Sparse Matrices Methods and Kriging Applications to Large Spatial Data Sets

SAMSI

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What are sparse matrices?

How to work with sparse matrices?

Sparse positive definite matrices in statistics.

Sparse matrices and fields.

Thanks NSF! DMS-0621118

Outline

What are sparse matrices?

How to work with sparse matrices?

Sparse positive definite matrices in statistics.

Sparse matrices and fields.

What is "sparse" or a sparse matrix?

According to Wiktionary/Wikipedia:

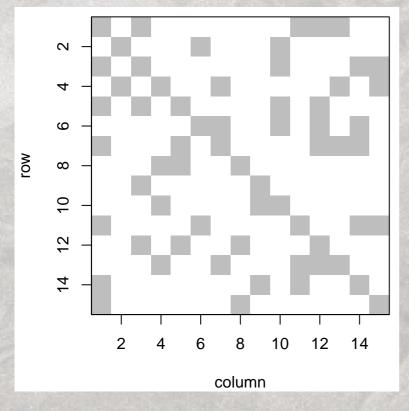
Sparse: (Adjective)

1. Having widely spaced intervals

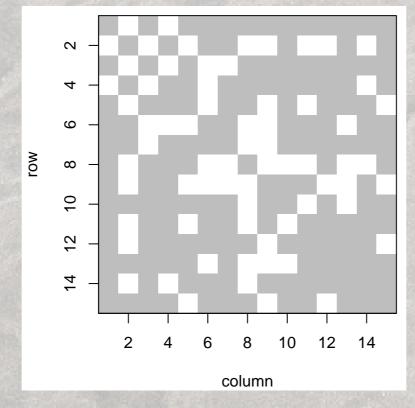
2. Not dense; meager

Sparse matrix: a matrix populated primarily with zeros.

- R> n <- 15
- $R > A <- array(runif(n^2), c(n,n)) + diag(n)$
- R > A[A < 0.75] <- 0



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- R> AtA <- t(A) %*% A



Why should we use sparse matrices?

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2. Savings in computing time

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- 2. Savings in computing time 0.066sec vs 0.003sec for $1,000 \times 1,000$ matrix multiplication

To exploit the savings need to exploit the sparsity.

We need a clever storage format and fast algorithms.

Let $\mathbf{A} = (a_{ij}) \in \mathbb{R}^{n \times m}$ and z the number of its nonzero elements.

1. Naive/"traditional"/classic format: one vector of length $n \times m$ and a dimension attribute.

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- 2. Triplet format:

three vectors of length z, (i, j, a_{ij}) and a dimension attribute.

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3. Compressed sparse row (CSR) format: eliminate redundant row indices.

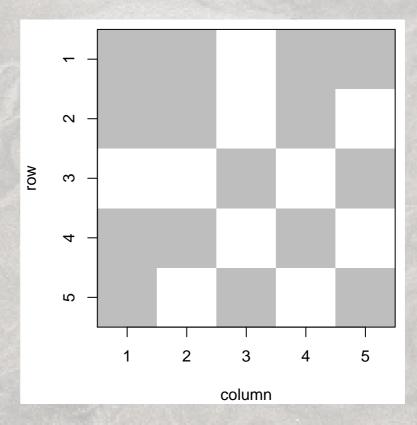
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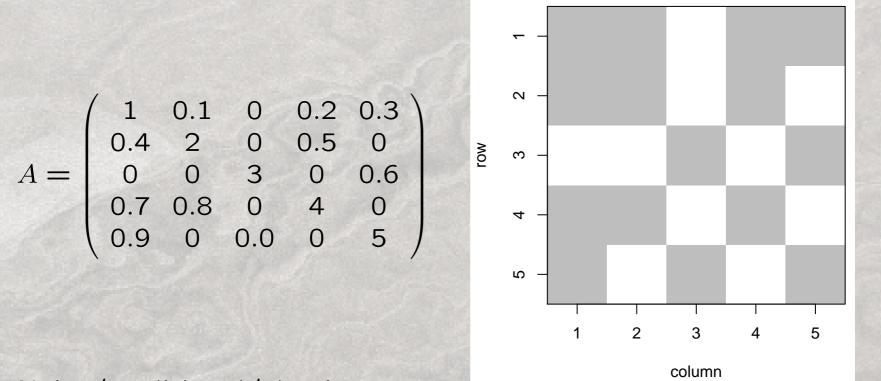
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three vectors of length z, (i, j, a_{ij}) and a dimension attribute.

- 3. Compressed sparse row (CSR) format: eliminate redundant row indices.
- 4. and about 10 more ...

