

More snow Examples

Luke Tierney

Department of Statistics & Actuarial Science
University of Iowa

September 27, 2007





Parallel Kriging

- Several R packages provide spatial prediction (kriging).
- Sgeostat has a pure R version, `krige`.
- Computation is a simple loop over points.
- Fairly slow when using only points within `maxdist`.
- Result structure is fairly simple.
- Easy to write a parallel version.



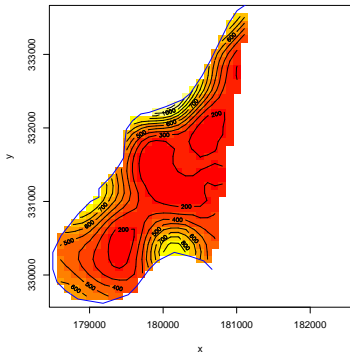
Parallel Version of kriging

```
parKriging <- function(cl, s, ...) {  
  # split the prediction points s  
  idx <- clusterSplit(cl, 1: dim(s)[1])  
  ssplt <- lapply(idx, function(i) s[i,])  
  
  # compute the predictions in parallel  
  v <- clusterApply(cl, ssplt, kriging, ...)  
  
  # assemble and return the results  
  merge <- function(x, f) do.call("c", lapply(x, f))  
  s.o <- point(s)  
  s.o$do <- merge(v, function(y) y$do)  
  s.o$zhat <- merge(v, function(y) y$zhat)  
  s.o$sigma2hat <- merge(v, function(y) y$sigma2hat)  
  return(s.o)  
}
```



Zink in Maas Flood Plane Ground Water

- Measurements at 155 points.
- Predict on $50m \times 50m$ grid.
- Use only data within 1 kilometer.
- Sequential version takes 2.53 seconds.
- Parallel version (10 nodes) takes 0.38 seconds.
- Only a factor of 6.7 speedup.





Load Balanced Kriging

- `clusterApplyLB`: load balanced `clusterApply`.
- Give more jobs n than cluster nodes p .
 - Places first p jobs on p nodes,
 - job $p + 1$ goes to first node to finish,
 - job $p + 2$ goes to second node to finish,
 - etc., until all n jobs are done.



Parallel Version of kriging with Load Balancing

```
parKrigingLB <- function(cl, s, ..., LBF = 4) {  
  # split the prediction points s  
  idx <- splitIndices(dim(s)[1], length(cl) * LBF) #****  
  ssplt <- lapply(idx, function(i) s[i,])  
  
  # compute the predictions in parallel  
  v <- clusterApplyLB(cl, ssplt, kriging, ...) #****  
  
  # assemble and return the results  
  merge <- function(x, f) do.call("c", lapply(x, f))  
  s.o <- point(s)  
  s.o$do <- merge(v, function(y) y$do)  
  s.o$zhat <- merge(v, function(y) y$zhat)  
  s.o$sigma2hat <- merge(v, function(y) y$sigma2hat)  
  return(s.o)  
}
```



- The result is a speedup of 8.5:

```
> system.time(pk1b <-  
+   parKrigingLB(cl,grid$point,maas.point,'zinc',maas.vmod,  
+               maxdist=1000,extrap=FALSE,border=maas.bank))  
   user  system elapsed  
0.108  0.007  0.297
```

- And the results are identical to the sequential version.

```
> identical(k, pk)  
[1] TRUE  
> identical(pk1b, pk)  
[1] TRUE
```

- Load balancing can improve performance.
- Load balancing does increase communication somewhat.
- Load balancing is hard to combine with reproducible simulation.
- Load balancing can be hard to use with distributed data.



Parallel Cross Validation

- Useful for choosing tuning parameters.
- Common structure:
 - Outer loop over tuning parameters
 - Inner loop over omitted data
 - Additional inner replication loop if random (`nnet`)
- Good initial approach:
 - parallelize loop over omitted data
 - replace loop by `lapply`; test and debug
 - replace `lapply` by `parLapply`



Nested loops

```
cv <- function(parameters, data)
  for (p in parameters) {
    v <- vector("list", length(data))
    for (d in data)
      v[[d]] <- fit for p, omitting d
    summarize result for p
  }
```

lapply in inner loop

```
lcv <- function(parameters, data)
  for (p in parameters) {
    fit <- function(p, d)
      fit for p, omitting d
    v <- lapply(data, fit)
    summarize result for p
  }
```

Parallel version

```
parCv <- function(cl, parameters, data)
  for (p in parameters) {
    fit <- function(p, d)
      fit for p, omitting d
    v <- parLapply(cl, data, fit)
    summarize result for p
  }
```

