover>
```

```
intersect %subshed_cov% %hrap_cov% sector_cov
```

For the Tenkiller watershed, `%subshed_cov%` = `tksubshedsc` and `%hrap_cov%` = `tk3geoccalb`. Intersect computes the geometric intersection of the subwatershed coverage and the HRAP coverage generating `sector_cov` which contains only areas common to the two input coverages. `sector_cov` is shown in [Figure 4.1](#). `sector_cov.pat` is built automatically after intersection and retains all unique items from `%subshed_cov%.pat` and `%hrap_cov%.pat`. Most importantly, the grid-code from `%subshed_cov%.pat` and the `hrapx` and `hrapy` attributes from `%hrap_cov%.pat` are retained. The items in `tksubshedsc.pat`, `tk3geoccalb.pat`, and `sector_cov.pat` are listed below.

TKSUBSHEDSC-ID	TK3GEOCCALB-ID	SECTOR_COV-ID
GRID-CODE	HRAPX	TKSUBSHEDSC#
	HRAPY	TKSUBSHEDSC-ID
		GRID-CODE
		TK3GEOCCALB#
		TK3GEOCCALB-ID
		HRAPX
		HRAPY

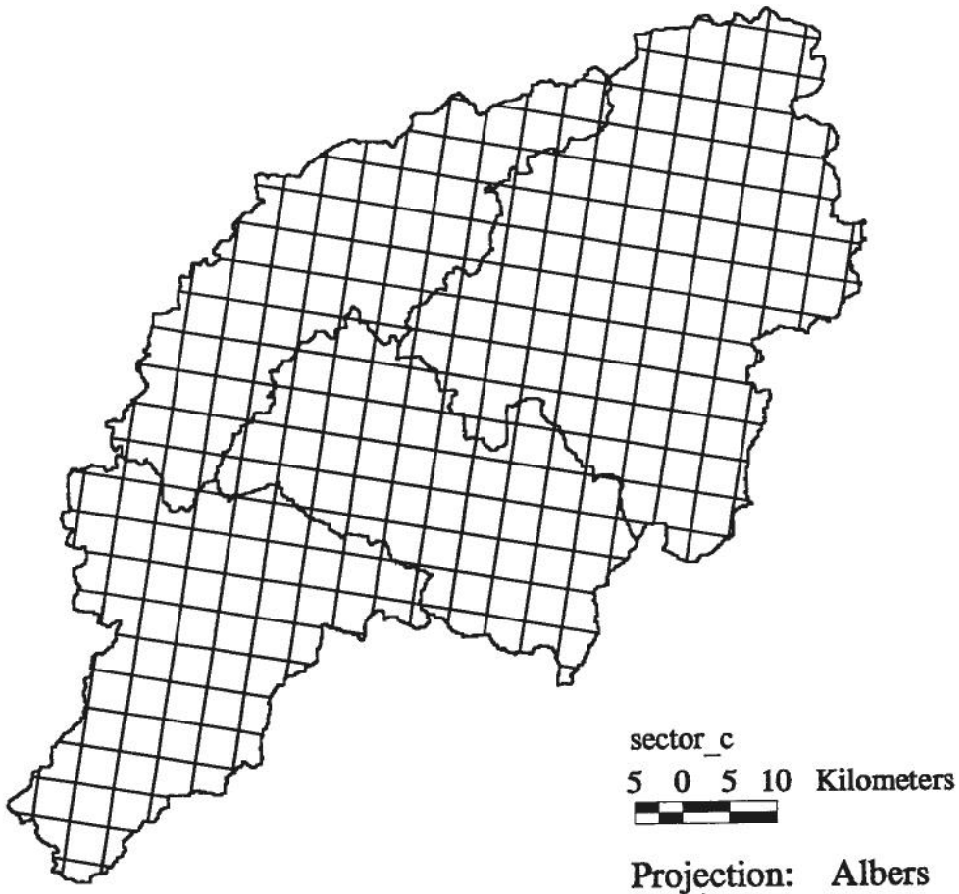


Figure 4.1: HRAP Coverage Intersected with a Subwatershed Coverage

<u>tksubshedsc.pat</u>	<u>tk3geoccalb.pat</u>	<u>sector_cov.pat</u>
AREA	AREA	AREA
PERIMETER	PERIMETER	PERIMETER
TKSUBSHEDSC#	TK3GEOCCALB#	SECTOR_COV#
TKSUBSHEDSC-ID	TK3GEOCCALB-ID	SECTOR_COV-ID
GRID-CODE	HRAPX	TKSUBSHEDSC#
	HRAPY	TKSUBSHEDSC-ID
		GRID-CODE
		TK3GEOCCALB#
		TK3GEOCCALB-ID
		HRAPX
		HRAPY

(2) POLYGRID(<cover>,{item},{lookup_table},{weight_table},{cell size})

sector_grid = polygrid (sector_cov,##,%,%cellsize%)

The Grid function Polygrid converts the coverage sector_cov into a grid in which all cells in a given sector (or zone) are assigned the value of the internal polygon number, sector_cov# by default. The cell size argument is read from the grid flmerge_grid and for the Tenkiller watershed is equal to 100 m. It should be noted that some polygons in sector_cov may be smaller than the size of one grid cell; these polygons do not retain a unique GRID-CODE during the vector to raster conversion. As a result, sector_grid.vat contains fewer records than sector_cov.pat and these small polygons in sector_cov.pat do not have an associated mean flowlength. The total area of these small polygons in the Tenkiller example with four subwatersheds was 0.0725 