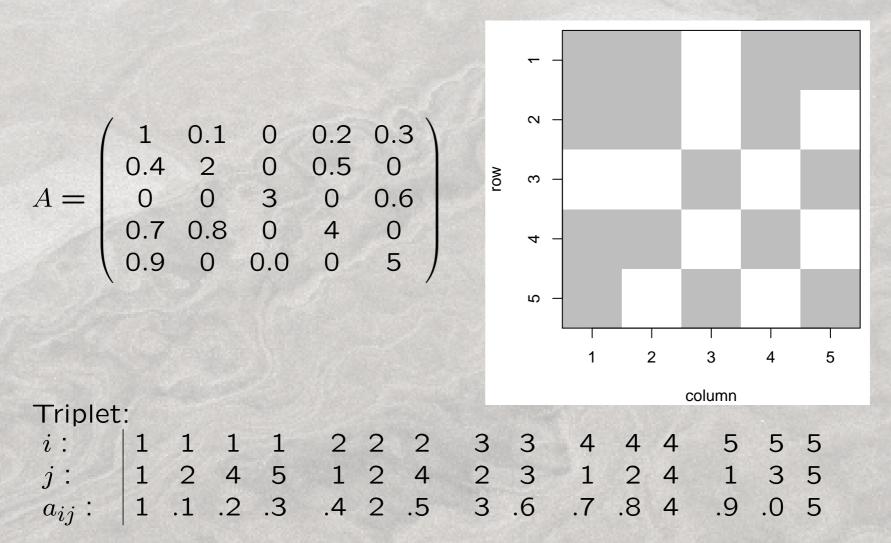
 $A = \begin{pmatrix} 1 & 0.1 & 0 & 0.2 & 0.3 \\ 0.4 & 2 & 0 & 0.5 & 0 \\ 0 & 0 & 3 & 0 & 0.6 \\ 0.7 & 0.8 & 0 & 4 & 0 \\ 0.9 & 0 & 0.0 & 0 & 5 \end{pmatrix}$

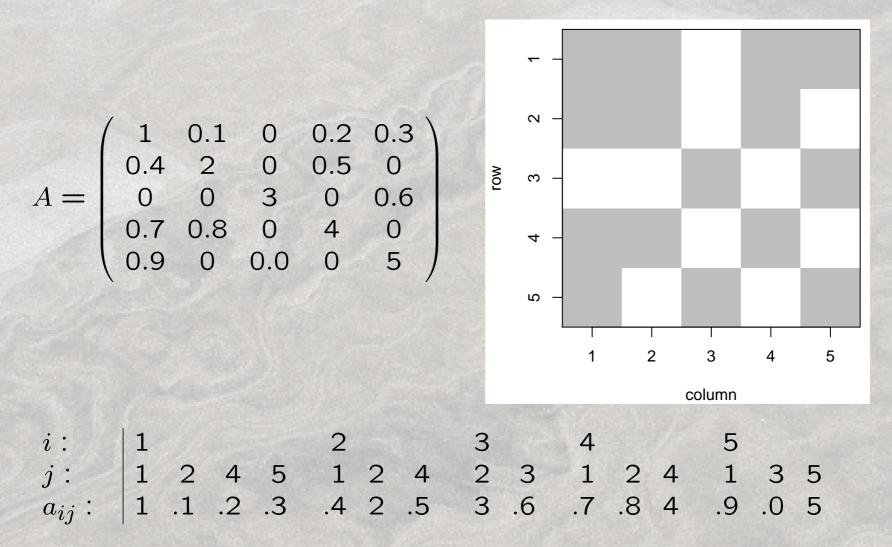


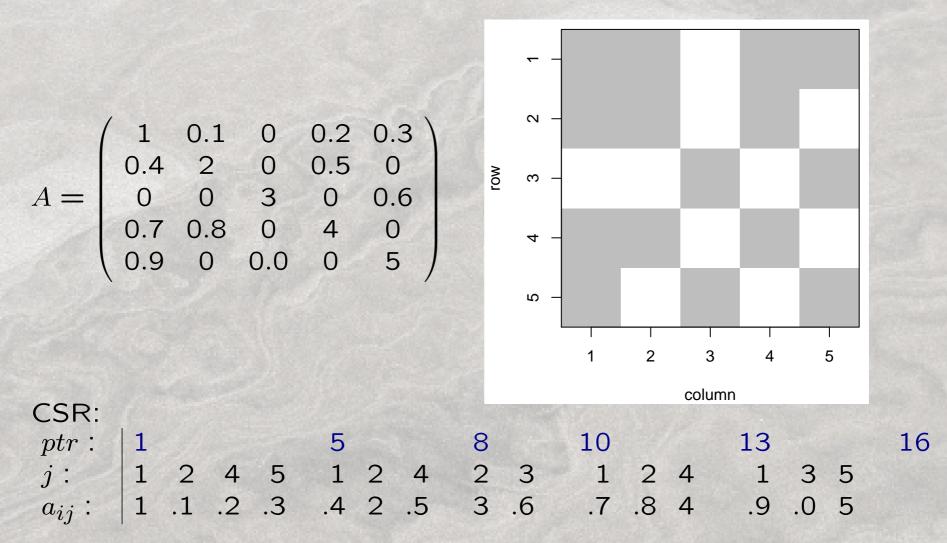


Naive/traditional/classic:

 $1,\ .4,\ 0,\ .7,\ .9,\ .1,\ 2,\ 0,\ .8,\ 0,\ 0,\ 3,\ 0,\ .0,\ .2,\ .5,\ 0,\ 4,\ 0,\ .3,\ 0,\ .6,\ 0,\ 5$







Compressed Sparse Row Format

- 1. the nonzero values row by row
- 2. the (ordered) column indices of nonzero values
- 3. the position in the previous two vectors corresponding to new rows, given as pointers
- 4. the column dimension of the matrix.

