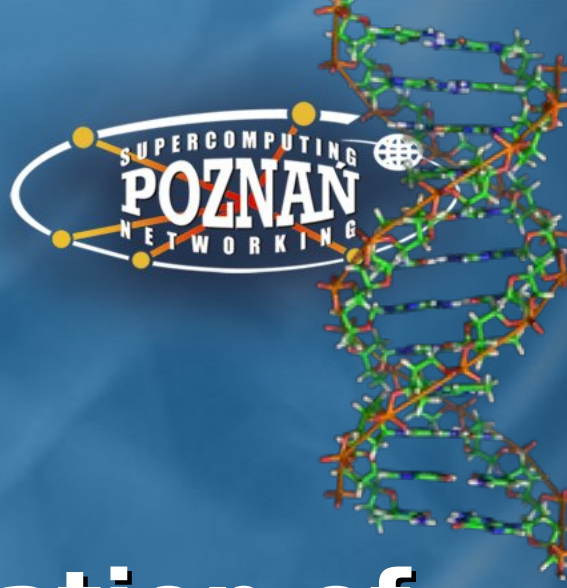
POZNAŃ
SUPERCOMPUTING AND
NETWORKING
CENTER



Discovery and visualization of network protocols with tools for biological sequence alignment

Mateusz Drygas, ***Tomasz Nowak***

PSNC Security Team

Me and my team

- Programmer and software security analyst
- PSNC Security Team
  - within Poznań Supercomputing and Networking Center
  - affiliated with Institute of Bioorganic Chemistry of PAS
  - operator of Poznań MAN and Polish NREN - PIONIER
- Independent security research –
  e.g. Browsers security tests (2010)
- http://security.psnc.pl

Agenda

- Motivation
- Inspiration
- Exploitation
  - Packets as proteins
  - Clustering for “packet families”
  - Finding patterns
  - Fuzzing

Motivation (1)

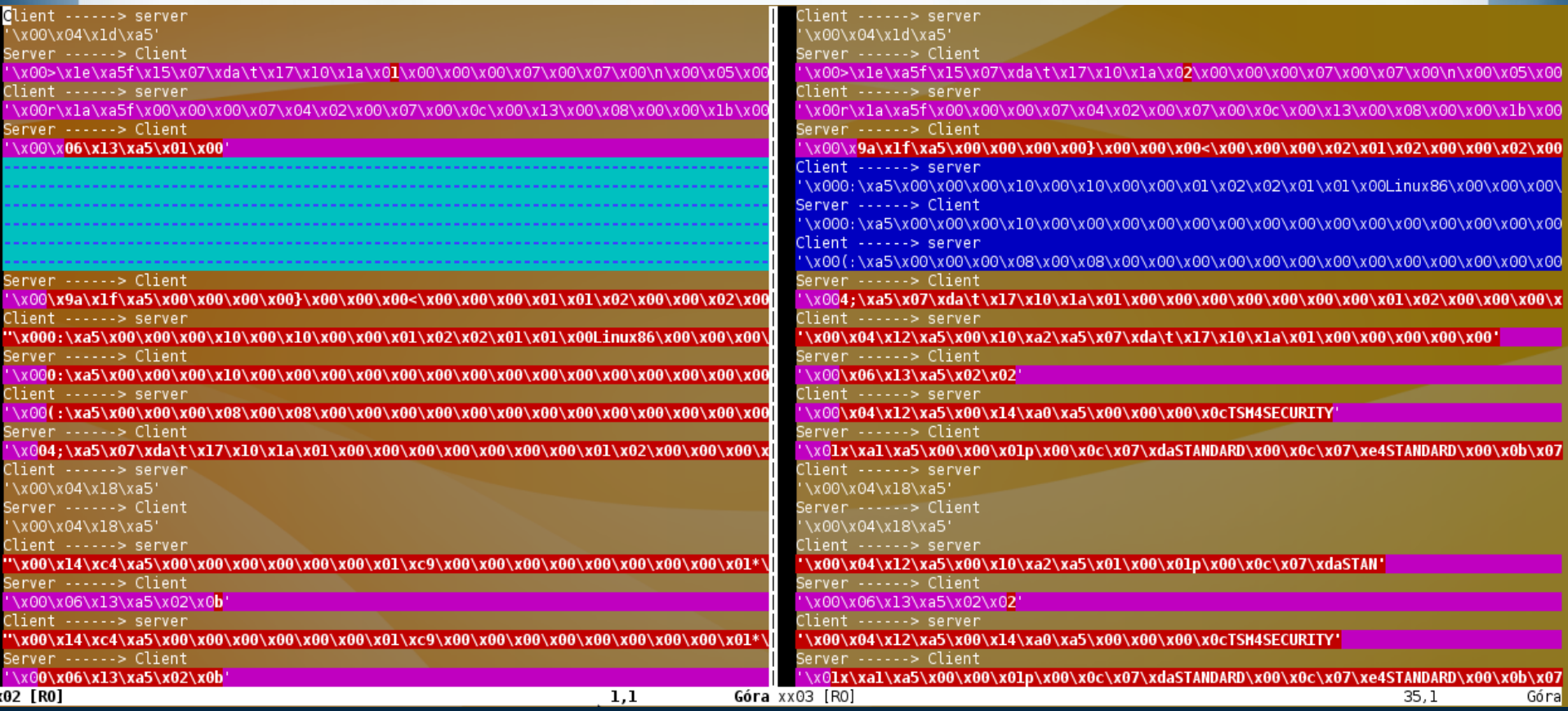
- Integration with a commercial backup/recovery product
- Client software is expensive
  - vendor provides dynamic client library for free
- Proprietary protocol for Library <=> Server communication
- We test libraries used in our projects
- Fuzzing seems to be a good way

