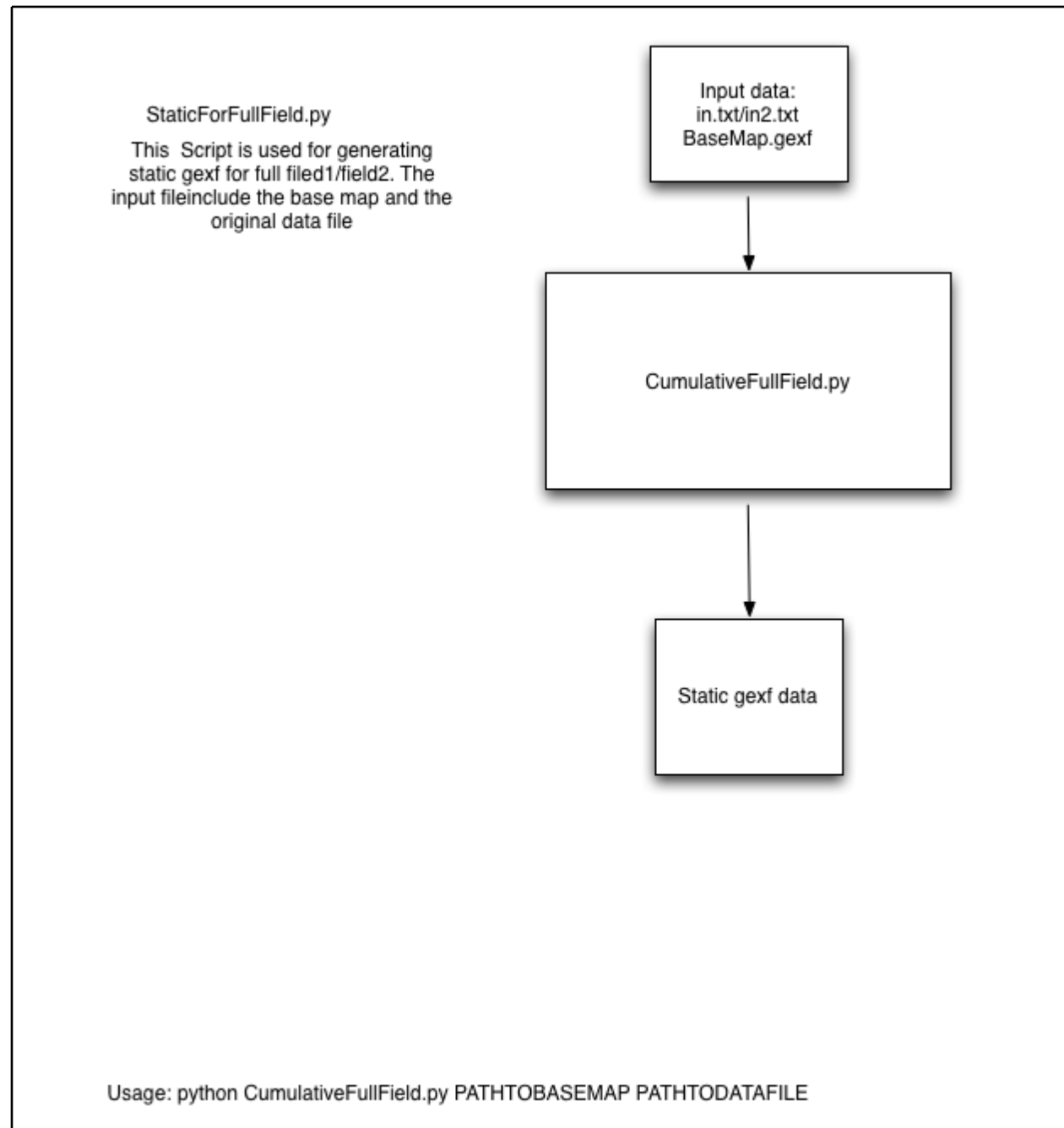


Appendix B



StaticForTopic.py

This Script is used for generating static gexf files for top topic areas filed1/field2. The input file include the base map and the original data file and the area-articleIDs pck file and the argument of filed number.

