

# Ecological Network Analysis Tutorial

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SYSTEMS ECOLOGY AND ECOINFORMATICS LABORATORY  
 @ UNIVERSITY OF NORTH CAROLINA WILMINGTON

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## ENA Workflow - Generalized

Data Theory  
Obs. Exp.

Trace conserved currency (energy, C, N, P)

Analyses

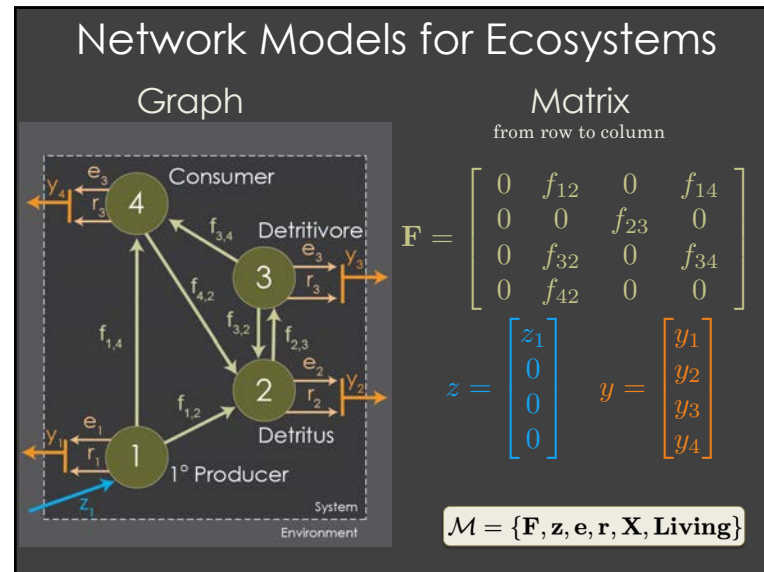
Knowledge, Insight, Understanding

**Model Construction**

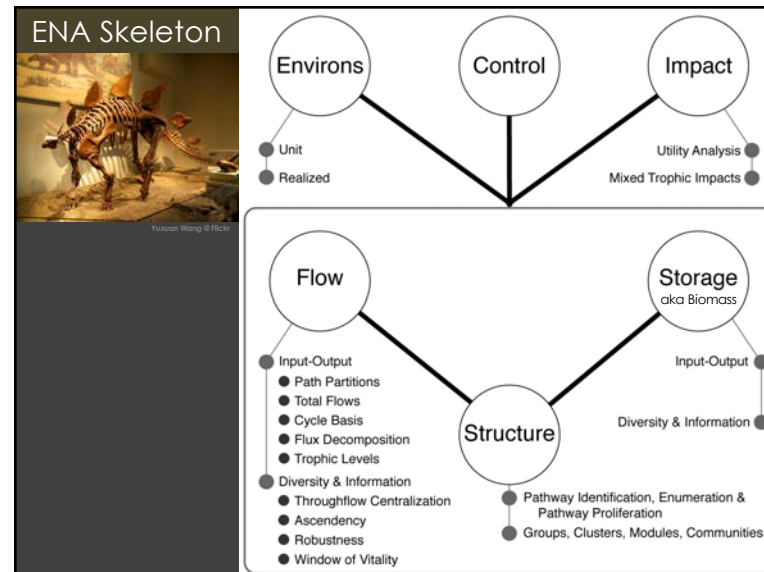
Phenomenological, Budget, Simulation, LIM

**Software Tools**

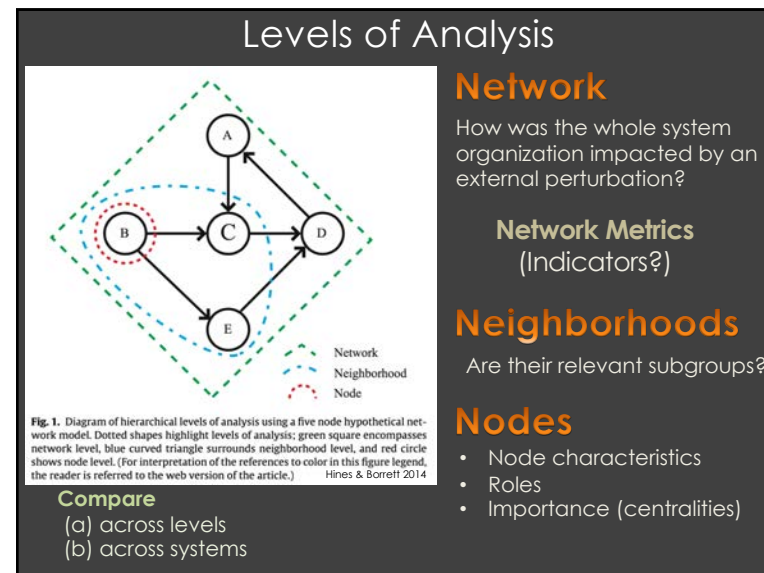
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# Introduction to