CSR:													
ptr :	1				5			8	10			13	16
j:	1	2	4	5	1	2	4	2 3	3 1	2	4	1 3 5	
a_{ij} :	1	.1	.2	.3	.4	2	.5	3.6	5.7	.8	4	1 3 5 .9 .0 5	

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Savings in storage and computation for sparse matrices Loss in storage and computation for full matrices Intuitive

3. Compressed sparse row (CSR) format:
Apart from intuitive, same as triplet
Faster element access
Many available algorithms
Arbitrary choice for "row" vs "column" format (CSC)

Implications

With a new storage format new "algorithms" are required ...

Is it worthwhile???

Setup:

```
R> timing <- function(expr)
+ as.vector( system.time( for (i in 1:N) expr)[1])</pre>
```

R> N <- 1000 # how many operations
R> n <- 999 # matrix dimension
R> cutoff <- 0.9 # what will be set to 0</pre>

```
R> A <- array( runif(n^2), c(n,n))
R> A[A < cutoff] <- 0
```

R> S <- somecalltomagicfunctiontogetsparseformat(A)
Compare timing for different operations on A and S.</pre>

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```
R> A <- array( runif(n^2), c(n,n))
R> A[A < cutoff] <- 0</pre>
```

R > S <- as.spam(A)

Compare timing for different operations on A and S.

```
R> timing( A + sqrt(A) )
[1] 0.058
R> timing( S + sqrt(S) )
[1] 0.065
```

```
R> timing( AtA <- t(A) %*% A )
[1] 1.567
R> timing( StS <- t(S) %*% S )
[1] 3.422</pre>
```

```
R> timing( A[1,2] <- .5 )
[1] 0.007
R> timing( S[1,2] <- .5 )
[1] 0.018</pre>
```

```
R> timing( A[n,n-1] <- .5 )
[1] 0.001
R> timing( S[n,n-1] <- .5 )
[1] 0.012</pre>
```

```
R> timing( xA <- solve(AtA, rep(1,n)) )
[1] 0.626
R> timing( xS <- solve(StS, rep(1,n)) )
[1] 0.831</pre>
```

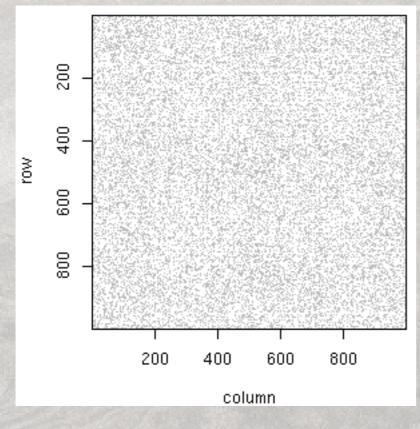
```
R> timing( RA <- chol(AtA) )
[1] 0.301
R> timing( RS <- chol(StS) )
[1] 0.824</pre>
```

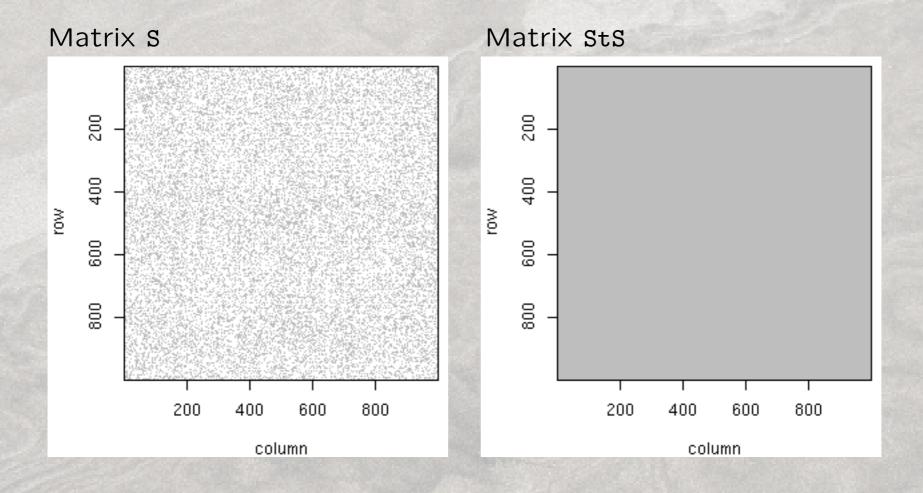
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R> timing( RS <- chol(StS) )
[1] 0.824</pre>
```

Is it really worthwhile? What is going on?

Matrix S





With cutoff 0.99:

R> timing(AtA <- t(A) %*% A)
[1] 1.536
R> timing(StS <- t(S) %*% S)
[1] 0.076</pre>

```
R> timing( RA <- chol(AtA) )
[1] 0.304
R> timing( RS <- chol(StS) )
[1] 0.451</pre>
```

Matrix chol(StS) Matrix StS HH. МO νo column column

Density of the factor is 41% with fill-in ratio 7.2.

Timing

With cutoff 0.999:

R> timing(AtA <- t(A) %*% A)
[1] 1.549
R> timing(StS <- t(S) %*% S)
[1] 0.004</pre>

```
R> timing( RA <- chol(AtA) )
[1] 0.304
R> timing( RS <- chol(StS) )
[1] 0.004</pre>
```

Timing

Matrix StS Matrix chol(StS) МO νo di. column column

Density of the factor is .6% with fill-in ratio 2.3.

Implications

With a new storage format new "algorithms" are required ...

Is it worthwhile??? Yes!

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Is it worthwhile??? Yes!

Especially since

spam: R package for sparse matrix algebra.