Input data:
in.txt/in2.txt
BaseMap.gexf
area-articleIDs.pck
1/2



CumulativeFullField.py



Static gexf files for
each top topic
area

Usage: python StaticForTopic.py PATHTOBASEMAP PATHTODATAFILE PATHTOarea-articleID.pck filed#

StaticForResearcher.py
This Script is used for generating static gexf for field1/field2 of highly productive researchers. The input file include the base map and the original data file and the authname-noderole.pck and authnames-articleIDs.pck

Input data:
in.txt/in2.txt
BaseMap.gexf
authname-
noderole.pck
authnames-
articleIDs.pck

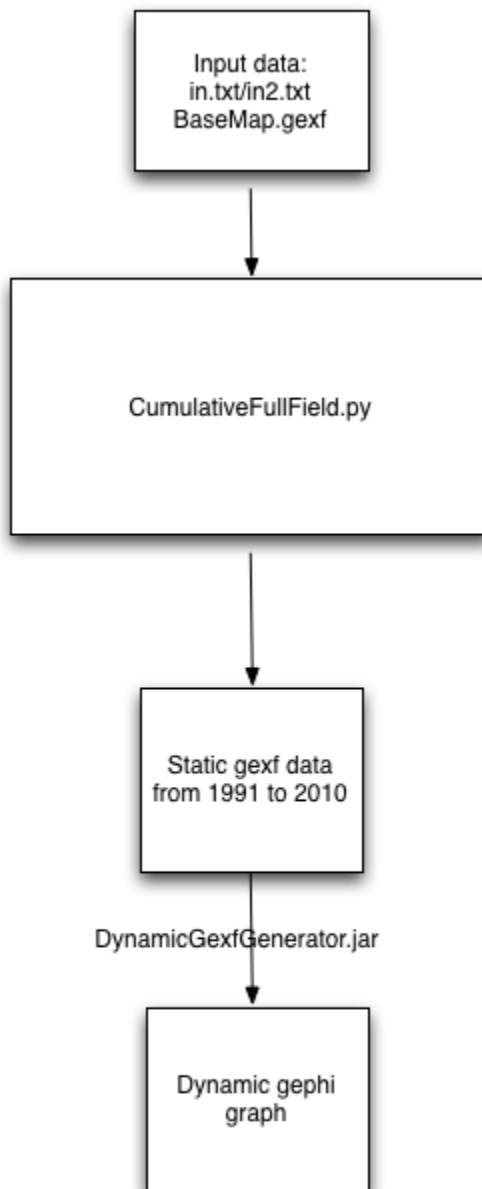
StaticForResearcher.py

Static gexf files for
top researchs



Cumulative FullField.py

This Script is used for generating static gexf files for cumulative time evolution. The input file include the base map and the original data file



Usage: `python CumulativeFullField.py PATHTOBASEMAP PATHTODATAFILE`

Put the jar file in the same directory as these static gexf file are.
`java -jar DynamicGexfGenerator.jar` ---> generate the final dynamic gexf file

CumulativeTopic.py

This Script is used for generating static gexf files for cumulative time evolution of top topic areas. The input file include the base map and the original data file and the area-articleIDs pck file and the argument of filed number.

Input data:
in.txt/in2.txt
BaseMap.gexf
area-articleIDs.pck
1/2

CumulativeTopic.py

Static gexf data
from 1991 to 2010

DynamicGexfGenerator.jar

Dynamic gephi
graph

Usage: python CumulativeFullField.py PATHTOBASEMAP PATHTODATAFILE PATHTOarea-articleID.pck filed#

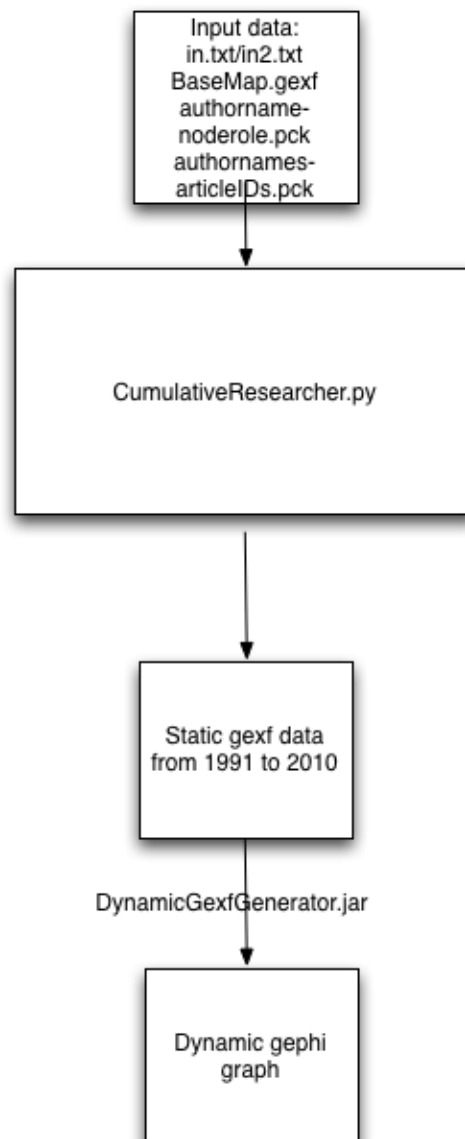
Put the jar file in the same directory as these static gexf file are.

