

最尤法による系統樹推定の理論と実際

- 1. 尤度原理、確率モデル、ベイズ推定
- 2. 系統樹推定の実際
- 3. 推定の信頼性評価

分子系統樹作成の手順:

- 1. アミノ酸配列や塩基配列などの分子データの収集
(EMBL/NCBI/DDBJなどのデータベースから)
- 2. 配列データの整列(alignment)
- 3. 最尤法による系統樹の構築
 - a) アミノ酸組成、塩基組成の変化の確認
 - b) アミノ酸置換、塩基置換モデルの選択
 - c) 配列内の進化速度の不均質性への考慮
- 4. 推定された最尤系統樹の信頼性の評価

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各データバンクから発表された配列データを手に入れることが可能し、更に**相同性検索**や**塩基配列・アミノ酸配列の多重整列と系統樹作成**([CLUSTALW](#))などのサービスも提供している。

WHAT'S NEW

Hot Topics: [アノテータ募集](#) (7/29)

- [ワークショップ「塩基配列のデータベース登録方法」のおしらせ](#) (7/19)

- [登録データの取り扱いについて](#) (7/11)

- [DDBJリリースに関するおしらせ](#) (定期リリース時期変更, 圧縮形式変更, 公開 DB に新形式追加)

DDBJへようこそ

- ・ [DDBJ/CIBとは?](#)
- ・ [DDBJing](#)
- ・ [DDBJの統計](#)
- ・ [DDBJ発行物オンライン](#)
- ・ [DDBJの連絡先](#)

塩基配列の登録

- ・ [塩基配列の登録入門](#)
- ・ [SAKURAによる登録](#)
- ・ [大量データの登録](#)
- ・ [塩基配列登録のための参考資料](#)

登録データの修正・更新

生命情報学へのとびら

- ・ [遺伝子とゲノム](#)
- ・ [遺伝研の生命情報webリンク](#)
- ・ [その他の生命情報webリンク](#)

データベース検索

- ・ [getentry](#) (アクセス番号などによる検索)
- ・ [SRS](#) (キーワード複合検索)
- ・ [相同性検索](#) (FASTA/BLAST/SSEARCHなど)
- ・ [TXSearch](#) (生物分類データベース検索)

データ解析

- ・ [ClustalW](#) (多重整列と系統樹作成)
- ・ [スパコンシステムの利用](#)

ゲノム解析

- ・ [DDBJ/CIBヒトゲノム情報工房](#)
- ・ [GIB](#) (微生物ゲノムの統合検索)
- ・ [GTOP](#) (ゲノム配列からタンパクの構造へ)

タンパク質のデータベース及び構造解析

- ・ [PMD](#) (変異タンパク質データベース)
- ・ [PDB Retriever](#) (PDBデータベースのブラウザ)
- ・ [SS-Thread](#) (タンパク質の二次構造予測)
- ・ [LIBRA](#) (タンパク質の立体構造予測)

LOCUS AB015962 16707 bp DNA VRT 08-APR-2000
 DEFINITION Mustelus manazo mitochondrial DNA, complete sequence.
 ACCESSION AB015962
 VERSION AB015962.1
 KEYWORDS .
 SOURCE Mustelus manazo liver mitochondrion DNA, clone:mtsh-1.
 ORGANISM Mustelus manazo
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
 Chondrichthyes; Elasmobranchii; Neoselachii; Galeomorphii;
 Galeoidea; Carcharhiniformes; Triakidae; Mustelus.

REFERENCE 1 (bases 1 to 16707)
 AUTHORS Cao,Y.
 TITLE Direct Submission
 JOURNAL Submitted (07-JUL-1998) to the DDBJ/EMBL/GenBank databases. Ying Cao, The Institute of Statistical Mathematics; 4-6-7 Minami-Azabu, Minato-ku, Tokyo 106-8569, Japan (E-mail:cao@ism.ac.jp, Tel:3-5421-8748, Fax:3-5421-8796)

REFERENCE 2
 AUTHORS Cao,Y., Waddell,P.J., Okada,N. and Hasegawa,M.
 TITLE The complete mitochondrial DNA sequence of the shark (Mustelus manazo): Evaluating rooting contradictions to living bony vertebrates
 JOURNAL Mol. Biol. Evol. 15, 1637-1646 (1998)

COMMENT
 FEATURES Location/Qualifiers
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BASE COUNT 5139 a 4077 c 2319 g 5172 t 0 others

ORIGIN

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121 caagtttcag ccctcctgtg agaatgccct aattaatcta ttaaataatt aggagcaggt
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241 cagtaataaa cattaattca tgagcgaag cttgaattag ttaaagtсga cagagttggт
301 таатctcgtg ccagccaccg cggттatacg agtaactcat attaacacac cccggcgtaa
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421 gcactcatga gtggaataat caacaacgaa agtgacttta catattaagg agcттtgatg
481 ccacgatagt tgagacccaa actaggatta gataccctac tatgcccac cataaactta
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分子系統樹作成の手順:

- 2. 配列データの整列(alignment)

実際に配列を解析するときには、位置合わせをする必要がある。特に進化距離が長くなってくると、その間に挿入や欠失が起こり、配列の中にいくつかGAPを入れることにより、それぞれの座位が対応づけられる。この位置合わせはアライメントと呼ばれている。

現在最もよく使われているソフトウェアは[CLUSTALW](#)などである。しかし、ソフトウェアで得られたものが時にはミスマッチがあるので、慎重な確認をお勧めする。

Search and Analysis

Search

[FASTA](#)

相同性検索
(長い配列の類似性を保っているものを検索)

[PSI-BLAST](#)

相同性検索
(局所的に高い類似性を有するものを繰り返し検索)

[BLAST](#)

相同性検索
(局所的に高い類似性を有するものを検索)

[SSEARCH](#)

相同性検索
(Smith-Waterman algorithmを採用した検索)

Analysis

[CLUSTALW](#)

多重整列と系統樹作成

[CLUSTALW DDBJ拡張版](#)

多重整列と系統樹作成
DOTとDISTANCEの機能追加

[LIBRA-I](#)

3D-1D法によるタンパク質の立体構造予測及び配列解析

Utility

[Result Viewer](#) 受付番号の入力による結果表示

Others

[What's New](#) 当ホームページの最新情報

[Traffic](#) サービス混雑情報

[About](#) このシステムについて

[Statistics](#) 統計情報

[Documents](#)
このシステムに関するドキュメント

Gap ---PQLNNTVWPTMITPMLLTL-FLITQKML-----PWEP-----

SB17F ---MPQLNNTVWPTMITPMLLTL-FLITQKMLNNTSYHLPPS-PKPMKMKNYNKPWEPKWTKICSLHSLPPQS*

CHIMP ---MPQLNTAVWPTMITPMLLTL-FLVTQKMLNSNYHLPPS-PKPMKMKNYNKPWEPKWTKIYSLHSLPPQS*

PyGC ---MPQLNTAVWPTTITPMLLTL-FLITQKMLNSNYHLPPS-PKPMKMKNYNKPWEPKWTKICSLHSLPPQS*

GORIL ---MPQLNNTVWPTMIAPMLLTL-FLITQKVLNTNYHLPLL-PKTMKMKNFCKPWEPKWTKIYSLHSLPPQS*

ORANG ---MPQLNNTTWTVTITPMLLTL-FLITQKLLNSHLHPPTP-PKFTKTKPHAKPWELKWTKIYSPHSLPPQS*

Ponpy ---MPQLNNTTWTPTITPMLLTL-FLITQKLLNSHLHPPTP-PKFTKPKLHAKPWGPKWTKVYLPHSLPPQY*

Hylla ---MPQLNNTVWPTIIMSLLAL-FLLMQKLTNTHYHPPAS-PKLTNPKPHNNPWEHKWTKIYSLHSLPPQF*

Papha ---MPQLDTSWFTIIMAMPLTL-YLITQKLLSMNYQPPL-TKNPNLQTHNTCWRPKWTKIYLPHSPQQQS*

Macsy ---MPQLDTSWSTIIMAMPLTL-YLITQKLLNTNYQPPL-TKNPNLQTHNIYQPEWTKICLPHSQPQ--*

Cebal ---MPQLDISPWPMTLSMILT-FYAMQKMLKFIFHTTPL-SKLTKIQNKQKTWELKWTKIYLPPLSMYQ--*

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Lemca ---MPQLDTSWTLITILSMILT-LIVFQLKISK-FNYPLNPMTKNINKDLYTNPWETKWTKIYLPPLSPQQS*