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 - wrap an as.spam() and go
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 - S4 and S3 syntax
- situated between SparseM and Matrix

Representation of Sparse Matrices

spam defines a S4 class spam containing the vectors: "entries", "colindices", "rowpointers" and "dimension".

R> slotNames("spam")
[1] "entries" "colindices" "rowpointers" "dimension"

R> getSlots("spam")
 entries colindices rowpointers dimension
 "numeric" "integer" "integer" "integer"

Representation of Sparse Matrices R> A

	[,1]	[,2]	[,3]	[,4]	[,5]			
[1,]	1.0	0.1	0	0.2	0.3			
[2,]	0.6	2.0	0	0.5	0.0			
[3,]	0.0	0.0	3	0.0	0.6			
[4,]	0.7	0.8	0	4.0	0.0			
[5,]	0.9	0.0	1	0.0	5.0			
Class 'spam'								
R> slotNames(A)								
[1] "entries" "colindices" "rowpointers" "dimension"								
R> A@entries								
[1] 1.0 0.1 0.2 0.3 0.6 2.0 0.5 3.0 0.6 0.7 0.8 4.0 0.9 1.0 5.0								
R> A@colindices								
[1] 1 2 4 5 1 2 4 3 5 1 2 4 1 3 5								
R> A@rowpointers								
[1] 1 5 8 10 13 16								
R> A@dimension								
[1] 5 5								

Creating Sparse Matrices

Similar coercion techniques as with matrix:

- spam(...)
- as.spam(...)

Special functions:

- diag.spam(...)
- nearest.dist(...)

Methods for spam

- Similar behavior as with matrices plot; dim; determinant; %*%; +; ...
- Slightly enhanced behavior print; dim<-; chol;
- Specific behavior
 Math; Math2; Summary; ...
- New methods display; ordering;

Create Covariance Matrices

Covariance matrix:

nearest.dist and applying a covariance function:

R> C <- nearest.dist(x, diag=TRUE, upper=NULL)</pre>

R> C@entries <- Wendland(C@entries, dim=2, k=1)

Create Covariance Matrices

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Precision matrix (GMRF):

— regular grids: nearest.dist with different cutoffs R> diag.spam(n) +

- + (b1-b2) * nearest.dist(x, delta=1, upper=NULL) +
- + b2 * nearest.dist(x, delta=sqrt(2), upper=NULL)

— irregular grids: using incidence list and spam R> incidence <- list(i=..., j=..., values) R> C <- spam(incidence, n, n)</p>

Solving Linear Systems

A key feature of spam is to solve efficiently linear systems.

To solve the system Ax = b, we

- perform a Cholesky factorisation $\mathbf{A} = \mathbf{U}^{\mathsf{T}}\mathbf{U}$
- solve two triangular systems $\mathbf{U}^{\mathsf{T}}\mathbf{z} = \mathbf{b}$ and $\mathbf{U}\mathbf{x} = \mathbf{z}$

But we need to "ensure" that U is as sparse as possible!

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But we need to "ensure" that **U** is as sparse as possible! Permute the rows and columns of \mathbf{A} : $\mathbf{P}^{\mathsf{T}}\mathbf{A}\mathbf{P} = \mathbf{U}^{\mathsf{T}}\mathbf{U}$.



Some technical details about a Cholesky decomposition:

 Determine permutation and permute the input matrix A to obtain P^TAP
 Symbolic factorization: the sparsity structure of U is constructed
 Numeric factorization: the elements of U are computed

BTW: efficient Cholesky factorization



efficient determinant calculation:

$$det(\mathbf{C}) = det(\mathbf{U}^{\mathsf{T}}) det(\mathbf{U}) = \prod_{i=1}^{n} \mathbf{U}_{ii}^{2}$$



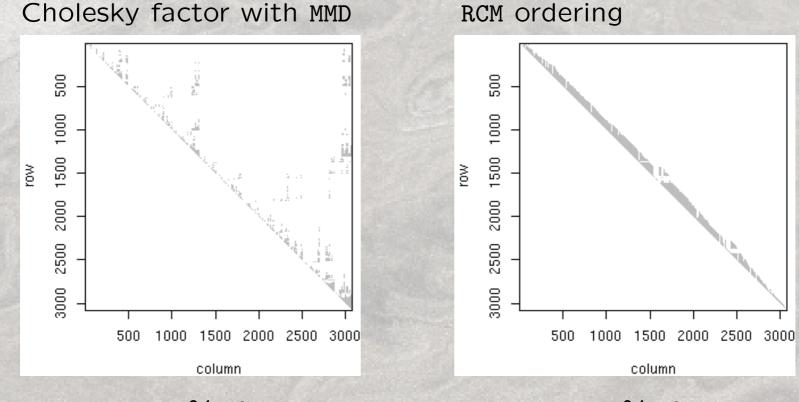
spam knows Cholesky!

— Several methods to construct permutation matrices ${\bf P}$

none, MMD, RCM

spam knows Cholesky!

Several methods to construct permutation matrices P



Density: 1.5%, fill-in: 4.7

Density: 2.7%, fill-in: 8.1

spam knows Cholesky!

- Several methods to construct permutation matrices P
 - update to perform only 'partial' Cholesky factors update(choleskyobject, covariancematrix) Performing the numerical decomposition only, [3]

spam knows Cholesky!