java -jar DynamicGexfGenerator.jar top1 ---> generate the final dynamic gexf file for top 1 area

java -jar DynamicGexfGenerator.jar top2 ---> generate the final dynamic gexf file for top 2 area

CumulativeResearcher.py

This Script is used for generating static gexf files for cumulative time evolution of highly productive researchers. The input file include the base map and the original data file and the authorname-noderole.pck and authornames-articleIDs.pck



Usage: python CumulativeResearcher.py PATHTOBASEMAP PATHTODATAFILE PATHTOauthorname-noderole.pck PATHTOauthornames-articleIDs.pck

Put the jar file in the same directory as these static gexf file are.

java -jar DynamicGexfGenerator.jar author1 ---> generate the final dynamic gexf file for top 1 author

java -jar DynamicGexfGenerator.jar author2 ---> generate the final dynamic gexf file for top 2 author

...

TimeSlideForFull.py
This Script is used for generating static gexf files for 2 -year-window. The input file include the base map and the original data file

Input data:
in.txt/in2.txt
BaseMap.gexf

TimeSlideForFull.py

Static gexf files for
each two years

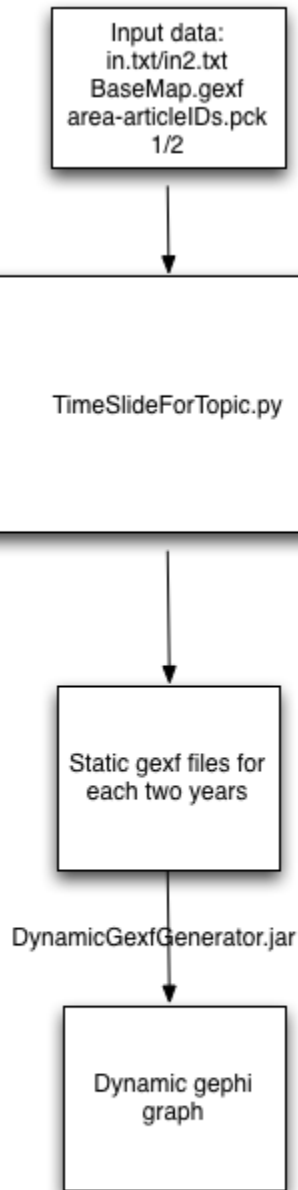
DynamicGexfGenerator.jar

Dynamic gephi
graph

Usage: python TimeSlideForFull.py PATHTOBASEMAP PATHTODATAFILE

Put the jar file in the same directory as these static gexf file are.
java -jar DynamicGexfGenerator.jar ---> generate the final dynamic gexf file

TimeSlideForTopic.py
This Script is used for generating static gexf files for 2-year-window of top topic areas. The input file include the base map and the original data file and the area-articleIDs pck file and the argument of filed number.



Usage: `python TimeSlideForTopic.py PATHTOBASEMAP PATHTODATAFILE PATHTOarea-articleID.pck filed#`

Put the jar file in the same directory as these static gexf file are.

`java -jar DynamicGexfGenerator.jar top1` ---> generate the final dynamic gexf file for top 1 area

`java -jar DynamicGexfGenerator.jar top2` ---> generate the final dynamic gexf file for top 2 area

TimeSlideForResearcher.py

This Script is used for generating static gexf files for 2 year window of highly productive researchers. The input file include the base map and the original data file and the authname-noderole.pck and authnames-articleIDs.pck

Input data:
in.txt/in2.txt
BaseMap.gexf
authname-
noderole.pck
authnames-
articleIDs.pck

TimeSlideForResearcher.py

Static gexf files for
each two years

DynamicGexfGenerator.jar

Dynamic gephi
graph

Usage: python TimeSlideForResearcher.py PATHTOBASEMAP PATHTODATAFILE
PATHTOauthname-noderole.pck PATHTOauthnames-articleIDs.pck

Put the jar file in the same directory as these static gexf file are.

java -jar DynamicGexfGenerator.jar author1 ---> generate the final dynamic gexf file for top 1 author
java -jar DynamicGexfGenerator.jar author2 ---> generate the final dynamic gexf file for top 2 author

...

