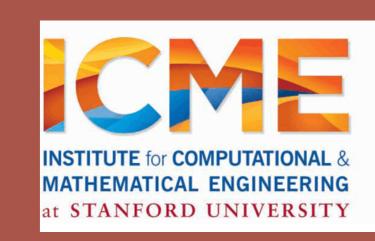
Numerical linear algebra and optimization tools for bioinformatics

Nick Henderson, Ding Ma, Yuekai Sun, and Michael Saunders

Institute for Computational and Mathematical Engineering, Stanford University



Bioinformatics problems

- Conservation analysis
 Find subgroups conserved by biological systems
- Flux balance analysis (FBA)
 Find fluxes in multiscale metabolic networks

Numerical software

- Sparse matrix factorization

 LUSOL S = LDU with L and possibly U well-conditioned SPQR (Davis 2011) SP = QR or $S^TP = QR$
- ► Sparse linear equations and least squares MINRES, MINRES-QLP

MINRES, MINRES-QLP Symmetric Ax = bLSQR, LSMR, LSRN Ax = b, min ||Ax - b||

- ► LP
 MINOS, SQOPT, CPLEX, Gurobi, Mosek, Soplex, Xpress, . . .
- NLP
 MINOS, SNOPT, PDCO, CONOPT, IPOPT, Knitro, ...
- Multiscale LP and NLP quad-MINOS

Conservation analysis S = stoichiometric matrix

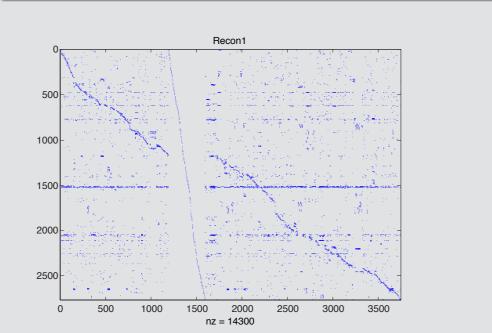
Reduces to finding rank(S) and null(S^T):

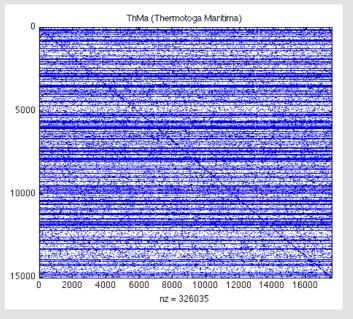
$$0 = \frac{d}{dt} \{z^T c(t)\} = z^T \frac{dc(t)}{dt} = z^T Sv(t)$$

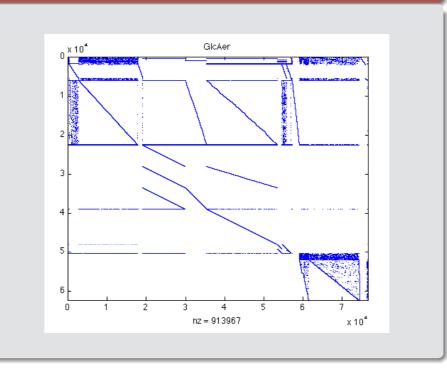
z is a conserved moiety (group of chemical species) Need $S^{T}z = 0$

- Partition rows of S into dependent and independent species: $PS = \begin{pmatrix} S_{\text{ind}} \\ S_{\text{dep}} \end{pmatrix}$
- Compute *link matrix* N that describes the relations among concentrations of dependent/independent species: $S = NS_{ind}$

Models 9, 10, 11







Davis (2011)

 $P_1SP_2 = LDU$

rank(S) by QR SPQR

Householder QR factorization SP = QR

- $P = \text{col perm } Q^TQ = I R \text{ diagonal } \text{rank}(S) = \text{rank}(R)$
- Nearly as reliable as SVD
- Dense QR Vallabhajosyula, Chickarmane, Sauro (2006)
- Sparse QR (SPQR) now available

model 9 (Recon1) 2800 × 3700 0.1 secs model 10 (ThMa) 15000 × 18000 2.5 secs model 11 (GlcAer) 62000 × 77000 0.2 secs(!)

rank(S) by LDU

LUSOL

Sparse LU with Threshold Rook Pivoting

▶ $P_1, P_2 = \text{perms}$ $D \text{ diagonal rank}(S) \approx \text{rank}(D)$ L, U well-conditioned

- ▶ $L_{ii} = U_{ii} = 1$, $|L_{ij}|$ and $|U_{ij}| \le 2.0$ (say)
- LUSOL: Main engine in optimizers MINOS, SQOPT, SNOPT
- ▶ model 9 (Recon1)
 2800 × 3700
 0.1 secs
 model 10 (ThMa)
 model 11 (GlcAer)
 15000 × 18000
 4.1 secs
 62000 × 77000
 186 secs