Motivation (2)

- Enabled core dumps
- Prepared a script to loop
  - zzuf for blind fuzzing (good parametrization)
  - proxyfuzz for redirection (good logging)
  - netcat & tee & bash for plumbing
- Too many rejected transactions (auth failures)
  - 0 knowledge fuzzing vs. challenge-response, nonces...
- How to avoid reverse engineering of the implementation?

Motivation (3)

- Just compare the packets and find patterns!

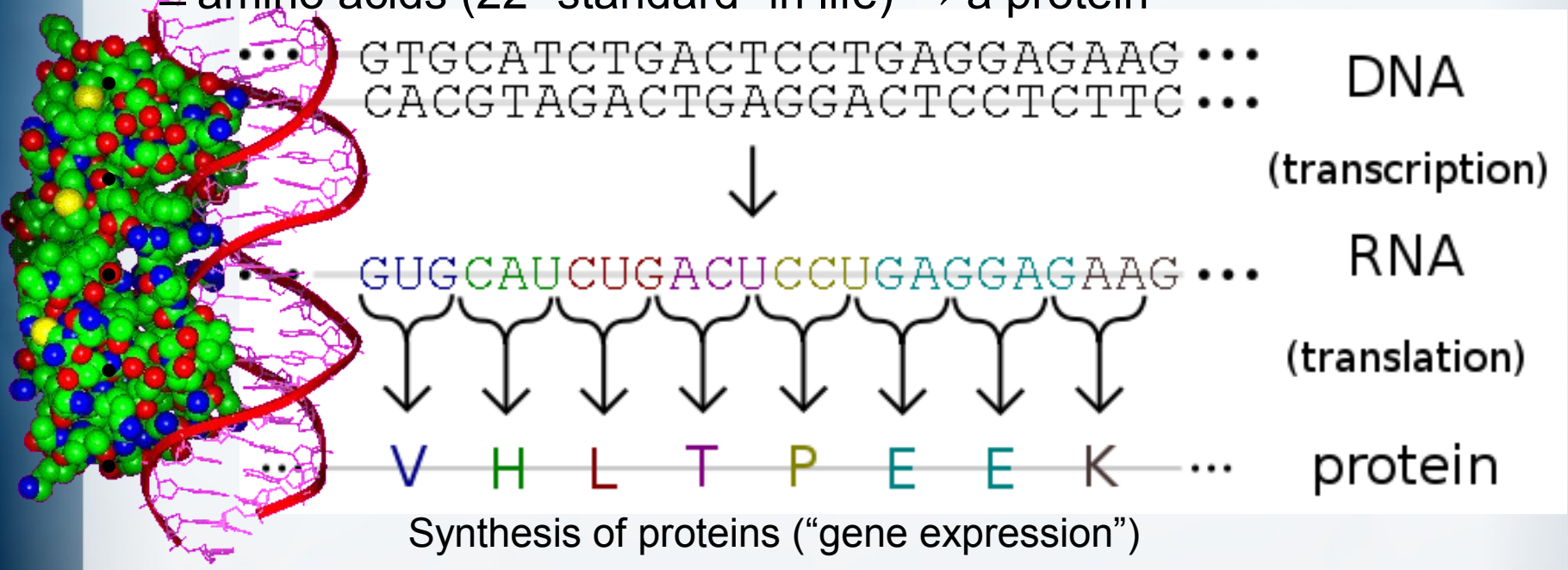


Motivation (4)

- Not far this way...
- How to embrace more byte sequences?
  - Available tools show differences between 2 or 3 files (diff, vimdiff, meld)
  - ... but we got hundreds of flows
- Bioinformatics deals with this problem for years!