Tupbe ---MPQLDTSWFTIIVSMLATL-FILFQLKLSK-YCYYNLPQTKMTKKQDTPWQKWTKIYLPPLSPRH--*

Phovi ---MPQLDTSWLMIMLSMILT-FITFQLKVS-KHYFTNPEPKHTPLLLKNSAPWEEKWTKIYSPSLPLQ--*

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Felca ---MPQLDTSWSTIIMSIMTL-FIVFQLKISK-YLYPSNPEKSMTLKQRNPWEKKWTKIYSPSLPQQ--*

Equca ---MPQLDTSWFINIVSMILT-FIVFQLKISK-HSYVTHPEVKTMTKHSAPWESKWTKIYSPSLPQQ--*

Equas ---MPQLDTSWFINIVSMILT-FIVFQLKISK-HSYVPMHEAKTTKMAKRLTPWESKWTKIYSPSLPQQ--*

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Lampa ---MPQLDTSWFTIITILSMLTL-FILFQLKLSK-HIYYPTPEPKFKSKTHKQNTPWETKWKIYLPPLLPQ--*

Sussc ---MPQLDTSWFTIITISMITL-FILFQLKISN-YSYPASPESIELKTQKHSPTWEMKWTKIYLPPLLP--*

Bosta ---MPQLDTSWTLTMLSMLFVL-FIIFQLKVS-KHNFYHNPETLPTKMLKQNTPWETKWTKIYLPPLLP--*

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Hipam ---MPQLDTSWFTIITILSMLTL-FIIFQLKISK-HTYHPNETLTPMTQKQTPWETKWTKIYSPSLPQLS*

Balpb ---MPQLDTSWLLTILSMLTL-FVLFLKISK-HSYSPNPKLAHTKTQKQAPWNTWTKIYLPPL----*

Balmu ---MPQLDTSWLLTILSMLTL-FVLFLKISK-HSYSPNPKLVPTKTQKQTPWNTWTKIYLPPL----*

Phyca ---MPQLDTSWFLTILSVMLTL-FTLQPKISM-HLYTPNPKMPTKTQKQHSWNTAWTKIYLPPL----*

Artja ---MPQLDTSWFTIITILATLTL-FIIMQLKIS-TYYHNSPEKTKMTKSLIPWEIKWTKIYSPSLPLR--*

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Chatu ---MPQLDTSWFTIIMSIALTL-FIMFQLKISK-HYYTYPEPLAIKQTHNTPWAKWTKIYLPPLSPQH--*

Rhipu ---MPQLDTSWFTIITILSMLTL-FIIMQLKVS-KHSFHSNPEPELVKSSKHTTPWETKWTKIYSPSLPQR--*

Pipab ---MPQLDTSWFTIIMSMLTL-YIIFQLKISK-HYIYNPEPSTTKSQKHTTPWETKWTKIYLPPLSLPH--*

Sorun ---MPQLDTSWFTIITISMITL-FIAFQLKISK-YLYPMSPELKSALKKHNPNWETKWTKIYSPSLPQQ--*

Taleu ---MPQLDTSWFTIITILATITL-FILFQLKISK-YIYPSPELKSMSKLNHTPWETKWTKIYSPSLPLQ--*

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Ratno ---MPQLDTSWFTIITISSMATL-FILFQLKIS-SQTFPAPPSPKTMATEKTNPNWESKWTKIYLPPLSPPQ--*

Musmu ---MPQLDTSWFTIITISSMITL-FILFQLKVS-SQTFPLAPSPKSLTMTKVKTPWELKWTKIYLPHSLPQQ--*

Scivu ---MPQLDTSWFTIITISMLAL-FMLFQSKIA-NHSYYSNPSHKDMKPTHTSPWEKKWTKIYLPPLSLPH--*

Loxaf ---MERMDIIWLLAVIVLITL-MIFLHLKTL-KIIRLLFISKELSKSCVFPKWKWTKNYPPSSMYP--*

Oryaf ---MPQLDTPWFITILSMIITL-FILFQSNMS-KYLYPLEPQKTLKTOLYNAPWETKWTKIYLPHSLHLH--*

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Eriue ---MPQLDTSWFTMILAMFLTL-FIIMQLKIN-SYKTYNMMETKQTLNLSLKPWEHKWTKIYLPPLLPPLHY*

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Corfr ---MPQLNPNPWFIMLTWTLTY-SMIIQPKLL-SFITMNPPLNK-TQTTLTSPWTPWWT-----*

Galga ---MPQLNPNPWFIMLLTWFTL-SLLIQPKLL-SFTLTNPNANK-IT-TTKPTPWTPWT-----*

Aytam ---MPQLNPAPWFSIMITWTL-ALLIQPKLL-TFTTNPPSSK-PSLTKPTWAWPWT-----*

Falpe ---MPQLNPNPWFIMLATWAL-LLIQPKLL-PFTPTNPNMKN-TNTSNKSPWTPWT-----*

Vidch ---MPQLNPNPWFIFIMISWTF-SMIIQPKIL-TFVSTNPPSK-TLTAPTTPWTPWT-----*

Smish ---MPQLNPNPWFIMLTWTF-SLLIQPKLT-LFIPNPPSTK-TSTPMKPSPNWTPWT-----*

RheamM ---MPQLNPNPWFIMIMSWAVF-LLLIQPKLL-SFTHTNLPNSK-PLSTPNTPWTPWT-----*

StrcaA ---MPQLNPNPWFIFMFSWTF-LFLMQPKLT-SFISTNSPNSKNKT-TLTPPWTPWWT-----*

Allmi2 ---MPQLNPEPWLTFILVWISL-IVILQPKIA-SLMLTSPTPYKAM---TIKTWFPWT-----*

AllmiJ4 ---MPQLNPEPWLTFILVWISL-IVILQPKIA-SLMLTSPTPYKAM---TIKTWFPWT-----*

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Eumeg ---MPQLNPAPWLLILLISWTL-MFIFKTKL-SSTPHNTPTAPDLL-THHTTPWNPWT-----*