Tool for Science & Innovation

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### enaR Software Design Objectives

Tools for Science & Innovation

**Collect**

**Available**


**Extensible**

**Connect**

Algorithms from both  
Ulanowicz and Patten ENA Schools

Illustrate some *enaR*  
functionality

Emphasize how it facilitates  
system comparisons



Additional *network* tools

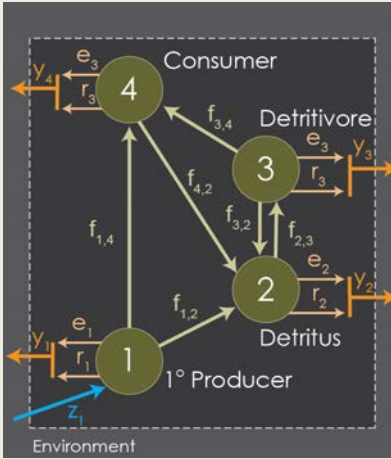
- Social network analysis
- ERGM

Existing R tools

- **Network** (Butts 2008)
- **sna** (Butts 2008)
- **Statnet** (Handcock, 2008)

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### Data Input: Model Data



**Node Names**

**F**: Flows from *i* to *j*

**z**: Inputs

**e**: Exports

**r**: Respirations

**y**: Outputs (e + r)

**X**: storage or biomass

Living: logical (T or F)

Data stored as a *network* object (Butts 2008)

**pack()** and **unpack()**

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Collect
Data Input: read.x

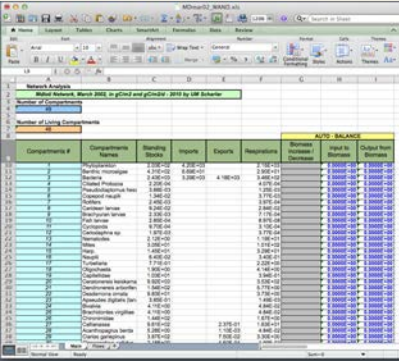
**NETWRK 4.2 - SCOR**  
read.scor()

```

SYSTEM REF: DAMEPATTEN, MAR. ECOL. PROG. SER. 5:115; KCAL/MZ/D; S&B-FIXED;
6 5
Filter: Feeders
Microbions
Meloforms
Deposit: Feeders
Predators
Deposited: Detritus
1 2.0000e+03
2 2.4321e+00
3 2.4321e+01
4 1.6274e+01
5 6.9237e+01
6 1.0000e+03
-1
1 4.1470e+1 \IMPORTS
-1
1 \EXPORTS
-1
1 \RESPIRATION
1 2.5166e+01
2 5.7600e+00
3 3.5794e+00
4 4.3030e-01
5 3.5940e-01
6 6.1793e+00
-1
1 \FLOWS
6 2 8.1721e+00
2 3 1.2064e+00
6 3 7.2745e+00
2 4 1.2064e+00
3 4 6.0090e-01
6 4 6.4310e-01
1 5 5.1350e-01
4 5 1.7210e-01
1 6 1.5791e+01
3 6 4.2403e+00
4 6 1.3070e+00
5 6 3.2500e-01
-1 -1
                
```

Plain text file

**WAND**  
read.wand()




read.enam(), read.nea(), read.EcoNet()

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## Main ENA functions

**Table 2. Ecosystem Network Analysis functions in enaR**

Function	Description	Example Reference
enaStructure	ENA Structural analysis returns the adjacency matrix and multiple common descriptive statistics (e.g. number of nodes, connectance, pathway proliferation rate)	Borrett, Fath & Patten (2007)
enaFlow	Calculates node throughflow and input- and output-oriented direct and integral flow intensity matrices. It also returns multiple whole-network descriptive statistics including total system throughflow, Finn Cycling Index, and average path length	Finn (1976)
enaAscendency	Performs ascendency analysis on the model flows and returns whole-network statistics including the average mutual information, ascendency, capacity and overhead	Ulanowicz (1997)
enaStorage	ENA Storage analysis considers how the model fluxes generate the node storage (e.g. biomass) in the system. This function returns the input- and output-oriented direct and integral storage matrices	Matis & Patten (1981)
enaUtility	ENA Utility analysis investigates the direct relationships among the network nodes as well as the integral relationships when all of the indirect interactions are also considered	Patten (1991)
enaMTI	Mixed trophic impacts assesses the net relationships among species in a food web	Ulanowicz & Puccia (1990)
enaControl	Control analysis determines the relative control one node exerts on another through the transaction network	Dame & Patten (1981)
enaEnviron	Returns the <i>n</i> unit and <i>n</i> realized input and output environs of the model	Patten (1978)