A biological sequence

- Single, continuous molecule compound of
  - nucleotides (ACGT) → a nucleic acid (RNA, DNA etc.)
  - amino acids (22 “standard” in life) → a protein



Synthesis of proteins (“gene expression”)

- Stored in ASCII file formats like FASTA

FASTA format

```
>HSBGPG Human gene for bone gla protein (BGP)
GGCAGATTCCCCCTAGACCCGCCCGCACCATGGTCAGGCATGCCCCTCCTCATCGCTGGGCACAGCCCAGAGGGT
ATAAACAGTGCTGGAGGCTGGCGGGGCAGGCCAGCTGAGTCCTGAGCAGCAGCCCAGCGCAGCCACCGAGACACC
ATGAGAGCCCTCACACTCCTCGCCCTATTGGCCCTGGCCGCACTTTGCATCGCTGGCCAGGCAGGTGAGTGCCCC
CACCTCCCCTCAGGCCGCATTGCAGTGGGGGCTGAGAGGAGGAAGCACCATGGCCCACCTCTTCTCACCCCTTTG
GCTGGCAGTCCCTTTGCAGTCTAACCACCTTGTTGCAGGCTCAATCCATTTGCCCCAGCTCTGCCCTTGCAGAGG
GAGAGGAGGGAAGAGCAAGCTGCCCGAGACGCAGGGGAAGGAGGATGAGGGCCCTGGGGATGAGCTGGGGTGAAC
CAGGCTCCCTTTCCTTTGCAGGTGCGAAGCCCAGCGGTGCAGAGTCCAGCAAAGGTGCAGGTATGAGGATGGACC
TGATGGGTTCCTGGACCCTCCCCTCTCACCCTGGTCCCTCAGTCTCATTCCCCCACTCCTGCCACCTCCTGTCTG
GCCATCAGGAAGGCCAGCCTGCTCCCCACCTGATCCTCCCAAACCCAGAGCCACCTGATGCCTGCCCCTCTGCTC
CACAGCCTTTGTGTCCAAGCAGGAGGGCAGCGAGGTAGTGAAGAGACCCAGGCGCTACCTGTATCAATGGCTGGG
GTGAGAGAAAAGGCAGAGCTGGGCCAAGGCCCTGCCTCTCCGGGATGGTCTGTGGGGGAGCTGCAGCAGGGAGTG
GCCTCTCTGGGTTGTGGTGGGGGTACAGGCAGCCTGCCCTGGTGGGCACCCTGGAGCCCCATGTGTAGGGAGAGG
AGGGATGGGCATTTTGCACGGGGGCTGATGCCACCACGTCGGGTGTCTCAGAGCCCCAGTCCCCTACCCGGATCC
CCTGGAGCCCAGGAGGGAGGTGTGTGAGCTCAATCCGGACTGTGACGAGTTGGCTGACCACATCGGCTTTCAGGA
GGCCTATCGGCGCTTCTACGGCCCGGTCTAGGGTGTCGCTCTGCTGGCCTGGCCGGCAACCCCAGTTCTGCTCCT
CTCCAGGCACCCTTCTTTCCTCTTCCCCTTGCCCTTGCCCTGACCTCCCAGCCCTATGGATGTGGGGTCCCCATC
ATCCCAGCTGCTCCCAAATAAACTCCAGAAG
```

- Sequence elements
  - Nucleic acids: A, C, G, T/U
  - Amino acids: 24 letters

Visualizing similarity: Sequence alignment

- Calculating similarity of sequences
- Interweaving sequences with the knowledge
- Aligns same characters in one column (by introducing dashes - “gaps”)
- Example (pairwise align.): ABFDEL, ABMNDE:

```
ABF-DEL
ABMNDE
```

- Many free tools available, e.g.
  - kalign
  - clustalw
  - muscle
  - blast
- Parameterizable heuristics, distributed algorithms