Pelue ---MPQLNPNPWFIFITWVIL-ILILPKIK-SHIPNNSPTNKNKM-LTTPMPWTPWT-----*

Chrpi ---MPQLNDPWFIMLSSSWLMY-ILILPKIS-SYLPNTDPTNKNK-TMHTNSWTWPTQHSINS-----*

Chatu ---MPQLDSTWFTITMSMIATL-FIMFQKISK-HYYTYPEPLAIKTQTHNTPWEAKWTKIYLPDLSLPQH-*
Rhipu ---MPQLDSTWFTITLMSMLTL-FIMMQLKVS-KHSFHSNPEPELVKSSKHTTPWETKWKIYSPDLSLPQR-*
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Orycu ---MPQLDSTWFTITVAMILSL-FILMQLKFIK-YTYPMNPVLKALESTSFPCPWETKWKIYSPDLSLPQH-*
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Gligl ---MPQLDSTWFTITLSTFSI-IHRLQLKLT-THIFSPNPTPKDLKTLKHHNPDWKKWKTYLPHSLHQH-*
Ratno ---MPQLDSTWFTITISSMATL-FILFQLKIS-SQTFPAPPSPKTMATEKINNPWESKWKTYLPHSLPPQO-*
Musmu ---MPQLDSTWFTITISSMITL-FILFQLKVS-SQTFPLAPPKSLTMTKVKTPWELKWKTYLPHSLPQO-*
Scivu ---MPQLDSTWFTITISMIIL-FMLFQSKIA-NHSYYSNP SHKDMKPTHS TPWEKKWKTYLPHSLPLH-*
Loxaf ---MERMDIIWLLAVVIVLTL-MIFLHLKTL-KIIRLFFPISKELSKSCVFPKWKTKNYPSSMYP-*
Oryaf ---MPQLDTPWFTITLMSIITL-FILFQSNMS-KYLYPLEPQPKTLKTLYNAPWETKWKTYLPHSLHLH-*
Echte ---MPQLDSTPWLISILSMFFTL-YLLMPKIS-KILINNDINCPSEITKSTNPNWKNWKTYLPHSLPLH-*
Eriue ---MPQLDSTSWFTMLAMFLTL-FIIMQLKIN-SYKTYNMMETKQTLNHLKLPWEHKWKTYLPLLLPLHY*
Macro ---MPQLDSTWLLTITLMLAL-FCIYQSKMINQTMISIPPQDKVIKPTQLPWEKWKTYLPHSSPLLS*
Didvi ---MPQLNTSTWTLTISLMIISL-FCIYQKMMNQTLIQTPTSTEQSKLTKHTLPEKKWKTYLPHSSHQO*
Isoma ---MPQLDSTWLLVIFLMIMAL-FCYQLKMLNQLKISIPQNDVITIKPQLPWEKKWKTYLPHSSPLQO*
Ornan LYDMPQLDSTWYTTITLMLAL-FCIFQLKMIKHLMYMNVPLILNQLQELFIKHQTPWHSKWKTYLPHSLLLQS*
Cicci ---MPQLNPNPWFYIMLATWTL-LLAIQPKLL-SFTTNQPSNK-LPTTKTPWAWPWT-----*
Cicbo ---MPQLNPNPWFYIMLATWTL-LLAIQPKLL-SFTTNQPSNK-LPTTKTPWAWPWT-----*
Corfr ---MPQLNPNPWFIMLTSWLTYSMIIQPKLL-SFITMNPPLNK-TQTLLTSPWTPWT-----*
Galga ---MPQLNPNPWFIMLTSWLTYSMIIQPKLL-SFTLNPNANK-IT-TTKTPWTPWWT-----*
Aytam ---MPQLNPAPWFSIMIMTWLTL-ALLIQPKLL-TFTTNPPSSK-PSLTKTPWAWPWT-----*
Falpe ---MPQLNPNPWFIMLTSWLTYSMIIQPKLL-SFTLNPNANK-IT-TTKTPWTPWWT-----*
Vidch ---MPQLNPNPWFIMLTSWLTYSMIIQPKLL-SFTLNPNANK-IT-TTKTPWTPWWT-----*
Smish ---MPQLNPNPWFIMLTSWLTYSMIIQPKLL-SFTLNPNANK-IT-TTKTPWTPWWT-----*
RheamM ---MPQLNPNPWFIMLTSWLTYSMIIQPKLL-SFTLNPNANK-IT-TTKTPWTPWWT-----*
StrcaA ---MPQLNPNPWFIMLTSWLTYSMIIQPKLL-SFTLNPNANK-IT-TTKTPWTPWWT-----*
Allmi2 ---MPQLNPNPWFIMLTSWLTYSMIIQPKLL-SFTLNPNANK-IT-TTKTPWTPWWT-----*
AllmiJ4 ---MPQLNPNPWFIMLTSWLTYSMIIQPKLL-SFTLNPNANK-IT-TTKTPWTPWWT-----*
Caicr ---MPQLNPNPWFIMLTSWLTYSMIIQPKLL-SFTLNPNANK-IT-TTKTPWTPWWT-----*
Dinse ---MPQLDITILMTHLWAWML-YLTTQ-KIK-TFIMTSHPMIY-HK---PNKQTPPTWTL-----*
Iguig ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Eumeg ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Pelu ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Chrpi ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Chemy ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Dogsu ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Xenla ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Ranni ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Typna ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Merlu ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Prodo ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Latch ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Cypca ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Crola ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Oncmy ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Salfc ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Salal ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Salsaa ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Salsa ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Corla ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Gadmo ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Carau ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Danre ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Parol ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Polja ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Dipta ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Gongr ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Musma ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Scyca ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Squac ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Rajra ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Polor ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Petma ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Myxgl ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Brala ---MPQLNPNPWFILLLLITWTL-ATFLNKTI-HSKFPPPTQKPN-QKTEPWTWPH-----*
Gap ---PQLNTPWPTMTPMLLTL-FLITLQKML-----PWP-----*

分子系統樹作成の手順:

3. 最尤法による系統樹の構築

現在広く一般的に使われている最尤法による分子系統樹推定のソフトウェアを紹介する。

a) MOLPHY

(<http://www.ism.ac.jp/software/ismlib/softother.html>)

b) PHYLIP

(<http://evolution.genetics.washington.edu/phylip.html>)

c) PAUP (<http://paup.csit.fsu.edu/>)

d) PAML

(<http://abacus.gene.ucl.ac.uk/software/paml.html>)

e) TREE-PUZZLE (<http://www.tree-puzzle.de/>)

分子系統樹作成の手順:

3. 最尤法による系統樹の構築

- a) アミノ酸組成、塩基組成の変化の確認
- b) アミノ酸置換、塩基置換モデルの選択
- c) 配列内の進化速度の不均質性への考慮

分子系統樹作成の手順:

3. 最尤法による系統樹の構築 (MOLPHYを例に)

- 入力ファイルのデータ処理
- アミノ酸組成、塩基組成の変化の知る
- アミノ酸置換、塩基置換モデルの選択
- 扱うOTUからすべての組み合わせを作る
- 近似尤度法ですべてのトポロジーを調べた上で、希望する上位のものを選び出す
- NJ法など他の方法で得られたトポロジーの周りを調べ、より尤度の高くなるトポロジーを探索する(局所探索法)
- 複数の遺伝子で得られた結果を総合的に評価

分子系統樹作成の手順:

3. 最尤法による系統樹の構築 (MOLPHYを例に)

- 入力ファイルのデータ処理
 - 1) 塩基データからアミノ酸データに変化する場合
`%nuc2ptn *.nuc > *.ptn` (Universal code);
`%nuc2ptn -m *.nuc > *.ptn` (Mitochondrial code).
 - 2) すべての塩基からコドンの1番目、2番目、3番目を取り分ける
`%molcodon -1 *.nuc > *.1st` (1番目の塩基のみ取出)
`%molcodon -2 *.nuc > *.2nd` (2番目の塩基のみ取出)
`%molcodon -3 *.nuc > *.3rd` (3番目の塩基のみ取出)
`%nuc2code *.nuc > *.code` (塩基を3つごとに分けられたファイル)
 - 3) 別のソフトウェアのデータファイルからMolphy用の入力ファイルに変化する
`%phy2mol (mol2phy) *.phy > *.mol`
`%mega2mol *.mega > *.mol`

Homsa Homo sapiens (human) # D38112

M-----PMANLLLLIVPILIAMAFMLLTERKILGYMQLRKGNVVGYPYGLLQPFADAM
 KLFKEPLKPKPATSTITLYITAPTLALTIALLLWAPLPMPNPLVNLNLGLLFFILATSSLAV
 YSILWSGWASNSNYALIGALRAVAQTISYEVTLAIILLSTLLMSGSFNLSTLITAQEH
 LLLPSWPLAMMWFISTLAETNRTPFDLAEGESELVSGFNIEYAAGPFALFFMAEYTNIIIM
 MNTLTITIFLGTTYDALSPELYTTYFVTKLLLSLFLWIRTAYPRFRYDQMLHLLWKNF
 LPLTLALLMWYVSMPTISSI-PP-QT----