DiversityForFull.py(has dependence with priodict.py)

This Script is used for generating diversity csv files for entire fields. The input files include the base map and edges.txt and the original data file and the field#

Input data:
BaseMap.gexf
in.txt/in2.txt
edges.txt
2

DiversityForFull.py

Input data:
BaseMap.gexf
in.txt/in2.txt
edges.txt
1

DiversityForFull.py

CSV files for field
1 and 2

CompareField1and2.R

diversity plots

Usage: python DiversityForFull.py PATHTOBASEMAP PATHTODATAFILE PATHTOedges.txt FIELD#

The CSV files should be in the same folder as R file is.

DiversityForMajorField1.py(has dependence with priodict.py)

This Script is used for generating diversity csv files for entire fields. The input files include the base map and edges.txt and the original data file and the field#

Input data:
BaseMap.gexf
in.txt
edges.txt
area-articleID.pck

DiversityForMajorField1

CSV files for field1

CompareField1MajorTopic.R

diversity plots

Usage: python DiversityForMajorField1 PATHTOBASEMAP PATHTODATAFILE PATHTOedges.txt
PATHTarea-articleID.pck

The CSV files should be in the same folder as R file is.

DiversityForMajorField2.py(has dependence with priodict.py)

This Script is used for generating diversity csv files for entire fields. The input files include the base map and edges.txt and the original data file and the field#

Input data:
BaseMap.gexf
in.txt
edges.txt
area-articleID.pck

DiversityForMajorField2

CSV files for field2

CompareField1MajorTopic.R

diversity plots

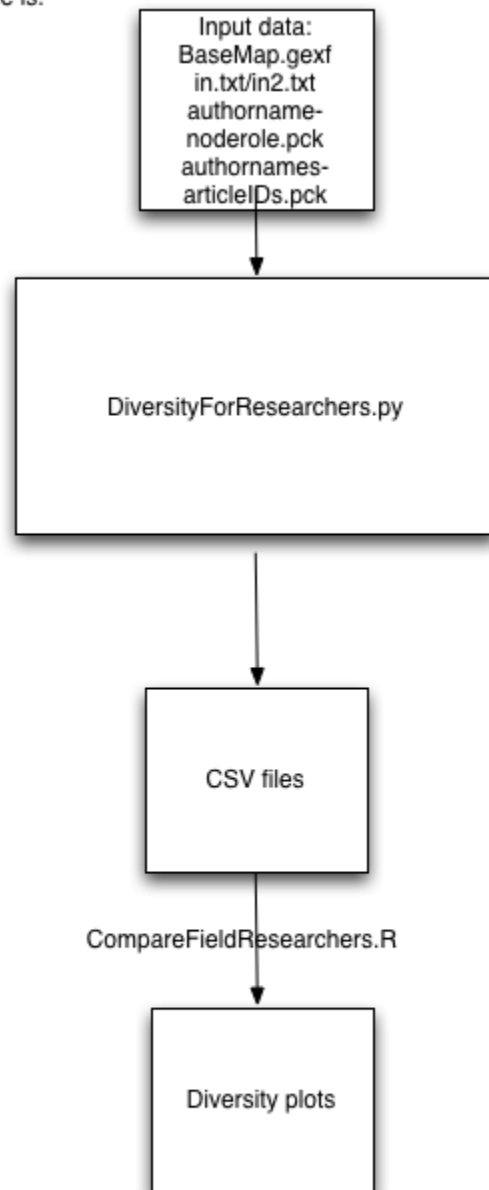
Usage: python DiversityForMajorField1 PATHTOBASEMAP PATHTODATAFILE PATHTOedges.txt
PATHTarea-articleID.pck

The CSV files should be in the same folder as R file is.

The CSV files should be in the same folder as R file is.

DiversityForResearchers.py

This Script is used for generating diversity csv files for top researchers. The input file include the base map and the original data file and the authorname-noderole.pck and authornames-articleIDs.pck



Usage: python DiversityForMajorField1 PATHTOBASEMAP PATHTODATAFILE PATHTOedges.txt
PATHTOauthorname-noderole.pck PATHTOauthornames-articleIDs.pck

The CSV files should be in the same folder as R file is.