SEAVIEW – GUI for seq. alignment

Multiple sequence alignment

- Discloses evolutionary events
  - point mutations
  - insertions / deletions (“indels”)
- Further analysis shows relationships between sequences
  - common ancestors

Transformation (1)

- Representing 256 states with some letters
- Ideas
  - patching all the software to support 256 values
    - introducing incompatibilities, time consuming
  - uuencode
    - 32 values, not so many amino-acids
  - base 2 – binary format, just two letters
    - too many alignments across byte boundary
  - using base 24; 2 digits are enough
    - the first one is hardly changing
  - hexadecimal!
    - use A-F and translate 0-9 to free amino-acid codes
- Correct FASTA file: header line with “>”, file extension

Transformation (2)

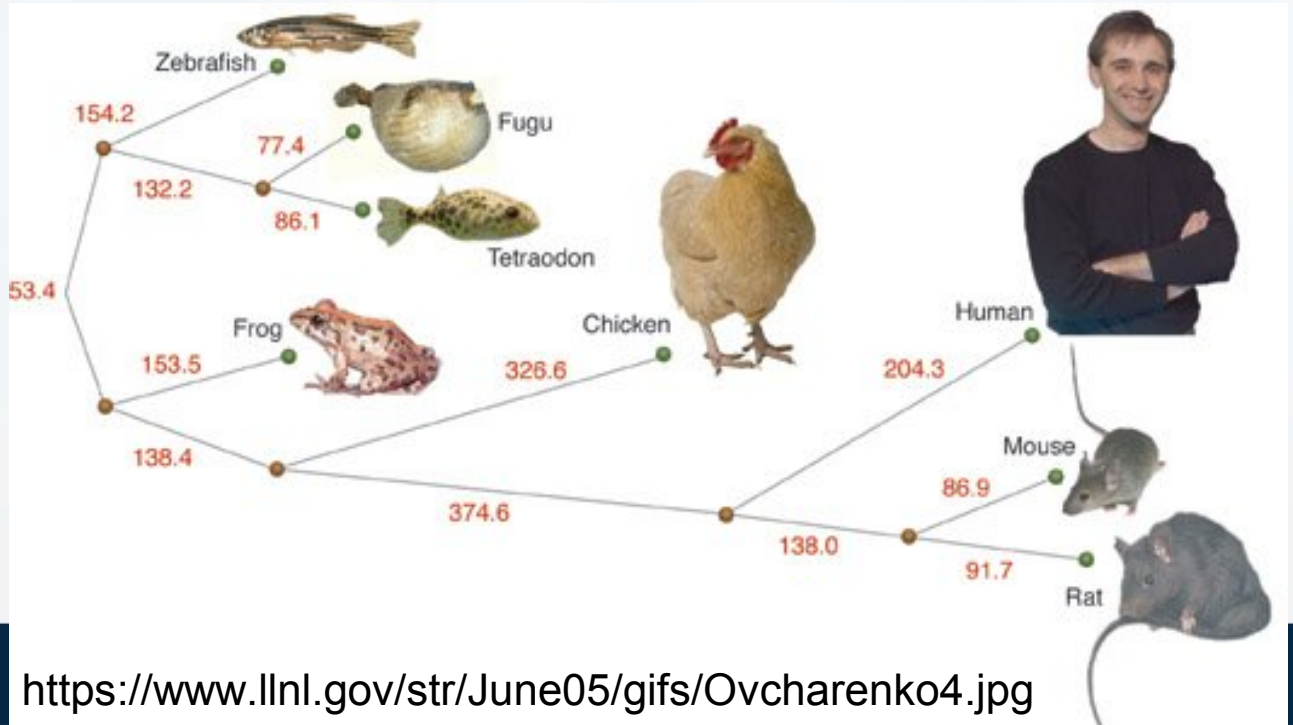
- Our tools transcode byte streams to amino-acid sequences
  - from proxyfuzz logs
  - from pcap dumps (using libpcap)
    - Ethernet, TCP and IP headers are preserved

```
$ ./pcap2fasta interesting.pcap
>pkt003 95 bytes
AACFFDMKBLEBAABQLLEWREDSAMAAEFAAAAFBAAAAEAAAEABBEABSRAPMABSQNKWTPAWSNLALAEPPA
ADSTCSSDAEPCLCRRQKWREBTDMLDKADBMTQMALEBENLEWFFLACKENEWADSNBLBRAKCFFWSQENEMBRF
DPDWNTKDBAQQSLLDCBSLFMDAEPRQKSFLSADF
>pkt004 95 bytes
AABQLLEWREDSAACFFDMKBLEBAMAAEFAAAAFBAAAAEAAADNBBELBSNKWTPAWSRAPMABSQAEPPNLALA
ADSPFLADALFKAMSLKMWWRNFBTTMCAFBDBRNNKKKWSPCCDNCQFDQLEKDKPTFFTSPRSBRCNMQAPEFWF
RPQPANDBALQBSPMMBWNALMQFWNMBCAMLFLDN
>pkt005 62 bytes
AACFFDMKBLEBAABQLLEWREDSAMAAEFAAAADADRRDEAAAEAAKWCNTRAPMABSQFQSKTSARQBTQBWMPQ
PSLEKRDDDADLLRPFABMADTPBPNKAAAAAMAAAAAAAAAAAA
```