- Several methods to construct permutation matrices P
- update to perform only 'partial' Cholesky factors
- Passing arguments and flags for avoiding sanity checks
 Using the specific call chol.spam

Passing memory=list(nnzR=..., nnzcolindices=...), pivot=...

Options safemode=c(FALSE,FALSE,FALSE), cholsymmetrycheck=FALSE, cholpivotcheck=FALSE

Options in spam

For "experts", flags to speed up the code:

R> powerboost()

```
R> noquote( format( spam.options()) )
```

eps	drop	printsize
2.220446e-16	FALSE	100
imagesize	trivalues	cex
10000	FALSE	1200
safemode	dopivoting	cholsymmetrycheck
TRUE, TRUE, TRUE	TRUE	TRUE
cholpivotcheck	cholupdatesingular	cholincreasefactor
TRUE	warning	1.25, 1.25
nearestdistincreasefactor	nearestdistnnz	
1.25	160000, 400	

Limits of spam

What can spam not do (yet)?

- LU decompositions
- SVD/eigendecompositions
- Non-double elements

. . .

But, please, comments to reinhard.furrer@math.uzh.ch!



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Sparse Matrices in Statistics

Where do large matrices occur?

- Location matrices
- Design matrices

Sparse Matrices in Statistics

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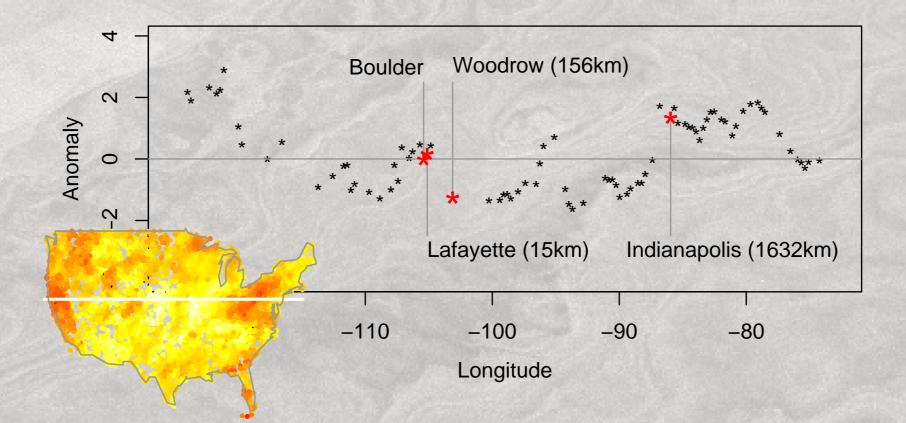
- Location matrices
- Design matrices
- Covariance matrices
- Precision matrices

Sparse Matrices in Statistics

- Covariance matrices: Compactly supported covariance functions Tapering
- Precision matrices: (Gaussian) Markov random fields (Tapering???)

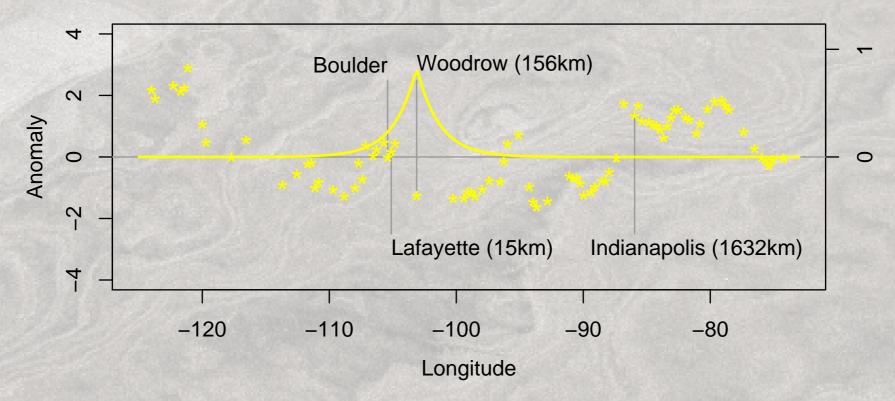
We have symmetric positive definite (spd) matrices.

Precipitation anomaly along 40° lat.



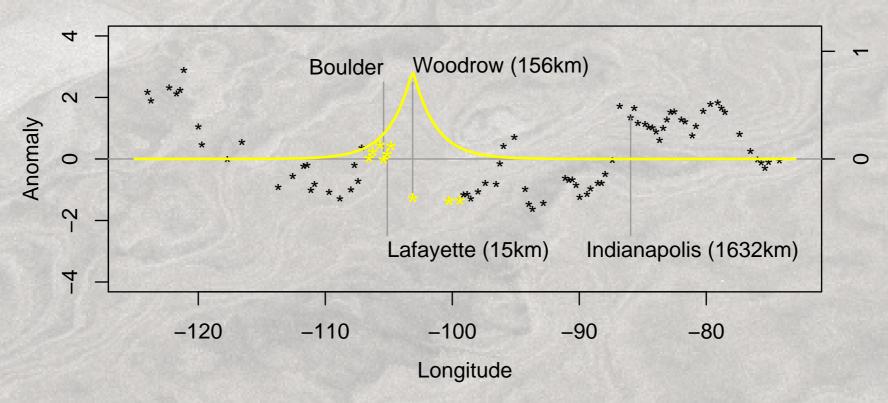
Precipitation anomaly along 40° lat.

