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[stabm4x] myprogram1 a successful conversion would produce user@host1\$./conv1.sh: /home/user/Projects/conv1: not a directory I know that I can modify the awk code to fix the filename, but I'm still stumped as to why this is happening, and what's causing the error. A: I assume your file name may vary so you could use a function for that purpose. You may have also the problem that the input file may be empty. #!/bin/bash infile="/home/user/Projects/conv1" outfile="/home/user/Projects/conv2" func() { filename="\$1" if [-f "\$infile/\$filename" "\$outfile" fi } while IFS= read -r line; do case \$line in user@host2) func \$line;; user@host3) func \$line;; user@host3) func \$line; user@host4) func \$line; u

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