Pantr Pan troglodytes (chimpanzee) # D38113

T-----PMTNLLLLIVPILIAMAFMLLTERKILGYMQLRKGNIVGYPYGLLQPFADAM
 KLFKEPLKPKPSTSTITLYITAPTLALTIALLLWTPMPNPLVNLNLGLLFFILATSSLAV
 YSILWSGWASNSNYALIGALRAVAQTISYEVTLAIILLSTLLMSGSFNLSTLVTTQEH
 LLLPTWPLAMMWFISTLAETNRTPFDLTEGESELVSGFNIEYAAGPFALFFMAEYMNIIIM
 MNTLTATIFLGATYNTHSPELYTTYFVTKALLLSLFLWIRTAYPRFRYDQMLHLLWKNF
 LPLTLASLMWYISMPTISSI-PP-QT----

Panpa Pan paniscus (bonobo) # D38116

T-----PMTNLLLLIVPILIAMAFMLLTERKILGYMQLRKGNIVGYPYGLLQPFADAM
 KLFKEPLKPKPSTSTITLYITAPTLALTIALLLWTPMPNPLVNLNLGLLFFILATSSLAV
 YSILWSGWASNSNYALIGALRAVAQTISYEVTLAIILLSTLLMSGSFNLSTLITTQEH
 LLLPTWPLAMMWFISTLAETNRTPFDLTEGESELVSGFNIEYAAGPFALFFMAEYMNIIIM
 MNTLTATIFLGTTYNTHSPELYTTYFVTKALLLSLFLWIRTAYPRFRYDQMLHLLWKNF
 LPLTLASLMWYISMPTISSI-PP-QT----

Gorgo Gorilla gorilla (gorilla) # D38114

M-----SMANLLLLIVPILIAMAFMLLTERKILGYMQLRKGNVVGYPYGLLQPFADAM
 KLFKEPLKPKPSTSTITLYITAPTLALTIALLLWTPMPNPLVNLNLGLLFFILATSSLAV
 YSILWSGWASNSNYALIGALRAVAQTISYEVTLAIILLSTLLMNGSFNLSTLIMTQEH
 LLLPTWPLAMMWFISTLAETNRTPFDLAEGESELVSGFNIEYAAGPLALFFMAEYMNIIIM
 MNTLTMTIFLGTTYNAHSPELYTVCFITKLLLSLFLWIRTAYPRFRYDQMLHLLWKNF
 LPLTLALLMWYISMPTISSI-PP-QT----

Ponpy Pongo pygmaeus (Bornean orangutan) # D38115

M-----PVINLLLLTMSILIAMAFMLLTERKILGYTQLRKGNIVGPGCLLQPFADAL
 KLFKEPLKPKPSTSTITLYIVSPALALTIALLLWTPMPNPLINLNLGLLFFILATSSLTV
 YSILWSGWASNSNYALIGTLRAVAQTISYEITLALILLSVLLMSGSFNLSTLITPQENSW
 LLLPSWPLALMWFISTLAETNRAPDLTEGESELVSGFNTEYAAGPFALFFMAEYTNIIIL
 MNALTAMIFLGTTFNIHSPELHTTLFTIKTLLLSLFLWIRQTYPRFRYDQMLHLLWKNF
 LPLTLALLMWHISMPITTSI-PP-QT----

Ponpy Pongo pygmaeus abelii (Sumatran orangutan) # X97707

M-----PMINLLLLIMSILIAMAFMLLTERKILGHTQLRKGNIVGYPYGLLQPFADAL
 KLFKEPLKPKPSTSTITLYIISPALALTIALLLWTPMPPIPLINLNLGLLFFILAASSLTV
 YSILWSGWASNSNYALIGALRAVAQTISYEITLALILLSVLLMSGSFNLSALITTQEH
 LLLPSWPLALMWFISTLAETNRAPDLTEGESELVSGFNTEYAAGPFALFFMAEYTNIIIL
 MNALTMTIFLGTTFNIHSPELYTTLFTIKTLLLSLFLWIRSTYPRFRYDQMLHLLWKNF
 LPLTLALLMWHISVPIATSGI-PP-QT---*

Hylla Hylobates lar (common gibbon) # X99256 (lar gibbon)

M-----PMINLLLLILPTLIAMAFMLLTERKILGYTQLRKGNIVGYPYGLLQPFADAM
 KLFKEPLKPKPSTSTALYIIAPTLALTIALLLWTPMPNPLINLNLGLLFFILATSSLTV
 YSILWSGWASNSNYALIGALRAVAQTISYEVTSAIILLSVLLMSGSFNLSTLITTQEH
 LLLPTWPLAMMWFISTLAETNRTPFDLTEGESELVSGFNTEYAAGPFALFFMAEYVNIIM
 MNALTMTIFLGTTHNAHRPELYTTCFTIKTLLLSLFLWIRTAYPRFRYDQMLYLLWKNF
 LPLTLTLLMWYISLSTMIASI-PP-QT---*

分子系統樹作成の手順:

3. 最尤法による系統樹の構築 (MOLPHYを例に)

- アミノ酸組成、塩基組成の変化の知る
 - 1) 各種の塩基配列やアミノ酸配列の組成を見る
 - `%nucst *.nuc > *.nucst`
 - `%protst *.ptn > *.ptnst`
 - アライメントを見たい場合 “-a” をつける
- ある種は他の種とかなり異なる塩基組成を持った場合、また塩基組成がよく似ている配列があった場合、塩基組成が似ている配列を近くに結びつける偏った系統樹を推定してしまう恐れがある。それに対して、頑健な距離推定としてLogDet変換は有力な方法である。

