Relative Pathnames

```bash
cat ..:/unixinst/quotation
```
Your Directory Hierarchy

unixstxx

dat

human
struct
seq
*.pdb
*.fasta

cow
struct
seq
*.pdb
*.fasta

rodent
struct
seq
*.pdb
*.fasta

others

UNIX Commands: No Redirection

sort

stdin
stdout
stderr

UNIX Commands: Redirect input

`sort < in.txt`
UNIX Commands: Redirect Output

```
sort > sorted.txt
```
UNIX Commands: Redirect Output

sort > sorted.txt 2> err.log
UNIX Commands: Combined Redirection

```
sort > sorted.txt 2>&1
```
UNIX Commands: More examples

sort < in.txt > sorted.txt
UNIX Commands: More examples

sort < in.txt >> sorted.txt
UNIX Commands: More examples

```
sort < in.txt > sorted.txt 2>&1
```
UNIX Commands: Pipes

egrep PAT < in.txt | sort | head -1 > first.txt
### The `csplit` Command

```bash
ccsplit seq.fasta '%^>%' '/^>/' '{3}'
csplit seq.fasta '%^>%' '/^>/' '/^>/' '/^>/' '/^>/' '/^>/'
```

#### 5 patterns = 6 groups

- **Lines before the first match.**
- **Lines from the first match up to (but not including) the second match.**
- **Lines from the second match up to (but not including) the third match.**
- **Lines from the third match up to (but not including) the fourth match.**
- **Lines from the fourth match up to (but not including) the fifth match.**
- **Lines from the fifth match up to the end of the file.**

---


<table>
<thead>
<tr>
<th>Pattern</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>xx00</td>
<td>&gt;seqA  MNSGVRMVTRS KVPVWEPOQNWQ</td>
</tr>
<tr>
<td>xx01</td>
<td>&gt;seqB  MEPPVPQSSVP GPPELAPTPAR</td>
</tr>
<tr>
<td>xx02</td>
<td>&gt;seqC  PDLDKGPTAPP CTNEDDEGSCA</td>
</tr>
<tr>
<td>xx03</td>
<td>&gt;seqD  SVICKAASGDT MNWNNITLTIV</td>
</tr>
<tr>
<td>xx04</td>
<td>&gt;seqE  SFRNFLGDIGC LISSNLLSYIK</td>
</tr>
</tbody>
</table>
Modes of vi

- SURF
  - Aa
  - Ii
  - Oo
- EDIT
- COMMAND
  - :wq
  - :q!

<Esc>