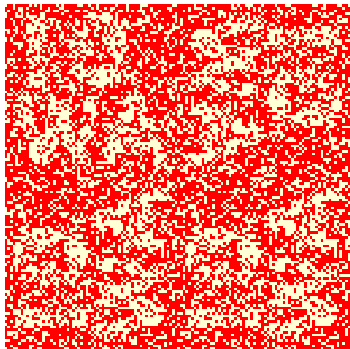
Simple Image Reconstruction

- Observe y_{ij} , a binary image with noise.
- True image is x_{ij} .
- Simple noise model:
 - $y_{ij}|x \sim p^{y_{ij}=x_{ij}}(1-p)^{y_{ij}\neq x_{ij}}$
 - pixel noise is independent
- A simple image prior distribution:

$$p(x) \propto \exp\{\beta N(x)\}$$

with $N(x)$ the number of neighbor pairs that are the same color.

- This is the *Ising model*.
- Simplest approach uses 4 neighbors.
- Dependence increases with β .

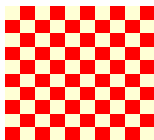


Simple Image Reconstruction

- Full conditionals are simple:

$$p(x_{ij} = c | y, \{x \setminus x_{ij}\}) = \exp\{\beta \times \text{number of neighbors with color } c\}$$

- Gibbs sampling is easy but can be slow in R using loops.
- Can vectorize using checkerboard order:



- Given the red pixels, the white pixels are independent.
- This also allows parallel computation.



A Vectorized Algorithm

Computing the number of neighbors with a specified color:

```
nn <- function(m, c) {  
  nr <- nrow(m)  
  nc <- ncol(m)  
  nn <- matrix(0, nr, nc)  
  nn[1:(nr)-1,] <- nn[1:(nr)-1,] + (m[2:nr,] == c)  
  nn[2:nr,] <- nn[2:nr,] + (m[1:(nr-1),] == c)  
  nn[,1:(nc)-1] <- nn[,1:(nc)-1] + (m[,2:nc] == c)  
  nn[,2:nc] <- nn[,2:nc] + (m[,1:(nc-1)] == c)  
  nn  
}
```

Simulating new pixel values:

```
simGroup <- function(m, l2, l1, beta, which) {  
  pp2 <- l2 * exp(beta * nn(m, 2))  
  pp1 <- l1 * exp(beta * nn(m, 1))  
  pp <- pp2 / (pp2 + pp1)  
  m[which] <- ifelse(runif(sum(which)) < pp[which], 2, 1)  
  m  
}
```



A Vectorized Algorithm

Computing the likelihood:

```
makeLik <- function(img, p)
  list(ifelse(img == 1, p, 1 - p), ifelse(img == 2, p, 1 - p))
```

Estimating the posterior mean image:

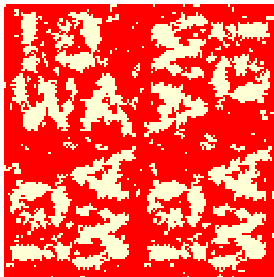
```
simImgPM <- function(img, beta, p, NN = 50, K = 50) {
  lik <- makeLik(img, p)
  white <- outer(1:nrow(img), 1:ncol(img), FUN='+') %% 2 == 1
  black <- ! white
  m <- img
  mm <- 0
  for (N in 0 : (NN - 1)) {
    for (i in 1 : K) {
      m <- simGroup(m, lik[[2]], lik[[1]], beta, white)
      m <- simGroup(m, lik[[2]], lik[[1]], beta, black)
    }
    mm <- (N / (N + 1)) * mm + (1 / (N + 1)) * m
  }
  mm
}
```



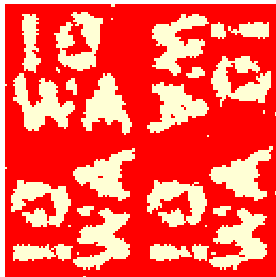
A Vectorized Algorithm

Some results for $NN = 500$, $K = 1$, and $p = 0.7$:

$\beta = 0.7$



$\beta = 0.9$



Timing:

```
> system.time(pm <- simImgPM(img4, 0.9,0.7,500,1))
  user  system elapsed
42.914   0.468  43.418
```



Towards a Simple Parallel Version

- Split image into two groups of columns.
- Each one needs edge of the other group.
- Find split point and label likelihood values:

```
n2 <- floor(ncol(img) / 2)
i1 <- 1 : n2; i1x <- c(i1, n2 + 1)
i2 <- (n2 + 1) : ncol(img); i2x <- c(n2, i2)
l1 <- lik[[1]]
l2 <- lik[[2]]
```

- Simulate “white” pattern in two steps

```
m[,i1] <- simGroup(m[,i1x], l2[,i1x], l1[,i1x], beta,
                  white[,i1x])[,-(n2 + 1)]
m[,i2] <- simGroup(m[,i2x], l2[,i2x], l1[,i2x], beta,
                  white[,i2x])[, -1]
```

- Do the same for “black” pattern.