		A Ala	R Arg	N Asn	D Asp	C Cys	Q Gln	E Glu	G Gly	H His	I Ile
1	SB17F	0.070	0.017	0.043	0.018	0.006	0.025	0.022	0.051	0.027	0.085
2	CHIMP	0.067	0.017	0.043	0.018	0.005	0.026	0.022	0.052	0.026	0.084
3	PyGC	0.065	0.017	0.044	0.017	0.006	0.025	0.022	0.051	0.026	0.083
4	GORIL	0.070	0.017	0.044	0.017	0.005	0.026	0.022	0.051	0.028	0.084
5	ORANG	0.067	0.017	0.041	0.018	0.006	0.025	0.022	0.051	0.029	0.086
6	Ponpy	0.069	0.017	0.039	0.018	0.005	0.024	0.021	0.051	0.030	0.089
7	Hylla	0.071	0.018	0.045	0.017	0.005	0.025	0.022	0.051	0.030	0.085
8	Papha	0.065	0.016	0.046	0.017	0.006	0.027	0.020	0.050	0.029	0.086
9	Phovi	0.068	0.018	0.039	0.018	0.006	0.024	0.024	0.054	0.027	0.088
10	Halgr	0.069	0.017	0.039	0.018	0.006	0.023	0.024	0.054	0.029	0.090
11	Canfa	0.067	0.018	0.041	0.017	0.007	0.024	0.024	0.055	0.026	0.091
12	Felca	0.069	0.018	0.039	0.018	0.006	0.025	0.024	0.054	0.026	0.088
13	Equca	0.064	0.018	0.040	0.017	0.006	0.025	0.024	0.053	0.029	0.091
14	Equas	0.065	0.018	0.041	0.017	0.006	0.025	0.024	0.053	0.028	0.094
15	Cersi	0.065	0.017	0.040	0.017	0.006	0.024	0.024	0.053	0.029	0.091
16	Rhiun	0.062	0.017	0.042	0.017	0.006	0.024	0.024	0.053	0.029	0.093
17	Sussc	0.070	0.018	0.041	0.017	0.006	0.024	0.024	0.053	0.028	0.089
18	Bosta	0.067	0.017	0.043	0.018	0.006	0.024	0.023	0.054	0.026	0.086
19	Oviar	0.065	0.018	0.044	0.018	0.006	0.024	0.023	0.053	0.027	0.091
20	Hipam	0.067	0.017	0.042	0.018	0.006	0.025	0.023	0.053	0.028	0.084
21	Balph	0.069	0.018	0.043	0.018	0.006	0.025	0.024	0.053	0.029	0.082
22	Balmu	0.069	0.018	0.042	0.018	0.006	0.025	0.023	0.052	0.027	0.084
23	Artja	0.067	0.018	0.039	0.018	0.006	0.023	0.023	0.053	0.027	0.088
24	Pteda	0.069	0.018	0.042	0.018	0.006	0.025	0.024	0.053	0.026	0.083
25	Ninin	0.068	0.018	0.037	0.019	0.006	0.024	0.024	0.054	0.029	0.085
26	abura	0.066	0.017	0.039	0.018	0.006	0.024	0.024	0.053	0.027	0.092
27	Sorex	0.067	0.018	0.041	0.018	0.006	0.025	0.024	0.053	0.025	0.091
28	Taleu	0.071	0.018	0.041	0.017	0.006	0.024	0.024	0.053	0.027	0.085
29	Dasno	0.066	0.018	0.039	0.017	0.006	0.024	0.023	0.054	0.028	0.091
30	Orycun	0.069	0.018	0.042	0.018	0.006	0.025	0.024	0.053	0.026	0.092
31	Gligl	0.060	0.020	0.044	0.018	0.007	0.024	0.023	0.055	0.026	0.095
32	Cavpo	0.067	0.017	0.041	0.018	0.007	0.024	0.024	0.053	0.027	0.089
33	Ratno	0.063	0.018	0.044	0.018	0.007	0.023	0.024	0.052	0.027	0.098
34	Musmu	0.063	0.018	0.043	0.019	0.007	0.022	0.023	0.052	0.027	0.099
35	Loxaf	0.062	0.018	0.042	0.018	0.006	0.023	0.025	0.052	0.028	0.085
36	Oryaf	0.067	0.018	0.039	0.017	0.007	0.023	0.024	0.054	0.029	0.100
37	Erieu	0.061	0.017	0.045	0.019	0.007	0.022	0.023	0.050	0.028	0.104
38	Macro	0.070	0.018	0.041	0.018	0.008	0.024	0.023	0.054	0.029	0.098
39	Didvi	0.061	0.018	0.043	0.017	0.007	0.025	0.023	0.054	0.026	0.102
40	Ornan	0.065	0.018	0.039	0.019	0.007	0.025	0.024	0.056	0.029	0.091
	mean	0.067	0.018	0.042	0.018	0.006	0.024	0.023	0.053	0.028	0.090

		L Leu	K Lys	M Met	F Phe	P Pro	S Ser	T Thr	W Trp	Y Tyr	V Val
1	SB17F	0.173	0.025	0.054	0.057	0.060	0.074	0.094	0.027	0.035	0.039
2	CHIMP	0.173	0.025	0.053	0.058	0.059	0.074	0.098	0.027	0.036	0.038
3	PyGC	0.173	0.025	0.054	0.058	0.059	0.074	0.098	0.027	0.036	0.040
4	GORIL	0.174	0.025	0.054	0.059	0.058	0.072	0.094	0.028	0.034	0.038
5	ORANG	0.177	0.025	0.050	0.055	0.061	0.074	0.101	0.027	0.033	0.036
6	Ponpy	0.177	0.025	0.049	0.054	0.062	0.074	0.099	0.027	0.034	0.036
7	Hylla	0.172	0.025	0.053	0.057	0.059	0.070	0.097	0.027	0.033	0.039
8	Papha	0.166	0.025	0.058	0.057	0.059	0.071	0.108	0.027	0.033	0.033
9	Phovi	0.158	0.026	0.065	0.061	0.054	0.074	0.086	0.028	0.035	0.046
10	Halgr	0.159	0.026	0.064	0.061	0.054	0.073	0.085	0.028	0.034	0.046
11	Canfa	0.158	0.026	0.065	0.062	0.053	0.075	0.081	0.027	0.037	0.046
12	Felca	0.159	0.027	0.067	0.059	0.053	0.073	0.083	0.028	0.037	0.046
13	Equca	0.163	0.025	0.060	0.063	0.052	0.080	0.084	0.028	0.033	0.044
14	Equas	0.164	0.025	0.059	0.062	0.052	0.079	0.083	0.028	0.034	0.041
15	Cersi	0.162	0.027	0.060	0.063	0.054	0.077	0.090	0.027	0.033	0.041
16	Rhiun	0.162	0.026	0.063	0.062	0.053	0.079	0.087	0.027	0.033	0.040
17	Sussc	0.156	0.026	0.069	0.059	0.052	0.074	0.084	0.028	0.036	0.045
18	Bosta	0.159	0.026	0.068	0.062	0.053	0.072	0.084	0.028	0.036	0.047
19	Oviar	0.159	0.025	0.068	0.064	0.053	0.071	0.086	0.028	0.033	0.043
20	Hipam	0.159	0.026	0.065	0.060	0.055	0.071	0.092	0.028	0.033	0.048
21	Balph	0.169	0.024	0.060	0.062	0.056	0.068	0.089	0.028	0.032	0.044
22	Balmu	0.168	0.025	0.058	0.063	0.057	0.069	0.090	0.028	0.033	0.045
23	Artja	0.165	0.024	0.065	0.060	0.055	0.072	0.090	0.028	0.036	0.044
24	Pteda	0.164	0.025	0.065	0.058	0.053	0.076	0.083	0.028	0.036	0.048
25	Ninin	0.166	0.024	0.057	0.062	0.053	0.077	0.086	0.029	0.032	0.051
26	abura	0.158	0.026	0.068	0.062	0.054	0.075	0.085	0.028	0.037	0.042
27	Sorex	0.161	0.026	0.059	0.062	0.051	0.076	0.083	0.028	0.037	0.048
28	Taleu	0.163	0.026	0.064	0.062	0.051	0.076	0.083	0.027	0.034	0.048
29	Dasno	0.160	0.026	0.069	0.060	0.055	0.072	0.089	0.027	0.036	0.041
30	Orycun	0.161	0.024	0.058	0.064	0.055	0.074	0.083	0.028	0.032	0.046
31	Gligl	0.161	0.025	0.057	0.069	0.050	0.084	0.082	0.028	0.031	0.041
32	Cavpo	0.163	0.025	0.062	0.062	0.051	0.081	0.081	0.027	0.036	0.043
33	Ratno	0.158	0.027	0.059	0.061	0.054	0.079	0.087	0.027	0.034	0.040
34	Musmu	0.156	0.027	0.065	0.064	0.054	0.077	0.084	0.027	0.032	0.041
35	Loxaf	0.166	0.025	0.067	0.057	0.053	0.073	0.093	0.028	0.036	0.043
36	Oryaf	0.166	0.025	0.057	0.063	0.055	0.078	0.078	0.028	0.036	0.037
37	Erieu	0.154	0.028	0.074	0.064	0.047	0.079	0.072	0.027	0.041	0.040
38	Macro	0.161	0.025	0.055	0.060	0.054	0.074	0.081	0.028	0.036	0.043
39	Didvi	0.157	0.026	0.069	0.060	0.052	0.080	0.080	0.028	0.036	0.036
40	Ornan	0.173	0.024	0.050	0.062	0.053	0.072	0.087	0.028	0.034	0.045
	mean	0.164	0.025	0.061	0.061	0.054	0.075	0.087	0.028	0.035	0.042

分子系統樹作成の手順:

3. 最尤法による系統樹の構築 (MOLPHYを例に)

アミノ酸置換、塩基置換モデルの選択

系統樹を推定する場合どのアミノ酸置換、塩基置換モデルを使う、
即ちモデル選択が必要である

塩基置換の統計モデル

- Jukes-Cantor model (1969)
- Kimura model (1980,1981)
- Felsenstein model (1981)
- HKY model (1985)
- Tamura & Nei model (1993)

アミノ酸置換の統計モデル

- Poisson model
- Proportional model
- Dayhoff model (Dayhoff *et al.* 1978)
- JTT model (Jones, Taylor & Thornton, 1992)
- mt-REV model (Adachi & Hasegawa, 1996)

NucML 2.3b6(December 16 1996) Maximum Likelihood Inference of Nucleic Acid Phylogeny

Copyright (C) 1992-1996 J. Adachi & M. Hasegawa. All rights reserved.