Ordinary kriging

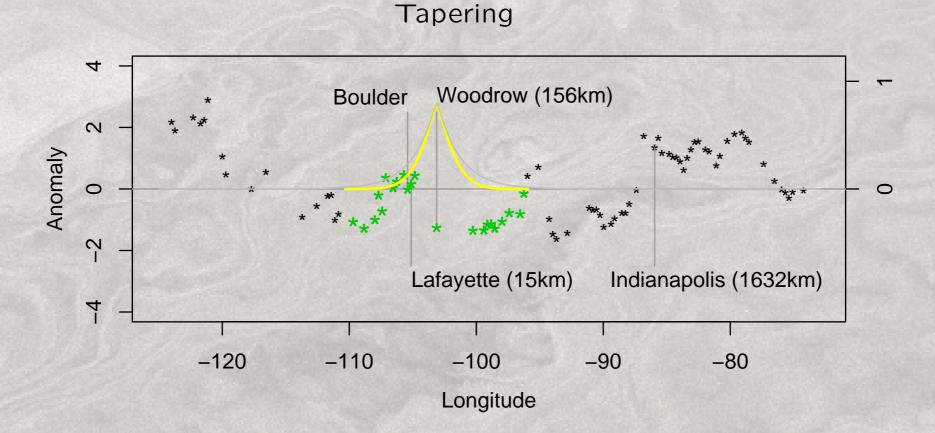


Precipitation anomaly along 40° lat.

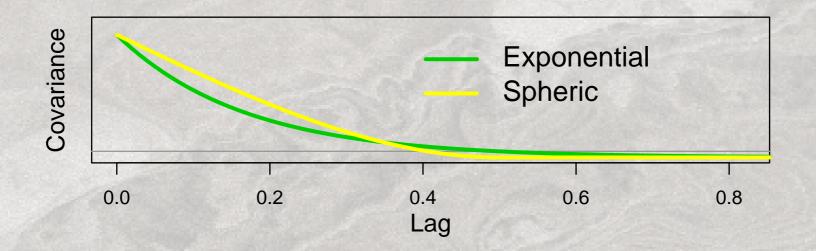
Nearest neighbor kriging with 8 observations



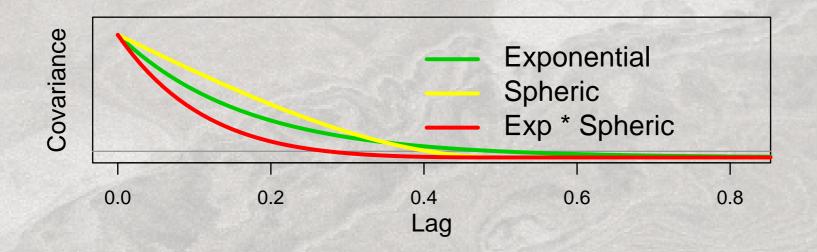
Precipitation anomaly along 40° lat.



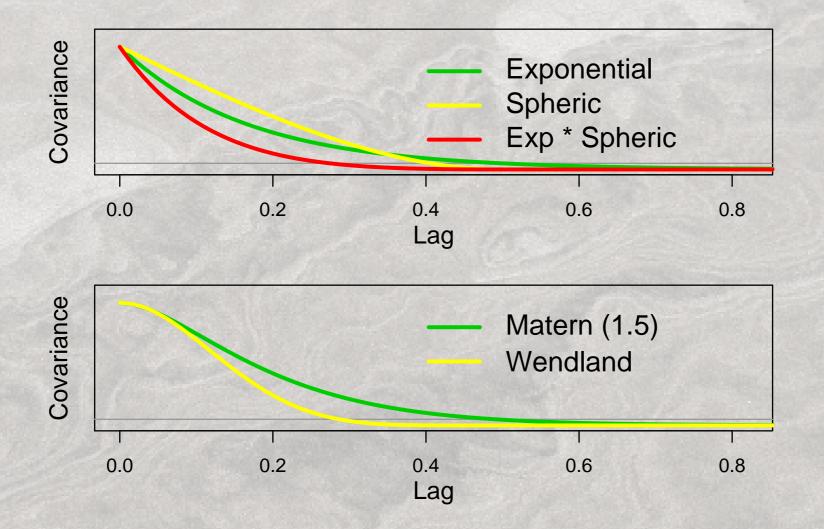
Examples



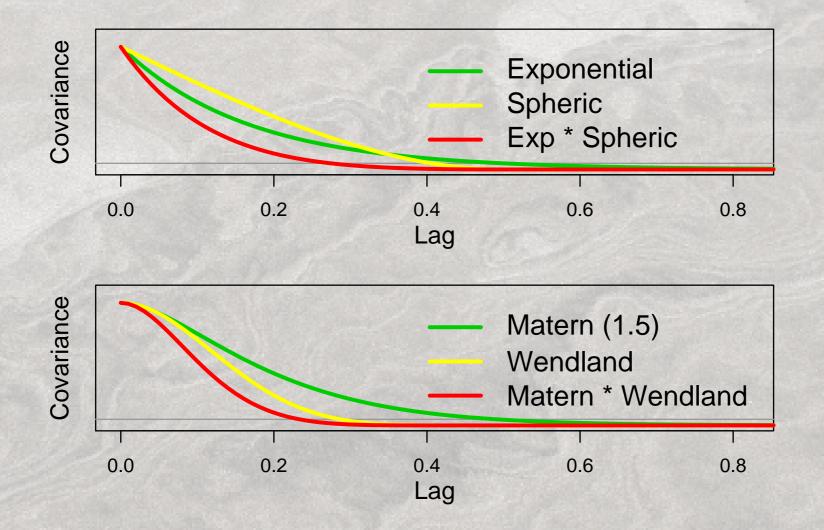
Examples



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Objective

For an isotropic and stationary process with Matérn covariance $C_0(h)$, find a taper $C_{\theta}(h)$, such that kriging with the product $C_0(h)C_{\theta}(h)$ is asymptotically optimal.

