

NAME

writea, reada – write and read gawk arrays to/from files

SYNOPSIS

```
@load "rvarray"
```

```
ret = writea(file, array)
ret = reada(file, array)
```

DESCRIPTION

The *rvarray* extension adds two functions named **writea()** and **reada()**, as follows.

writea()

This function takes a string argument, which is the name of the file to which dump the array, and the array itself as the second argument. **writea()** understands multidimensional arrays. It returns one on success, or zero upon failure.

reada() is the inverse of **writea()**; it reads the file named as its first argument, filling in the array named as the second argument. It clears the array first. Here too, the return value is one on success and zero upon failure.

NOTES

The array created by **reada()** is identical to that written by **writea()** in the sense that the contents are the same. However, due to implementation issues, the array traversal order of the recreated array will likely be different from that of the original array. As array traversal order in AWK is by default undefined, this is not (technically) a problem. If you need to guarantee a particular traversal order, use the array sorting features in *gawk* to do so.

The file contains binary data. All integral values are written in network byte order. However, double precision floating-point values are written as native binary data. Thus, arrays containing only string data can theoretically be dumped on systems with one byte order and restored on systems with a different one, but this has not been tried.

EXAMPLE

```
@load "rvarray"
...
ret = writea("arraydump.bin", array)
...
ret = reada("arraydump.bin", array)
```

SEE ALSO

GAWK: Effective AWK Programming, *filefuncs(3am)*, *fnmatch(3am)*, *fork(3am)*, *inplace(3am)*, *ordchr(3am)*, *readdir(3am)*, *readfile(3am)*, *revoutput(3am)*, *time(3am)*.

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