Usage: **nucml** [**switches**] **sequence_file** [**topology_file**]

sequence_file = MOLPHY_format | Sequential(-S) | Interleaved(-I)

topology_file = users_trees(-u) | constrained_tree(-e)

Model:

-t n1 n1: Alpha/Beta ratio (default:4.0) Hasegawa, Kishino & Yano(1985)

-t n1,n2 n2: AlphaY/AlphaR ratio (default:1.0) Tamura & Nei(1993)

-p Proportional -pf Poisson (-f with OTU data Frequencies)

-r users RSR-F -rf users RSR (Relative Substitution Rate)

Search strategy or Mode:

-u Users trees (need users_trees file)

-R local Rearrangement search -RX LBP only

-e Exhaustive search (with/without constrained_tree file)

-s Star decomposition search (may not be the ML tree)

-q Quick add OTUs search (may not be the ML tree)

-D maximum likelihood Distance matrix --> NJDIST

Others:

-n num retained top ranking trees (default -e:105,-q:50)

-P num Per cent (default -e:30, if possible trees<=945 : 200)

-b no RELL-BP -M Minimum evolution (with -e)

-S Sequential format -I Interleaved format

-v verbose to stderr -i, -w output some information

ProtML 2.3b6(December 16 1996) Maximum Likelihood Inference of Protein Phylogeny

Copyright (C) 1992-1996 J. Adachi & M. Hasegawa. All rights reserved.

Usage: **protml** [switches] **sequence_file** [topology_file]

sequence_file = MOLPHY_format | Sequential(-S) | Interleaved(-I)

topology_file = users_trees(-u) | constrained_tree(-e)

Model:

-j JTT (default) -jf JTT-F Jones, Taylor & Thornton(1992)

-d Dayhoff -df Dayhoff-F Dayhoff et al.(1978)

-m mtREV24 -mf mtREV24-F Adachi & Hasegawa(1996)

-p Poisson -pf Proportional (-f: with data Frequencies)

-r users RSR -rf users RSR-F (Relative Substitution Rate)

Search strategy or Mode:

-u Users trees (need users_trees file)

-R local Rearrangement search -RX LBP only

-e Exhaustive search (with/without constrained_tree file)

-s Star decomposition search (may not be the ML tree)

-q Quick add OTUs search (may not be the ML tree)

-D maximum likelihood Distance matrix --> NJDIST

Others:

-n num retained top ranking trees (default -e:105,-q:50)

-P num Per cent (default -e:30, if possible trees<=945 : 200)

-b no RELL-BP -M Minimum evolution (with -e)

-S Sequential format -I Interleaved format

-v verbose to stderr -i, -w output some information

分子系統樹作成の手順:

3. 最尤法による系統樹の構築 (MOLPHYを例に)

- 最尤系統樹の探索方法に関して
扱うOTUの数は多くなると探索すべき系統樹のtopologyの数も爆発的に増えるが、最尤系統樹探索の方法としては近似法ですべてのtopologyを調べた上で足りるする方法がMOLPHYが提供している。またNJ法など別の方法で得られた系統樹のtopologyの周りを調べてより尤度の高くなるtopologyを探索していく方法(局所探索法)などのヒューリスティックな方法が用意されている。

```
% protml -mf -e -n 10000 sequence_file constrained_file > topology_file
```

```
% protml -mf -u sequence_file topology_file > ML_file
```

```
% protml -mfD sequence_file > distance_file
```

```
% njdist -o n distance_file > NJtree_file (njdiat.tplファイルが自動的にできる)
```

```
% protml -mfR sequence_file NJtopology_file > MLtreelr_file
```

constrained_file

```
(Hipam,Phyca,{Balmy,  
(Eubau,Eubgl),  
Capma,  
Escro,  
(Balac,Balbon),  
(Balbor,Baled),  
Balmu,  
Balph,  
Megno});
```

10000 / 2027025 protml 2.3b6 "mtREV24-F" 14 OTUs 3535 sites. nd1 nd2 cox1 cox2 atp8 atp6 cox3 nd3 nd41 nd4 nd5 cob

<= 10000 trees (top ranking for approx. ln L) in the top 30.0% range of TBL

# range	TBL	trees
# <	36.77	0
# 5%	37.26	1164
# 10%	37.75	21656 *
# 15%	38.25	95722 *****
# 20%	38.74	166432 *****
# 25%	39.23	551569 *****
# 30%	39.72	930987 *****
# 35%	40.22	259482 *****
# 40%	40.71	13
# 45%	41.20	0
# 50%	41.70	0
# 55%	42.19	0
# 60%	42.68	0
# 65%	43.17	0
# 70%	43.67	0
# 75%	44.16	0
# 80%	44.65	0
# 85%	45.15	0
# 90%	45.64	0
# 95%	46.13	0
# 100%	46.62	0
#	over	0

approx. ln L -18191.3 ... -18350.9 diff 159.7, TBL 36.8 ... 37.7 diff 0.9

(Hipam,Phyca,((Balmy,(Eubau,Eubgl),(Capma,(Escro,((Balac,Balbon),((Balbor,Baled),Balmu),(Balph,Megno)))))); 0.0
(Hipam,Phyca,((Balmy,(Eubau,Eubgl),(Capma,(Escro,((Balac,Balbon),((Balbor,Baled),Balmu),(Balph,Megno)))))); 6.5
(Hipam,Phyca,((Balmy,(Eubau,Eubgl),(Capma,(Escro,((Balac,Balbon),(Balph,Megno),(Balbor,Baled),Balmu))))); 6.8
(Hipam,Phyca,((Balmy,(Eubau,Eubgl),(Capma,((Escro,(Balac,Balbon),((Balbor,Baled),Balmu),(Balph,Megno)))))); 19.3
(Hipam,Phyca,((Balmy,(Eubau,Eubgl),(Capma,((Escro,((Balbor,Baled),Balmu),(Balph,Megno)),(Balac,Balbon))))); 19.6
(Hipam,Phyca,(((Balmy,(Eubau,Eubgl),Capma),(Escro,((Balac,Balbon),((Balbor,Baled),Balmu),(Balph,Megno)))))); 23.0
(Hipam,Phyca,(((Balmy,(Eubau,Eubgl),(Escro,((Balac,Balbon),((Balbor,Baled),Balmu),(Balph,Megno))),Capma)); 23.2
(Hipam,Phyca,((Balmy,(Eubau,Eubgl),(Capma,((Escro,((Balac,Balbon),((Balbor,Baled),Balmu)),(Balph,Megno)))))); 25.6
(Hipam,Phyca,((Balmy,(Eubau,Eubgl),(Capma,((Escro,(Balac,Balbon),(Balph,Megno),(Balbor,Baled),Balmu)))))); 25.8
(Hipam,Phyca,((Balmy,(Eubau,Eubgl),((Capma,((Balac,Balbon),((Balbor,Baled),Balmu),(Balph,Megno))),Escro)); 27.5
(Hipam,Phyca,((Balmy,(Eubau,Eubgl),(Capma,((Escro,((Balac,Balbon),(Balph,Megno)),(Balbor,Baled),Balmu)))))); 28.2
(Hipam,Phyca,((Balmy,(Eubau,Eubgl),(Capma,(Escro,((Balac,Balbon),(((Balbor,Baled),Balmu),Megno),Balph)))))); 29.0
(Hipam,Phyca,((Balmy,(Eubau,Eubgl),(Capma,((Escro,(Balph,Megno),(Balac,Balbon),(Balbor,Baled),Balmu)))))); 29.0
(Hipam,Phyca,((Balmy,(Eubau,Eubgl),((Capma,Escro),(Balac,Balbon),((Balbor,Baled),Balmu),(Balph,Megno))))); 29.1
(Hipam,Phyca,((Balmy,(Eubau,Eubgl),(Capma,(Escro,((Balac,Balbon),(((Balbor,Baled),Balmu),Balph),Megno)))))); 29.9