SVD, SPQR, LUSOL on stoichiometric S

SVD and sparse QR

ThMa | 15024 17582

GlcAer | 62212 76664

1	m n	. 1	rank(S)			time	<u> </u>
model		SVD	SPQR nnz(S) nnz(Q)	nnz(R)	SVD	SPQR
Recon1 27	66 3742	2674	2674 1430	0 2750	21093	17.5	0.1
ThMa 150	24 17582	14983	14983 32603	5 844096	10595016	11hrs	2.5
GlcAer 622	12 76664	?	62182 91396	7 1287	916600	infty	0.2

LUSOL with Threshold Rook Pivoting: S = LDU, $|L_{ij}|$, $|U_{ij}| \le 2.0$ model | m n rank(S) | nnz(S) nnz(L) nnz(U) | time

LUSOL with Threshold Partial Pivoting: S = LU, $|L_{ij}| \leq 2.0$

62182 | 913967

	rank(S) nnz(S) 	nnz(L) 	nnz(U) 	time
Recon1	2674 14300	721	13585	0.1
ThMa	14983 326035	7779	324483	0.2
GlcAer	62182 913967	533	913781	0.4

LUSOL with TPP finds rank(S) efficiently, and also S_{ind} , S_{dep}

Multiscale FBA quad-precision MINOS

Step 1: double-MINOS, cold start, scaling

Problem name	GlcAerWT	EXIT the problem is infeasible			
No. of iterations	62856	Objective value	-2.4489880182E+04		
No. of infeasibilities	41	Sum of infeas	1.5279397622E+01		
No. of degenerate step	s 33214	Percentage	52.84		
Max x (scaled)	68680 4.4E+06	Max pi (scaled)	54979 1.4E+02		
Max x	62607 1.0E+09	Max pi	25539 3.0E+02		
Max Prim inf(scaled)	134382 6.5E+00	Max Dual inf(scaled)	70913 1.2E-05		
Max Primal infeas	129844 1.0E+04	Max Dual infeas	23177 2.0E-05		
Time for solving probl	em 9707.28	seconds			

Step 2: quad-MINOS, warm start, scaling

Prob	olem nam	e	(GlcAerWT	EXI	Γ (optimal solu	tion found	£
No.	of iter	ations		5580	Obje	ective	e value	-7.0382449)681E+05
No.	of dege	nerate steps		4072	Per	centag	ge		72.97
Max	X	(scaled)	59440	3.7E+00	Max	pi	(scaled)	40165	8.1E+11
Max	X		61436	6.3E+07	Max	pi		25539	2.4E+07
Max	Prim in	f(scaled)	83602	3.8E-16	Max	Dual	<pre>inf(scaled)</pre>	11436	4.4E-19
Max	Primal	infeas	83602	1.7E-07	Max	Dual	infeas	24941	8.6E-27
Time	e for so	lving problem	m	3995.58	secon	ds			

Step 3: quad-MINOS, warm start, no scaling

Problem name	GlcAerWT	EXIT optimal	solution found
No. of iterations	4	Objective value	-7.0382449681E+05
No. of degenerate steps	0	Percentage	0.00
Max x	61436 6.3E+07	Max pi	25539 2.4E+07
Max Primal infeas	142960 1.3E-19	Max Dual infeas	6267 9.4E-22
Time for solving proble	m 60.07	seconds	

References

- ► Davis (2011). Algorithm 915, SuiteSparseQR: Multifrontal multithreaded rank-revealing sparse QR factorization, *ACM TOMS* 38(1), 8:1–8:22
- ► Fleming, Maes, Saunders, Ye, and Palsson (2012)., A variational principle for computing nonequilibrium fluxes and potentials in genome-scale biochemical networks, *J. Theor. Biol.* 292:71–77
- ► Gill, Murray, and Saunders (2005).

 SNOPT: An SQP algorithm for large-scale constrained optimization,

 SIAM Review 47(1):99–131 (includes description of LUSOL)
- ► Henderson (2013). Matlab interface to LUSOL, https://github.com/nwh/lusol
- Henderson, Ma, Saunders, Sun, Fleming, and Thiele (2014).
 Conservation analysis of genome-scale biochemical networks,
 Bioinformatics, in preparation
- ► Ma and Saunders (2014). Solving multiscale linear programs using the simplex method in quadruple precision, Springer, to appear
- ▶ Vallabhajosyula, Chickarmane, and Sauro (2006). Conservation analysis of large biochemical networks, *Bioinform.* 22(3), 346–353
- http://web.stanford.edu/group/SOL/multiscale/ http://web.stanford.edu/group/SOL/software.html

Funding

DOE DE-FG02-09ER25917 NIH U01-GM102098