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For an isotropic and stationary process with Matérn covariance $C_0(h)$, find a taper $C_{\theta}(h)$, such that kriging with the product $C_0(h)C_{\theta}(h)$ is asymptotically optimal.

$$\frac{\mathsf{MSE}(\mathbf{x}^*, C_0 C_\theta)}{\mathsf{MSE}(\mathbf{x}^*, C_0)} \to 1$$

 $\frac{\varrho(\mathbf{x}^*, C_0 C_\theta)}{\mathsf{MSE}(\mathbf{x}^*, C_0)} \to \gamma$ $\varrho(\mathbf{x}^*, C) = C(0) - \mathbf{c}^{*\mathsf{T}} \mathbf{C}^{-1} \mathbf{c}^*$

Misspecified Covariances

In a series of (Annals) papers, Stein gives asymptotic results for misspecified covariances.

Under appropriate conditions, tapering is a form of misspecification.

The taper has to be

- as differentiable at the origin as the original covariance
- more differentiable throughout the domain than at the origin



Tapering is an (asymptotically and computationally) efficient technique to create sparse covariance matrices.

Taper range can be justified by computing resources. However, 20– 30 locations within the taper range is often sufficient.

"Classical" tapers are:

• spherical:
$$C_{\theta}(h) = \left(1 - \frac{|h|}{\theta}\right)^2_+ \left(1 + \frac{|h|}{\theta}\right)$$

• Wendland-type: $C_{\theta}(h) = \left(1 - \frac{|h|}{\theta}\right)_{+}^{\ell+k}$ polynomial in $\frac{|h|}{\theta}$ of deg k

Positive Definite Matrices

A (large) covariance (often) appears in:

- drawing from a multivariate normal distribution
- calculating/maximizing the (log-)likelihood
- linear/quadratic discrimination analysis
- PCA, EOF, ...

But all boils down to solving a linear system and possibly calculating the determinant . . .

'Sparse PCA' is sparse in a different sense . . .



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- fields is not bound to a specific sparse matrix format
- All heavy lifting is done in mKrig Or Krig.engine.fixed
- For a specific sparse format, requires the methods: chol, backsolve, forwardsolve and diag as well as elementary matrix operations need to exist
- If available uses operators to handle diagonal matrices quickly
- \rightsquigarrow The covariance matrix has to stem from particular class.

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fields uses spam as default package!

Example mKrig

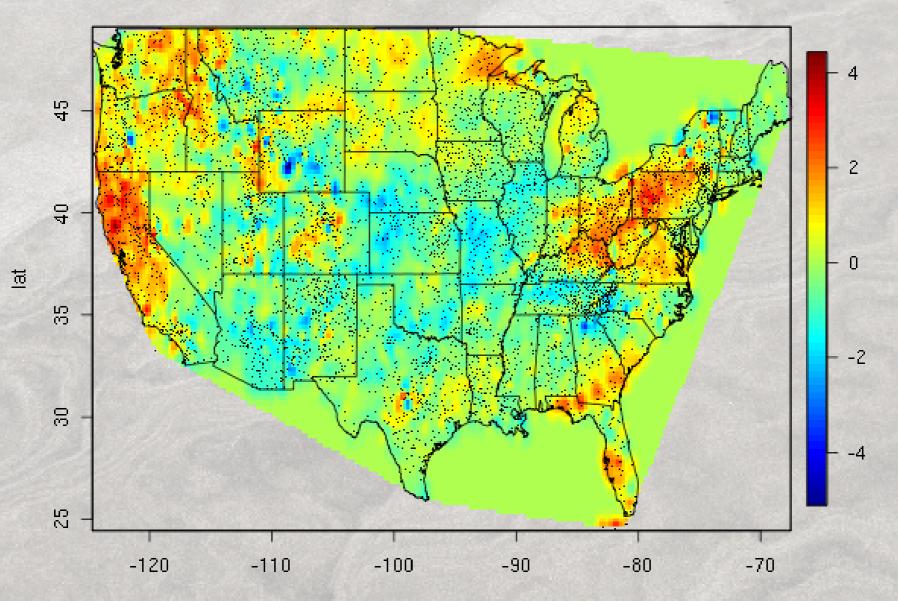
With appropriate covariance function:

```
R> x <- USprecip[ precipsubset, 1:2] # locations
R> Y <- USprecip[ precipsubset, 4] # anomaly</pre>
```

R> out <- mKrig(x,Y, m=1, cov.function="wendland.cov",theta=1.5)

```
R> out.p <- predict.surface( out, nx=220, ny=120)
R> surface(out.p, type='I')
R> US(add=T)
R> points(x,pch='.')
```

Example mKrig



Example Krig

R> out <- Krig(x,Y, m=1, cov.function="wendland.cov",theta=1.5, + lambda=0)