A Simple Parallel Version

- Replace the “white” step by

```
v <- clusterMap(cl, fun,  
               list(m[,i1x], m[,i2x]),  
               list(l2[,i1x], l2[,i2x]),  
               list(l1[,i1x], l1[,i2x]),  
               list(white[,i1x], white[,i2x]))  
m[,i1] <- v[[1]][,-(n2 + 1)]  
m[,i2] <- v[[2]][,-1]
```

with `fun` created by

```
makeSimImgHelper <- function(beta)  
  function(m, l2, l1, which)  
    simGroup(m, l2, l1, beta, which)
```

Need to export `nn` and `simGroup` to nodes.

- Timing: 104 seconds—almost 3 times *slower*.
- Problem: too much communication.
- Solution: maintain state on the nodes.



Maintaining Sampler State

```
makeImgSampler <- function(img, beta, p, white.first = FALSE) {  
  m<-img  
  mm<-img  
  <<more setup code>>  
  stepWhite <- function() {  
    m <<- simGroup(m, l2, l1, beta, white)  
    invisible(NULL)  
  }  
  stepBlack <- function() ...  
  accumulate <- function() ...  
  getColumn <- function(i) m[,i]  
  setColumn <- function(i, v) m[,i] <<- v  
  pm <- function() mm  
  list(stepWhite = stepWhite, stepBlack = stepBlack,  
       accumulate = accumulate,  
       getColumn = getColumn, setColumn = setColumn, pm = pm)  
}
```



Serial Algorithm Using Sampler State

- The code:

```
simImgPM <- function(img, beta, p, NN = 50, K = 50) {  
  smp <- makeImgSampler(img, beta, p)  
  for (i in 1:NN) {  
    for (i in 1:K) {  
      smp$stepWhite()  
      smp$stepBlack()  
    }  
    smp$accumulate()  
  }  
  smp$pm()  
}
```

- This is an *object oriented* design.
- `smp` is a sampler object with mutable state.
- The algorithm proceeds by sending messages to `smp`.



- Create two objects and get the border columns:

```
wf2 <- if (nc2 %% 2 == 0) FALSE else TRUE
smp1 <- makeImgSampler(img[,1:(nc2+1)], beta, p)
smp2 <- makeImgSampler(img[,nc2:nc], beta, p, wf2)
c1 <- smp1$getColumnName(nc2)
c2 <- smp2$getColumnName(2)
```

- “White” step:

```
v <- list(stepWhite2(smp1, nc2 + 1, c2, nc2),
          stepWhite2(smp2, 1, c1, 2))
c1 <- v[[1]]
c2 <- v[[2]]
```

with

```
stepWhite2 <- function(smp, i, v, j) {
  smp$setColumn(i, v)
  smp$stepWhite()
  smp$getColumnName(j)
}
```



- Sampler will be in a global variable `smp` on each node:

```
nodePutSmp <- function(v) {  
  assign("smp", v, envir = .GlobalEnv);  
  NULL  
}  
clusterApply(cl, list(smp1, smp2), nodePutSmp)
```

Some utility functions that use this global value:

```
nodeStepWhite2 <- function(i, v, j) {  
  stepWhite2(smp, i, v, j);  
  NULL  
}  
nodeStepBlack2 <- function(i, v, j) ...  
nodeAccumulate <- function() { smp$accumulate(); NULL }  
nodePM <- function() smp$pm()
```

- Need to export `stepWhite2` and `stepBlack2` to nodes:



- Body of the parallel code:

```
for (i in 1:NN) {  
  for (j in 1:K) {  
    v <- clusterMap(c1, nodeStepWhite2,  
                   c(nc2 + 1, 1), list(c2, c1), c(nc2, 2))  
  
    c1 <- v[[1]]  
    c2 <- v[[2]]  
    <<same for black pixels>>  
  }  
  clusterCall(c1, nodeAccumulate)  
}  
v <- clusterCall(c1, nodePM)  
cbind(v[[1]][,-(nc2+1)], v[[2]][,-1])
```

- Timings for $NN = 500, K = 1$:

Serial version:	31.57 seconds
Parallel version:	17.56 seconds



Some Open Issues

- Fault tolerance:
 - nodes/communication can fail
 - R processes can crash
- Error handling
 - Some computations may result in R-level errors.
 - Currently these are returned as results of class `try-error`.
- Interrupt handling
- Load balancing issues:
 - load balancing and reproducible simulations
 - integrating load balancing with `clusterApply`, `parLapply`, etc..
 - convenient control options for load balancing (e.g. chunk size)
- Support for
 - intermediate communication between nodes
 - maintaining state on nodes

The BSP model may be useful to explore.