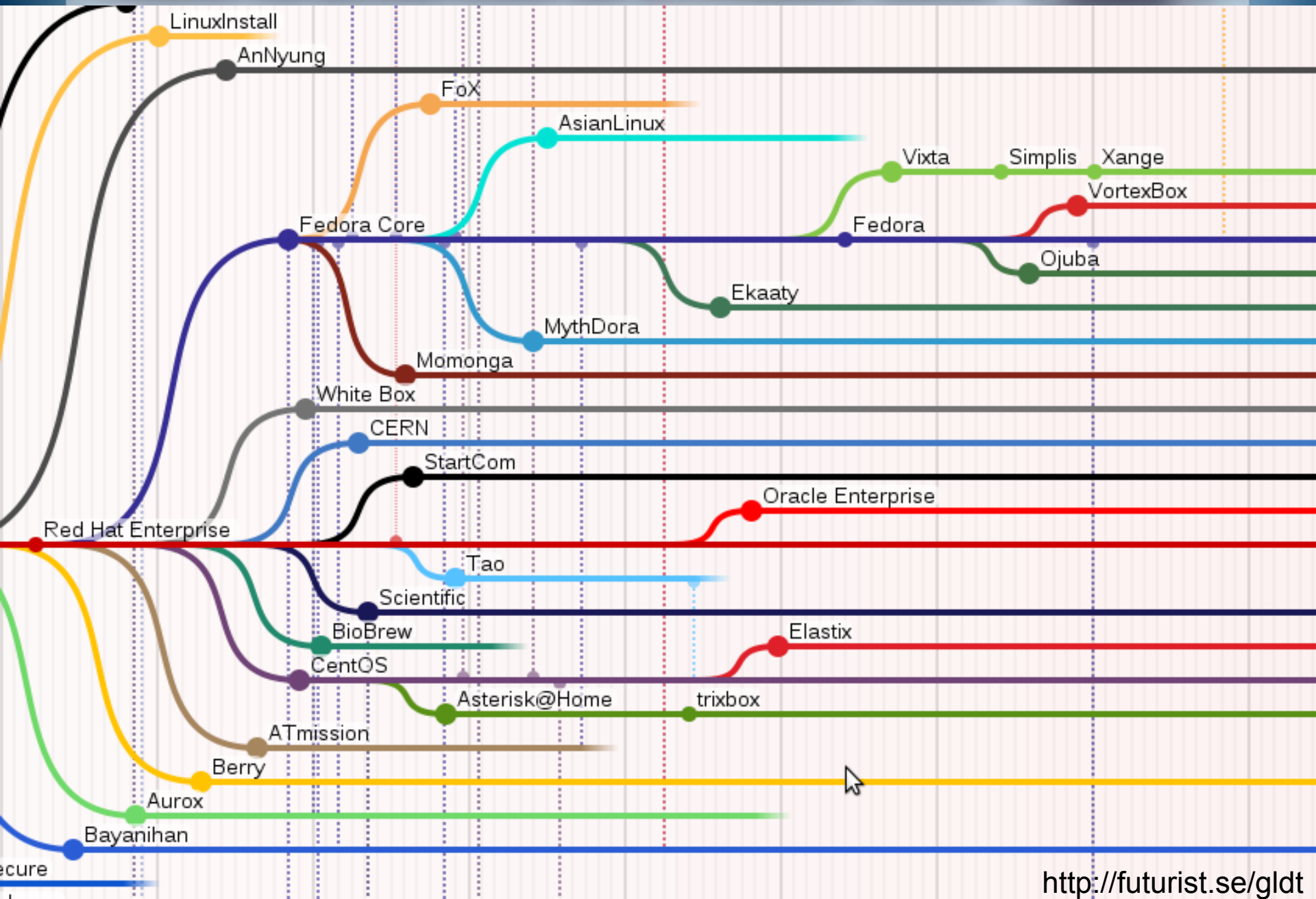
Transformation example (ping) DEMO

Phylogeny (1)