km² — only 0.002% of the total watershed area. This small area does not literally disappear during raster to vector conversion because the total number of cells in the raster representation is adjusted to reflect the total area in the vector representation as closely as possible. For example, the area of each 100 m raster cell at Tenkiller is 0.01 km² ; therefore, the area of sector_grid is equal to that of sector_cov to within 0.01 km².

(3) ZONALSTATS(<zone_grid>, <value_grid>, {stats_name}, {DATA | NODATA})

flength.stat = zonalstats(sector_grid,flmerge_grid)

With the grid of zones established from polygrid, the Zonalstats function creates an INFO file that stores the statistics on cells in the <value_grid> that belong to a common zone in the <zone_grid>. There will be one record in the INFO file flength.stat for each sector with items VALUE, COUNT, MEAN, MIN, and MAX. VALUE is equal to sector_cov# and COUNT is equal to the number of cells in that sector. By default, when the user does not specify a statistic, Zonalstats will compute MEAN, MIN, and MAX. A sample of the file flength.stat is printed here. The units for MEAN, MIN, and MAX Flowlength are meters.

Enter Command: **sel flength.stat**
315 Records Selected.

Enter Command: **list**

Record	VALUE	COUNT	MEAN	MIN	MAX
1	2	474	173727.594	172363.859	175119.500
2	3	609	174331.188	172570.969	176250.875
3	4	61	172292.359	171042.531	172698.172
4	5	1593	169481.859	166014.094	172449.641
5	6	9	172387.531	172198.172	172522.438
6	7	1650	170554.547	167101.109	174770.969
7	8	1071	169612.250	166496.938	172798.172
8	9	159	176609.047	175526.609	177499.406
.
.

Note that the cells in the input grids sector_grid and flmerge_grid to the Zonalstats function may not be aligned precisely with one another but such misalignment will not alter computational results to a hydrologically significant degree.

(4) Establishing and using a Relate in TABLES.

sel sector_cov.pat	
relate add	/* Add a relate to sector_cov.pat
relfl	/* Relation name.
flength.stat	/* Name of table to be related.
info	/* Type of table to be related.
sector_cov#	/* Relate item
value	/* Related item
ordered	/* Type of sorting (i.e, linear, ordered)