protml 2.3b6 mtREV24-F 14 OTUs 3535 sites. nd1 nd2 cox1 cox2 atp8 atp6 cox3 nd3 nd41 nd4 nd5 cob

```
#1
:-----1 Hipam
:
:-----14 Phyca
:
:      :-11 Balmy
:      :--16
:      : : :-9 Eubau
:      : : :-15
:      : : :-12 Eubgl
:-----25
:      :-----13 Capma
:-----24
:      : :---10 Escro
:-----23
:      :      :--8 Balac
:      :      :--17
:      :      : : :-7 Balbon
:-----22
:      :      : : :-6 Balbor
:      :      : : :-18
:      :      : : :-5 Baled
:      :      : : :-19
:      :      : : :--3 Balmu
:-----21
:      :      : : :--2 Balph
:-----20
:      :      : : :--4 Megno
```

No.1	ext.	branch	S.E.	int.	branch	S.E.
Hipam	1	11.65	0.62	15	0.62	0.14
Balph	2	1.45	0.21	16	1.10	0.19
Balmu	3	1.02	0.18	17	1.07	0.18
Megno	4	1.37	0.20	18	0.80	0.16
Baled	5	0.88	0.16	19	0.45	0.12
Balbor	6	0.40	0.11	20	0.42	0.12
Balbon	7	0.67	0.14	21	0.17	0.09
Balac	8	1.32	0.20	22	0.36	0.12
Eubau	9	0.07	0.05	23	0.45	0.13
Escro	10	2.18	0.26	24	0.59	0.15
Balmy	11	0.68	0.14	25	2.53	0.32
Eubgl	12	0.24	0.08	TBL :	40.26	iter: 4
Capma	13	3.28	0.31	ln L:	-18168.04	+ - 302.04
Phyca	14	6.50	0.47	AIC :	36424.09	

```
#2
:-----1 Hipam
:
:-----14 Phyca
:
:      :-11 Balmy
:      :--16
:      : : :-9 Eubau
:      : : :-15
:      : : :-12 Eubgl
:-----25
:      :-----13 Capma
:-----24
:      : :---10 Escro
```

Tree	ln L	Diff ln L	S.E.	#Para	AIC	Diff AIC	TBL	RELL-BP
1	-18168.0	0.0 <-best		44	36424.1	0.0	ME	0.2609
2	-18170.6	-2.5	9.0	44	36429.1	5.0	0.0	0.1739
3	-18171.9	-3.8	8.7	44	36431.7	7.7	0.0	0.1069
4	-18180.7	-12.6	12.3	44	36449.4	25.3	0.1	0.0496
5	-18186.0	-18.0	10.6	44	36460.1	36.0	0.2	0.0035
6	-18195.9	-27.8	12.0	44	36479.7	55.7	0.3	0.0005
7	-18192.9	-24.8	12.4	44	36473.7	49.6	0.1	0.0041
8	-18190.0	-22.0	17.1	44	36468.1	44.0	0.2	0.0064
9	-18190.4	-22.4	16.1	44	36468.8	44.7	0.2	0.0101
10	-18195.1	-27.1	12.3	44	36478.2	54.1	0.3	0.0005
11	-18197.7	-29.7	16.1	44	36483.4	59.4	0.3	0.0008
12	-18189.8	-21.7	14.3	44	36467.6	43.5	0.1	0.0236
13	-18198.0	-29.9	15.2	44	36484.0	59.9	0.3	0.0000
14	-18191.1	-23.1	12.9	44	36470.2	46.1	0.2	0.0075
15	-18196.9	-28.8	12.7	44	36481.8	57.7	0.2	0.0001
16	-18198.8	-30.8	15.2	44	36485.7	61.6	0.3	0.0001
17	-18198.4	-30.3	15.0	44	36484.8	60.7	0.3	0.0005
18	-18195.8	-27.8	15.6	44	36479.7	55.6	0.1	0.0019
19	-18196.3	-28.2	15.1	44	36480.6	56.5	0.1	0.0011
20	-18200.4	-32.4	13.9	44	36488.8	64.7	0.3	0.0000
21	-18186.6	-18.6	17.4	44	36461.3	37.2	0.2	0.0141
22	-18202.9	-34.9	17.2	44	36493.8	69.7	0.2	0.0001
23	-18183.8	-15.8	19.4	44	36455.7	31.6	0.2	0.0687
24	-18193.6	-25.6	14.1	44	36475.2	51.2	0.2	0.0022
25	-18202.5	-34.5	15.4	44	36493.0	68.9	0.3	0.0000
26	-18192.4	-24.3	14.5	44	36472.8	48.7	0.2	0.0024
27	-18185.7	-17.6	17.1	44	36459.3	35.2	0.2	0.0365
28	-18192.0	-23.9	14.8	44	36471.9	47.8	0.2	0.0067
29	-18187.8	-19.7	18.4	44	36463.5	39.4	0.2	0.0136
30	-18195.9	-27.8	18.5	44	36479.8	55.7	0.2	0.0126
31	-18191.1	-23.0	15.2	44	36470.2	46.1	0.2	0.0062
32	-18204.5	-36.4	16.1	44	36496.9	72.9	0.3	0.0001
33	-18203.4	-35.4	16.5	44	36494.8	70.8	0.2	0.0000
34	-18212.7	-44.7	15.8	44	36513.4	89.3	0.3	0.0000
35	-18209.7	-41.7	16.3	44	36507.4	83.3	0.3	0.0001
36	-18201.1	-33.0	18.0	44	36490.1	66.0	0.2	0.0037
37	-18201.8	-33.8	16.8	44	36491.7	67.6	0.2	0.0011
38	-18195.5	-27.4	17.9	44	36478.9	54.9	0.2	0.0093
39	-18209.6	-41.5	17.2	44	36507.1	83.1	0.4	0.0003
40	-18205.2	-37.2	17.4	44	36498.4	74.4	0.2	0.0005
41	-18212.3	-44.2	15.7	44	36512.6	88.5	0.3	0.0000
42	-18210.0	-41.9	15.9	44	36508.0	83.9	0.3	0.0001
43	-18212.1	-44.1	15.9	44	36512.2	88.1	0.4	0.0000
44	-18212.9	-44.8	17.6	44	36513.7	89.7	0.3	0.0005
45	-18205.5	-37.5	19.2	44	36499.0	74.9	0.2	0.0080
46	-18214.0	-46.0	21.2	44	36516.1	92.0	0.3	0.0003
47	-18220.3	-52.3	19.8	44	36528.7	104.6	0.5	0.0000
48	-18218.4	-50.4	21.0	44	36524.8	100.7	0.4	0.0000
49	-18218.4	-50.4	19.9	44	36524.8	100.7	0.5	0.0000
50	-18204.3	-36.3	18.9	44	36496.7	72.6	0.3	0.0028
51	-18217.8	-49.8	21.4	44	36523.7	99.6	0.3	0.0008