**Methods in Ecology and Evolution**  
Stuart R. Borrett<sup>1,2</sup> and Matthew K. Lu<sup>2,3</sup>

Functions require model input as network data object (e.g., created with pack())

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## Selected Other Functions

**Table 3.** Selected enaR auxiliary functions and analyses

Function	Description	Example Reference
<b>Specialty Analyses</b>		
enaAll	Runs all of the primary ENA algorithms	None
get.ns	Returns the whole-network statistics from enaStructure, enaFlow, enaAscendency, enaStorage and enaUtility	None
eigenCentrality	Calculates the average eigenvalue centrality for any input matrix	Fann & Borrett (2012)
environCentrality	Returns the input, output and average environ centralities for a matrix	Fann & Borrett (2012)
TET	Returns the total environ throughflows	Whipple <i>et al.</i> (2007)
TES	Returns the total environ storages	Matis & Patten (1981)
<b>Auxiliary Functions</b>		
get.orient	Determine the orientation of the results (row-to-column vs. School)	None
set.orient	Set the orientation of the results (row-to-column vs. School)	None
mExp	This function lets users calculate matrix exponents	None

Currently more than 45 functions in the package

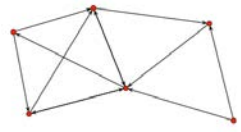
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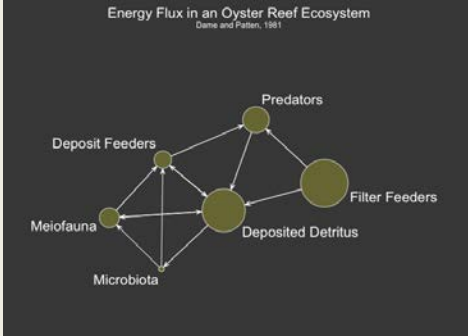
Connect
Visualization