- Studies on evolution of life forms
- Tree of life forms and their similarity ("phylogenetic tree" or "cladogram") based on:
  - phenotype (observable traits): pterodactyl ~ stork
  - genotype (DNA sequence): human ~ pig
- Similar forms are supposed to a have common ancestor
- Length of edges may have a meaning (time, difference)

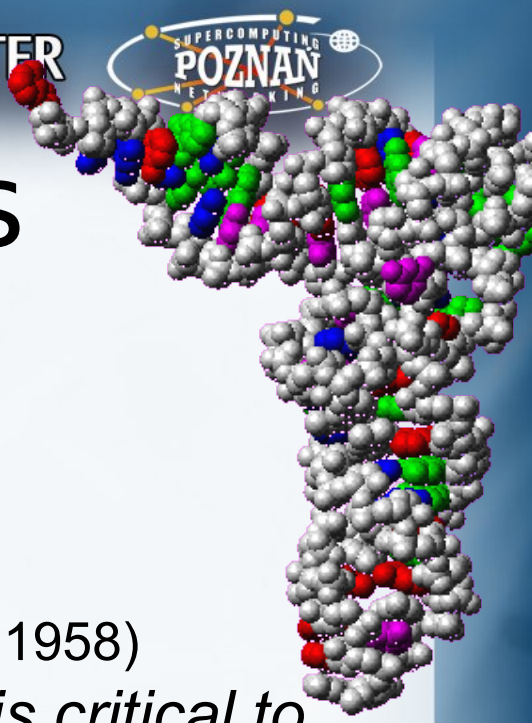


https://www.llnl.gov/str/June05/gifs/Ovcharenko4.jpg


LinuxInstall
AnNyung
FoX
AsianLinux
Vixta
Simplis
Xange
VortexBox
Fedora Core
Fedora
Ojuba
Ekaaty
MythDora
Momonga
White Box
CERN
StartCom
Oracle Enterprise
Red Hat Enterprise
Tao
Scientific
BioBrew
Elastix
CentOS
Asterisk@Home
trixbox
ATmission
Berry
Aurox
Bayanihan

Analogies

- Similar packets have a common "ancestor"
  - generated by a specific function
  - a template
- Discovering the "template" helps in reverse engineering
  - nonces/cookies, encrypted data
  - headers, parameters
- (And then fuzzing only non-random data)



Protein families

- Descend from a common ancestor
- Similar functions, 3D structure, sequence
- Example: globins
  - Hemoglobin
  - Myoglobin (first protein sequenced to atoms, 1958)
- *"Reliable identification of protein families is critical to*
  - *phylogenetic analysis*
  - *functional annotation*
  - *the exploration of diversity of protein function in a given phylogenetic branch"* - reverse engineering! (wikipedia)

Clustering packets (finding “families”)

- The famous original BLAST package (Basic Local Alignment Search Tool) from NCBI
- Tool: **blastclust**, input: FASTA packets
  - finds pairs of significantly similar sequences
  - clusters them in a lists

```
$ cat *.fasta | blastclust -S 1 -L 0.5
Nov 22, 2010  9:46 PM Start clustering of 33 queries
pkt000 pkt001 pkt002 pkt021 pkt022 pkt023 pkt030 pkt031 pkt032
pkt010 pkt014 pkt015 pkt018 pkt020
pkt009 pkt011 pkt017 pkt019
pkt004 pkt025 pkt028
pkt024 pkt029
pkt027 pkt026
pkt012
pkt016
pkt013
pkt008
```

Extracting family traits

- Creating a profile for each cluster
  - Take sequences from the cluster
  - Aligning cluster members once more
  - Extracting constant “sites” for families
    - Clustalx:
      Quality → Save Column Scores to File
    - Copy columns with 100 (%) score
    - Discard other – insert a gap
    - Join lines & fold

```
sed 's:\(.\).*100$:\1:' |
sed 's:..\+:-:' |
tr --delete '\r\n' |
fold --width 70
```

```
A A A A A A A A A A      100
F F F F F F F F F F      100
E E E E E E E E E E      100
B D N A K R M S R C       17
Q R N C C D D T E E       16
M B P E E D F P K E       12
.....................
```

```
AFE---QLLEWREDSAACFFDMKBLEBAMAAEFAAAAFE-
EAAAWLAB----SEESKEKFRAPMABSQAAAA----ASRA
AAF---TBWAER----ASAAAMANAPAQARASATAWBABB
BCBDBEBFBKBLBMBNBPBQBRBSBTBWCACBCCCDCECF
```