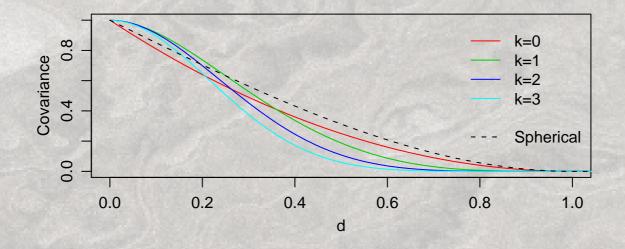
R> out.q <- predict.surface(out, nx=220, ny=120)

R> sum((out.q\$z-out.p\$z)^2, na.rm=T)
[1] 1.616783e-20

Krig/predict is slower (here 2.1/3.7 vs 10.4/3.9 seconds).

Wendland family

wendland.cov (based on Wendland) produces a spam matrix. All matrix functions are appropriately overloaded ...



To create sparse covariance matrices based on other covariance functions, use wendland.cov as skeleton.

Tapering can be performed with stationary.taper.cov. Arguments are (selection):

```
Covariance = "Exponential"
```

```
Taper = "Wendland"
```

Taper.args = NULL: arguments for the taper function

Dist.args = NULL: arguments passed to nearest.dist

... : arguments passed to covariance function

All arguments can also be passed from mKrig/Krig

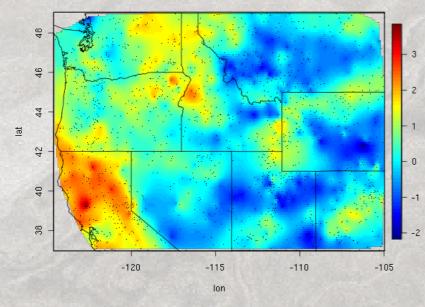
Compare the predicted surfaces without and with tapering:

```
R> out1 <- mKrig( xr,Yr, m=1, theta=1.5) )
R> out1.p <- predict.surface( out1, nx=220, ny=120) )</pre>
```

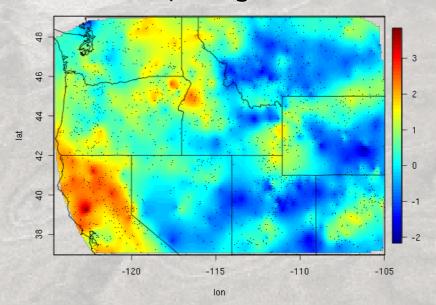
```
R> out2 <- mKrig( xr,Yr, m=1, theta=1.5,
+ cov.function="stationary.taper.cov",
+ Taper.args = list(k=0, theta=3)))
R> out2.p <- predict.surface( out2, nx=220, ny=120))</pre>
```

(timing yields 4/22 and 1/9 seconds)

Exponential covariance

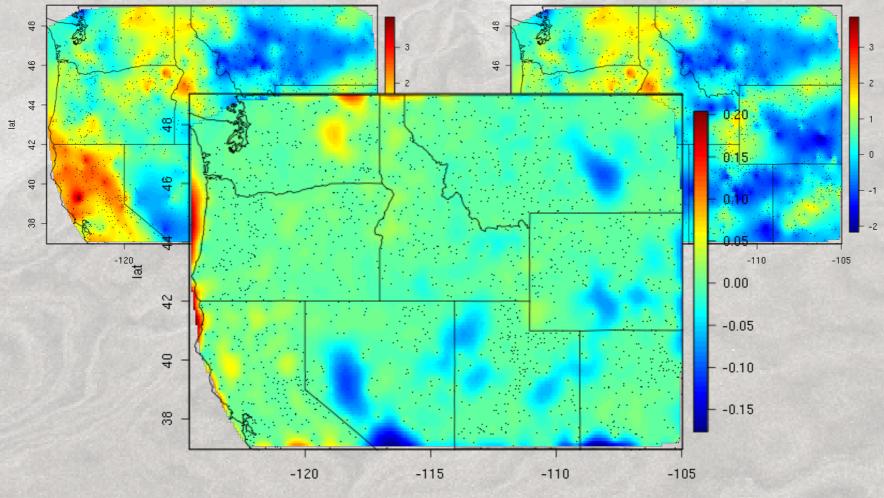


and with tapering



Exponential covariance

and with tapering



lon



The following arguments of mKrig/Krig are linked to spam:

Dist.args: arguments passed to nearest.dist

chol.args: arguments passed to chol

Use their help for fine tuning.

predict.se.Krig, predict.surface.se.Krig are very inefficient because nrow(x) equations need to be solved.

How Big is Big?

Upper limit to create a large matrix is the minimum of:

- (1) available memory (machine and OS/shell dependent)Error: 'cannot allocate vector of size'
- (2) addressing capacity $(2^{31} 1)$ Error: 'cannot allocate vector of length'

However, R is based on passing by value, calls create local copies (often 3–4 times the space of the object is used).

R> help("Memory-limits")

And Beyond?

Parallelization: nws, snow, Rmpi, ...

Memory "Outsourcing": Matrices are not (entirely) kept in memory: ff, filehash, biglm, ...

(S+ has the library BufferedMatrix)

References

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Furrer, R. and Sain, S. R. (2008). spam: A Sparse Matrix R Package with Emphasis on MCMC Methods for Gaussian Markov Random Fields. Submitted.