Simple Plot

```
> data(oyster)
> plot(oyster)
```

Fancier Plot

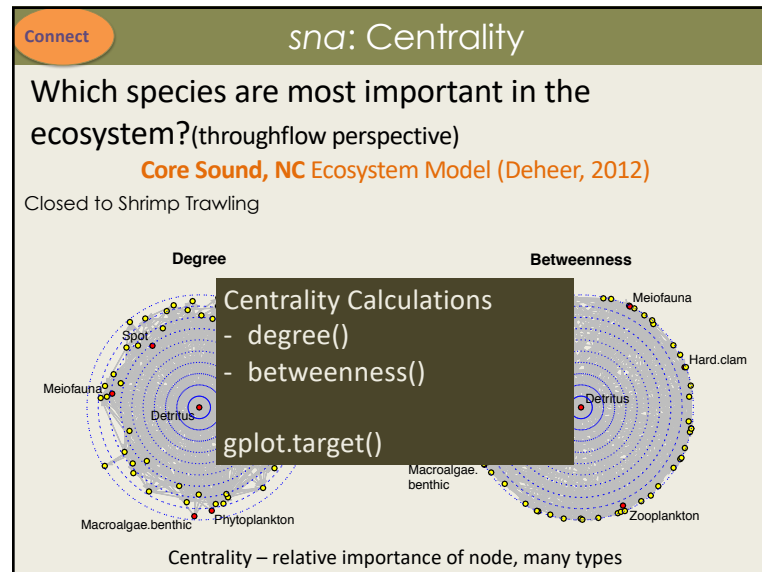




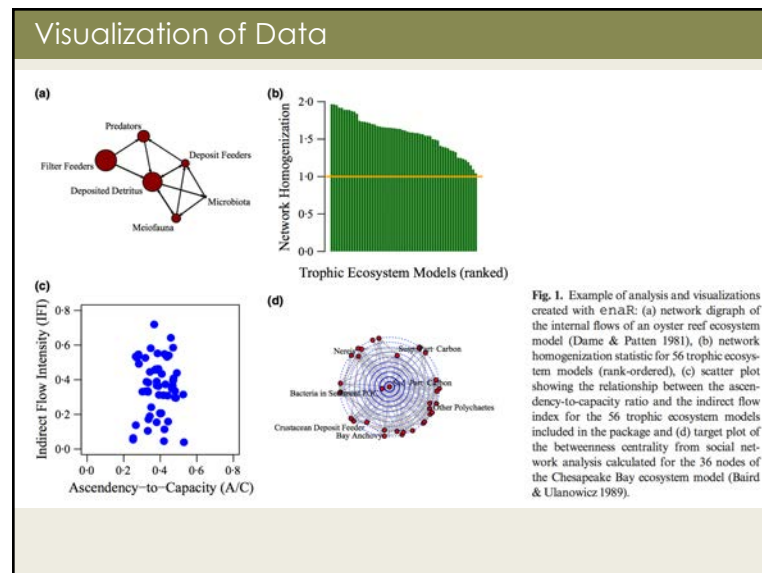
**Internal Fluxes**

Borrett, 2013

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**Model Library** Collect Extend

104 Empirically-based ecosystem models (previously published)

- ▲ 59 Trophic networks (food-web core, carbon or energy)
- 43 Biogeochemical cycling networks (i.e., nitrogen, phosphorus)
- 2 urban, socio-economic

...and Growing

Thanks to many contributors

Source: ERI, Chlo.org, HERE, SimTom, Intermag, Inademant P Corp., GEBCO, USGS, FAO, NPS, NRCAN, GEBCO, IGN, France, Survey, Esri, Japan, METI, Esri/China (Hong Kong), Swisstopo, and the GIS User Community

**Library enables new, comparative, and meta-analyses.**  
**Testing data for new theoretical developments**

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**Where to get help**

**Introduction: MEE**

**Methods in Ecology and Evolution**

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**enAR: An R package for Ecosystem Network Analysis**

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**Summary**

1. Network analysis is a useful approach for investigating complex and relational data in many fields including ecology, molecular and evolutionary biology.

2. Here, we introduce enAR, an R package for Ecosystem Network Analysis (ENA) as an analytical tool well suited to ecosystem ecology with over 30 years of development that examines the structure and dynamics of matter and energy movement between discrete ecological compartments (e.g. a food web).

3. In addition to describing the primary functionality of the package, we highlight several features including a library of 100 empirical ecosystem models, the ability to analyze and compare multiple models simultaneously, and connections to other ecological network analysis tools.

**Keywords:** network analysis, ecosystems, open-source software, network ecosystem analysis, ascendancy, input-output analysis, food web, Ecopath, NETWORK, WAND

<http://onlinelibrary.wiley.com/doi/10.1111/2041-210X.12282/abstract>

**Vignette**

**Ecosystem Network Analysis with R: A guide for using enAR**

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August 4, 2015

**Abstract**

Ecosystem Network Analysis (ENA) provides a framework for investigating the structure, function and dynamics of ecological systems, primarily ecosystem models with physically conserved units. This paper documents the enAR R package that codifies the core ENA functions including those developed by the Ulmerwitz and Patten schools. We detail how to use the primary functions for the analysis of single models as well as simultaneous, synthetic analysis of multiple ecosystem models.

**Keywords:** ecology, ENA, ecosystems, network ecology, food web, network ecosystem analysis, species interactions, networks, R

**1 Introduction**

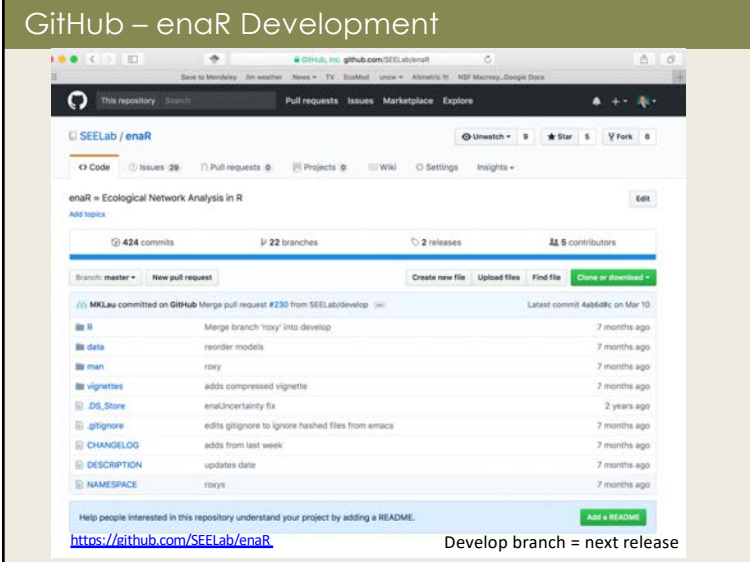
Network models have provided an in-road to a variety of complex systems (Barabási, 2012; Newman et al., 2006; Newman, 2001; Wasserman and Faust, 1994; Watts and Strogatz, 1998), and although the network approach has deep roots (Newman et al., 2006), its use has been expanding rapidly in a variety of disciplines including ecology (Borrett et al., 2014; Iago et al., 2009) and investigators are recently building a science of networks (Brandes et al., 2013; National Research Council, Committee on Network