```

ro                                /* Relate access (ro = read only)
.
.
.
reselect sector_cov# = relfl//value /* Reduce the selection to rows in
                                        /* sector_cov.pat and flength.stat for which
                                        /* sector_cov# = value. This is all rows
                                        /* except small polygons that were dropped.

reselect grid-code = [value basin%loops%] /* Select rows in both tables that
                                        /* belong to a given watershed.

```

Once the statistics file has been written, a Relate is set up in the TABLES subprogram so that the mean Flowlength and area for sectors with a common grid-code (or sectors that are within the same watershed) can be unloaded to a data file. The Relate is set up between sector_cov.pat and flength.stat and the Relate items that link these two INFO tables are SECTOR_COV# and VALUE respectively. Thus, as a set of rows with a common GRID-CODE in sector_cov.pat is selected, the related rows in flength.stat are also selected.

```

(5)  UNLOAD <out_file> {item...item} {DELIMITED | COLUMNAR
      <format_file>} {INIT}
      unload %.outfile% grid-code hrapx hrapy relfl//mean area delimited

```

A loop controls the selection of columns and rows to be written to an ASCII file. The total number of subwatersheds is written at the top of the file followed by data for subwatershed1, subwatershed2, etc. The items GRID-CODE, HRAPX, HRAPY, MEAN (Flowlength), and AREA are written for each selected record. Because it was difficult to unload data in the exact format requested for the modClark parameter file using AML, a simple FORTRAN code, moutput.f, rewrites the ASCII file into the desired form. In this study, moutput.f read tk3file.out and created tk3modc.in.

4.2 RESULTS

The final product of this procedure is a file named tk3modc.in that lists HRAP cell characteristics required as input for the modClark (HEC, 1995) program. A sample from an output file is printed below. The characteristics listed for each cell are hrapx, hrapy,

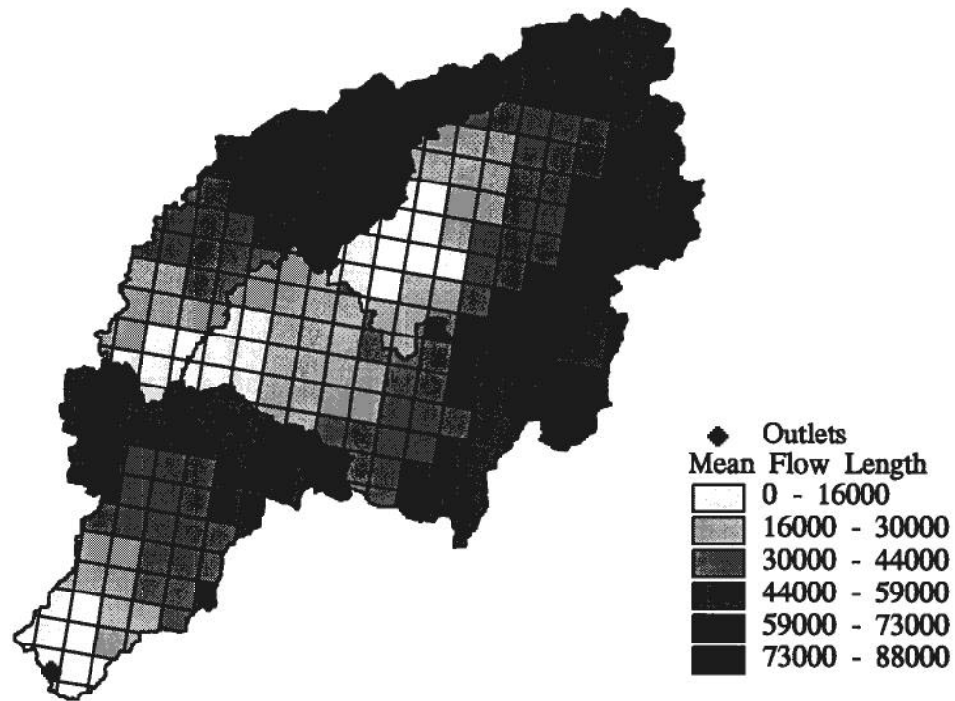


Figure 4.2: Mean Flow Length from HRAP Cells to Subwatershed Outlets

mean Flowlength to watershed outlet, and contributing area. Note that an HRAP cell may be split by a watershed boundary and therefore may be listed under more than one subwatershed. It is also possible that a watershed boundary may enter a cell, exit a cell, and re-enter a cell along a single side. With this scenario, the same HRAP-ID could be listed more than once for the same subwatershed.

```

SUBBASIN: 85
GRIDCELL: 633 359 86.8365 2.8668
GRIDCELL: 634 359 87.4707 0.3250
GRIDCELL: 632 358 81.4101 12.4244
GRIDCELL: 633 358 84.4681 15.7702
GRIDCELL: 634 358 87.3691 2.9036
GRIDCELL: 630 358 71.8893 0.7228
GRIDCELL: 631 358 76.4309 2.7685
GRIDCELL: 629 357 67.4486 9.0327
. . .
GRIDCELL: 625 346 7.3406 0.0158
END:
SUBBASIN: 86
GRIDCELL: 637 361 57.7422 4.7428
GRIDCELL: 638 361 58.3458 6.0854
. . .
GRIDCELL: 636 361 56.3070 0.6148
. . .

```

Figure 4.2 is a shaded map of the resulting travel lengths for each sector.