Applying to packets or files

- Intercept a byte sequence
- Find best matching profile & align with them
- Calculate byte ranges corresponding to constant sites (our tool)
  - Sample output: 2,3,4,14,15,16,34,
- Use ranges as a parameter for fuzzer
  - zzuf --bytes=ranges
- Forward the fuzzed data to application / network

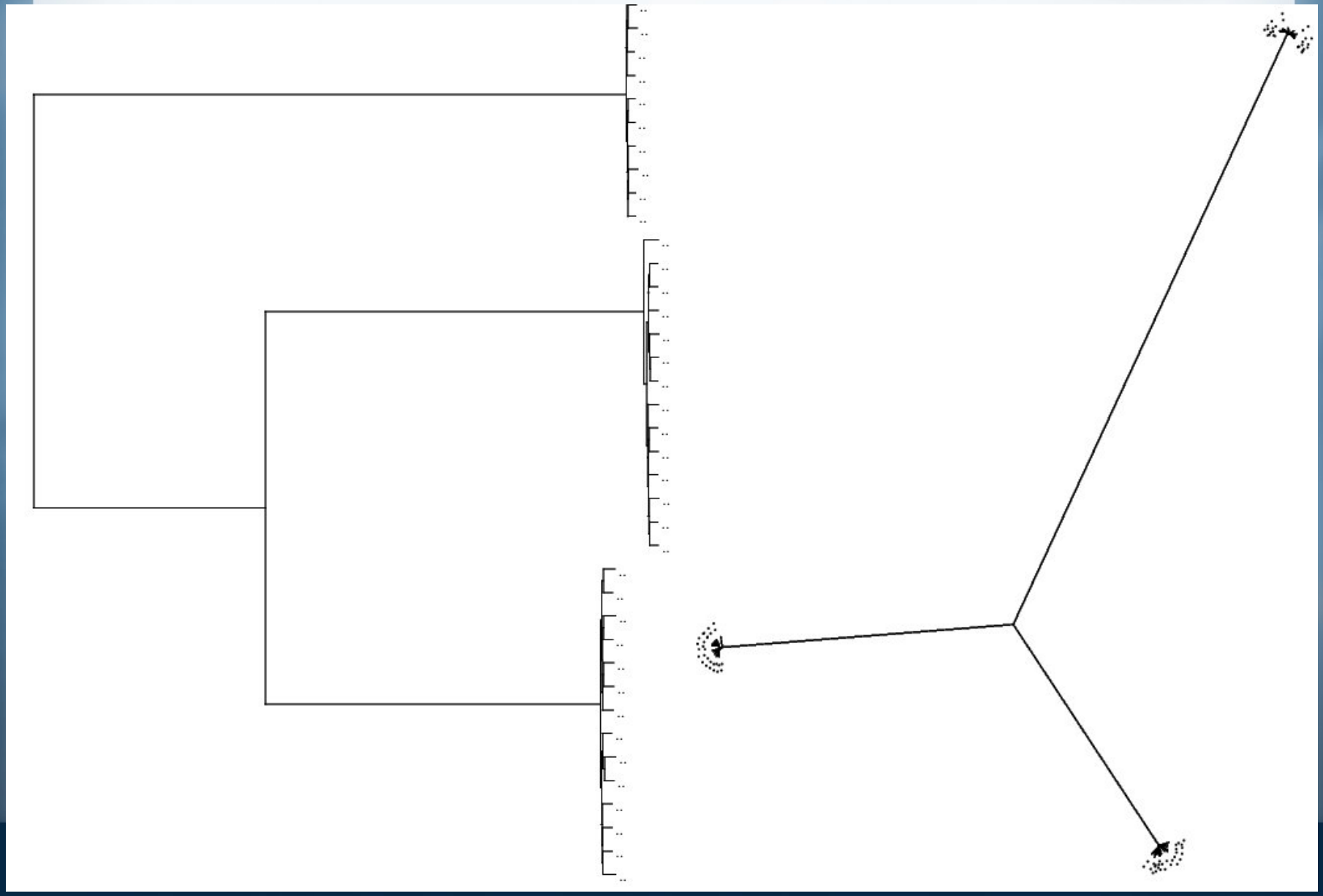
Classifier

- Convert to regexp
- Drop byte halves (-X or X-)
- Decode “aminal” base encoding back to 256 values
- Use in ngrep or anywhere