<https://github.com/SEELab/enAR/blob/develop/vignettes/enAR-vignette.pdf>

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## GitHub – enaR Development



enaR = Ecological Network Analysis in R

424 commits 22 branches 2 releases 5 contributors

Branch: master - New pull request

Latest commit 4ab6dc on Mar 10

File	Commit Message	Time Ago
R	Merge branch 'roxy' into develop	7 months ago
data	reorder models	7 months ago
man	roxy	7 months ago
vignettes	adds compressed vignette	7 months ago
_DS_Store	enaUncertainty fix	2 years ago
.gitignore	edits .gitignore to ignore hashed files from emacs	7 months ago
CHANGELOG	adds from last week	7 months ago
DESCRIPTION	updates date	7 months ago
NAMESPACE	roxy's	7 months ago

<https://github.com/SEELab/enaR> Develop branch = next release

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# 5 ENA Exercises

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### Exercise #1 – Getting Started with enaR Activity

Download script from tutorial website SC Oyster Reef Model

1. Open R
2. Load enaR library
3. Load model from model data(oyster)
4. Examine model properties
5. Plot model
6. Apply selected analyses

**Challenge Problems -- Test Your Understanding**

1. Find the **number of nodes** in the *Swartkops Estuary* model
2. Create a barplot of the **effective trophic levels** of the *Bothnian Sea* model
3. Find the **A/C** and **FCI** of the *Florida Bay (wet)* model

The diagram shows the following energy flows (values in parentheses):

- Filter Feeders (Node 1): 25.1646 (input), 0.3594 (output to Predators)
- Predators (Node 5): 0.3594 (input from Filter Feeders), 0.4303 (output to Deposit Feeders)
- Deposited Detritus (Node 6): 6.1759 (input), 5.7600 (output to Microbiota)
- Deposit Feeders (Node 4): 0.4303 (input from Predators), 3.5974 (output to Meiofauna)
- Microbiota (Node 2): 5.7600 (input from Deposited Detritus), 3.5974 (output to Meiofauna)
- Meiofauna (Node 3): 3.5974 (input from both Deposited Detritus and Microbiota)

Dame and Patten 1981

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### Exercise #2 – Loading a model into R Activity

Method 1: Manual using pack()

## Micro-modeling

$M = \{F, z, e, r, X, \text{Living}\}$

1. Draw a network model as a flow diagram with 3 nodes
2. Create objects for each of your model components
3. "Pack" your model into a network object
4. "Unpack" your network and look at the parts
5. Plot
6. Investigate some network metric you're interested in

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## Exercise #2 – Loading a model into R

Activity

Method 1: Manual using pack()

## Micro-modeling

M = {F, z, e, r, X, Livin...

1. Draw a network
2. Create object
3. "Pack" your
4. "Unpack" your
5. Plot
6. Investigate

## Micro-modeling (Solution 1)

```
library(enaR)
F <- c(0,5,0,
      0,0,1,
      0,0,0)
F <- matrix(F,nrow=3,byrow=TRUE)
z <- c(10,0,0)
e <- c(3,3,3)
r <- c(1,1,1)
X <- c(10,3,1)
liv <- c(TRUE,TRUE,FALSE)
toy <- pack(F,z,e,r,X,liv)
```

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## Exercise #3 – Comparing Models &amp; Batch Processing

Activity

Download script from tutorial website

1. Load enaR library
2. Load model from model library (troModels)
3. Use lapply() function to apply selected analyses to a list of models
4. Plot results

## Challenge Problems -- Test Your Understanding

1. Plot ID.F for troModels with n > 10
2. Find min, max, mean, and standard deviation of the troModels FCI
3. Look for correlations among selected indices by plotting FCI vs. A/C, IFI, synergism.F
4. Compare the TST and FCI of the two Crystal River Models

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