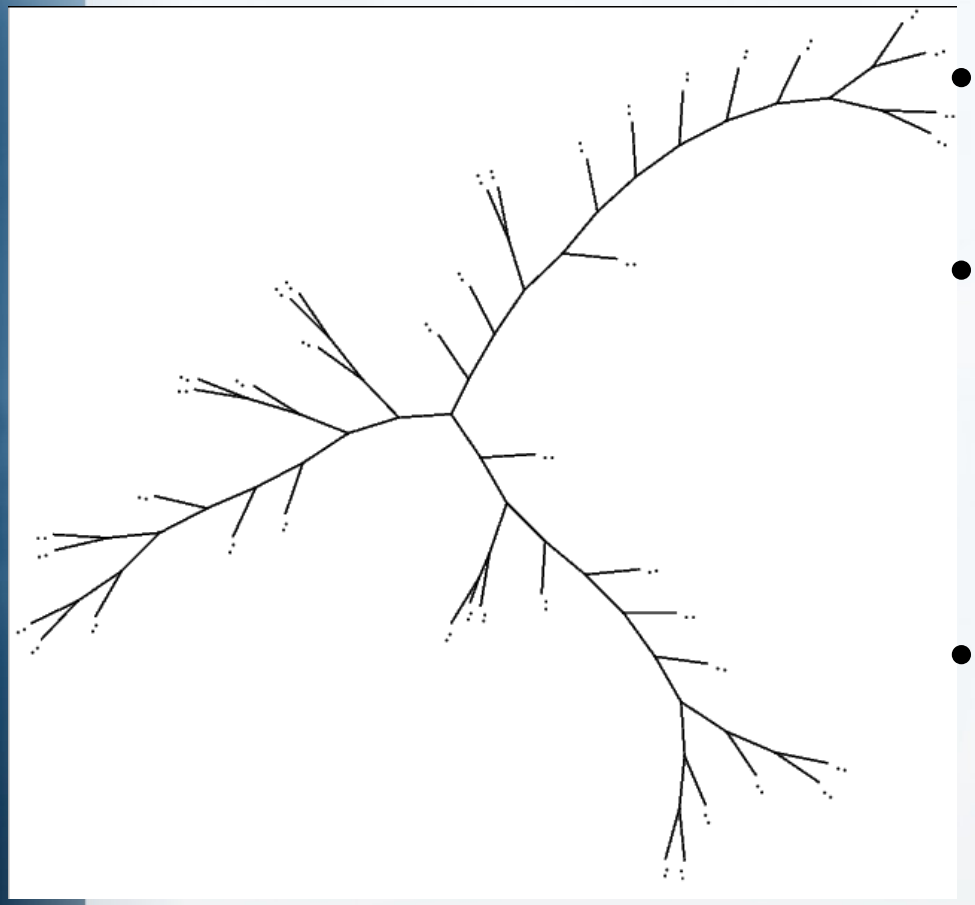
Other surprises

- Amino-acid distance matrix in alignment
  - Specifies probability of amino-acid replacement
  - In our case must be set to “identity”
- Some tools crashing when incorrectly used :)

Backup solution transmissions tree



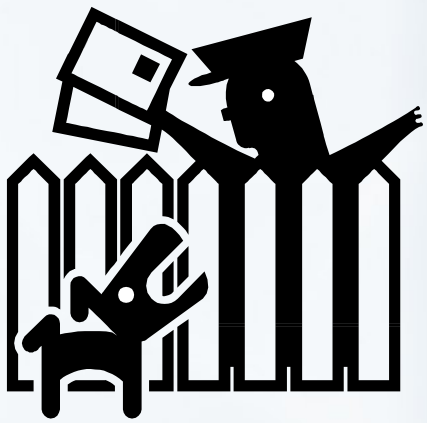
Backup solution transmission tree



- Each transaction split into 3 conversations
- Different
  - sizes
  - header parameters
  - positions of auth info
- Specialized fuzzing that doesn't break auth

Contact details

- Tomasz
  - tomasz.nowak@man.poznan.pl
- PSNC Security Team
  - http://security.psnc.pl
  - security@man.poznan.pl



Thank you for watching!

Questions, discussion...?