14 3535 sites mtREV24-F nd1 nd2 cox1 cox2 atp8 atp6 cox3 nd3 nd41 nd4 nd5 cob

Hipam Hippopotamus amphibius (hippopotamus)
0.00000000000 0.153580525863 0.152341133796 0.151332783168 0.154100981904
0.151740699891 0.151384309969 0.152927634810 0.151231079281 0.151776098041
0.152494603302 0.152069177505 0.158653083608 0.173257287807

Balph Balaenoptera physalus (fin whale)
0.153580525863 0.00000000000 0.027861710165 0.027404145088 0.035190847377
0.030482220514 0.031910037028 0.038960084185 0.039462576534 0.042835529946
0.041894923216 0.041829729679 0.053327901901 0.107486453535

Balmu Balaenoptera musculus (blue whale)
0.152341133796 0.027861710165 0.00000000000 0.028289243438 0.024794483896
0.020420925868 0.029496610867 0.035331685494 0.038948648668 0.036196198259
0.038051509922 0.040120942278 0.050363073264 0.104786677038

Megno Megaptera novaeangliae (Humpback whale)
0.151332783168 0.027404145088 0.028289243438 0.00000000000 0.032404039101
0.029486715894 0.032751311032 0.038843575223 0.040670432928 0.040305238223
0.041263185592 0.041832834680 0.049738366917 0.104817245281

Baled Balaenoptera edeni (Bryde's whale)
0.154100981904 0.035190847377 0.024794483896 0.032404039101 0.00000000000
0.012580464517 0.033631193639 0.039174305753 0.042488823733 0.039211572680
0.042462637654 0.043072749274 0.050023868060 0.104225746502

Balbor Balaenoptera borealis (Sei whale)
0.151740699891 0.030482220514 0.020420925868 0.029486715894 0.012580464517
0.00000000000 0.032159531065 0.035046051142 0.040132044288 0.037153245901
0.039240687397 0.041305235984 0.047639492109 0.103350050478

Balbon Balaenoptera bonaerensis (Antarctic minke whale)
0.151384309969 0.031910037028 0.029496610867 0.032751311032 0.033631193639
0.032159531065 0.00000000000 0.019788277844 0.038625544093 0.037401807203
0.039564209075 0.039503464854 0.050997249360 0.102593094788

Balac Balaenoptera acutorostrata (North Atlantic minke whale)
0.152927634810 0.038960084185 0.035331685494 0.038843575223 0.039174305753
0.035046051142 0.019788277844 0.00000000000 0.046559861473 0.043295975025
0.047187474786 0.048033263921 0.053837374383 0.106310304179

Eubau Eubalaena australis (Southern right whale)
0.151231079281 0.039462576534 0.038948648668 0.040670432928 0.042488823733
0.040132044288 0.038625544093 0.046559861473 0.00000000000 0.044571119424
0.013682619178 0.003118727878 0.052391890505 0.097736656928

Escro Eschrichtius robustus (Grey whale)
0.151776098041 0.042835529946 0.036196198259 0.040305238223 0.039211572680
0.037153245901 0.037401807203 0.043295975025 0.044571119424 0.00000000000
0.044320382285 0.044806243269 0.053606001107 0.102507043017

Balmy Balaena mysticetus (Bowhead whale)
0.152494603302 0.041894923216 0.038051509922 0.041263185592 0.042462637654
0.039240687397 0.039564209075 0.047187474786 0.013682619178 0.044320382285
0.00000000000 0.015122707747 0.052609295950 0.097840413246

Eubgl Eubalaena glacialis (Northern right whale)
0.152069177505 0.041829729679 0.040120942278 0.041832834680 0.043072749274
0.041305235984 0.039503464854 0.048033263921 0.003118727878 0.044806243269
0.015122707747 0.00000000000 0.053611075154 0.097723878711

Capma Caperea marginata (Pygmy right whale)
0.158653083608 0.053327901901 0.050363073264 0.049738366917 0.050023868060
0.047639492109 0.050997249360 0.053837374383 0.052391890505 0.053606001107
0.052609295950 0.053611075154 0.00000000000 0.114025556143

Phyca Physeter catodon (sperm whale)
0.173257287807 0.107486453535 0.104786677038 0.104817245281 0.104225746502
0.103350050478 0.102593094788 0.106310304179 0.097736656928 0.102507043017
0.097840413246 0.097723878711 0.114025556143 0.00000000000

njdist 1.2.5 14 OTUs 3535 sites mtREV24-F nd1 nd2 cox1 cox2 atp8 atp6 cox3 nd3 nd41 nd4 nd5
cob

```
      :--2 Balph
      :-22
      :  :--4 Megno
      :-25
      :  :  :--3 Balmu
      :  :-23
      :    :  :-5 Baled
      :    :-18
      :      :-6 Balbor
      :-24
      :  :  :-7 Balbon
      :  :-19
      :    :--8 Balac
      :-21
      :  :---10 Escro
      :-20
      :  :----13 Capma
:--15
:  :  :-9 Eubau
:  :  :-16
:  :  :  :-12 Eubgl
:  :--17
:    :-11 Balmy
:
:-----14 Phyca
:
:-----1 Hipam
```

njdist.tpl:

```
(((((Balph,Megno),(Balmu,(Baled,Balbor))),(Balbon,Balac)),Escro),Capma),((Eubau,Eubgl),Balmy),Phyca,Hipam);
```

~

protml 2.3b6 mtREV24-F 14 OTUs 3535 sites. nd1 nd2 cox1 cox2 atp8 atp6 cox3 nd3 nd41 nd4 nd5 cob
 ((((((Balph,Megno),(Balmu,(Baled,Balbor))), (Balbon,Balac)), Escro), Capma), ((Eubau,Eubgl), Balmy)), Phyca, Hipam);

```

      :--2 Balph
      :-15 94
      : :--4 Megno
      :-18 48
      : : :--3 Balmu
      : :-17 98
      : : : -5 Baled
      : :-16 100
      : : -6 Balbor
      :-20 84
      : : : -7 Balbon
      : :--19 100
      : :--8 Balac
      :-21 97
      : :--10 Escro
      :-22 99
      : :--13 Capma
      :--25 100
      : : : -9 Eubau
      : : : -23 100
      : : : -12 Eubgl
      : :--24 100
      : : -11 Balmy
      :
      :-----14 Phyca
      :
      :-----1 Hipam
  
```

No.1	ext.	branch	S.E.	int.	branch	S.E.	LBP	2nd	pair
Hipam	1	11.65	0.62	15	0.42	0.12	0.940	0.058	17&4
Balph	2	1.45	0.21	16	0.80	0.16	1.0	0.0	3&6
Balmu	3	1.02	0.18	17	0.45	0.12	0.981	0.019	3&15
Megno	4	1.37	0.20	18	0.17	0.09	0.478	0.307	19&17
Baled	5	0.88	0.16	19	1.07	0.18	1.0	0.0	7&18
Balbor	6	0.40	0.11	20	0.36	0.12	0.837	0.142	10&19
Balbon	7	0.67	0.14	21	0.45	0.13	0.966	0.028	13&10
Balac	8	1.32	0.20	22	0.59	0.15	0.990	0.009	21&24
Eubau	9	0.07	0.05	23	0.62	0.14	1.0	0.0	11&12
Escro	10	2.18	0.26	24	1.10	0.19	1.0	0.0	22&11
Balmy	11	0.68	0.14	25	2.53	0.32	1.0	0.0	14&24
Eubgl	12	0.24	0.08	TBL :		40.26	iter: 1		
Capma	13	3.28	0.31	ln L:	-18168.04	+ -	302.04		
Phyca	14	6.50	0.47	AIC :	36424.09				

分子系統樹作成の手順:

3. 最尤法による系統樹の構築 (MOLPHYを例に)

- 複数の遺伝子で得られた結果を総合的に評価
分子系統樹推定における最尤法の利点の一つは、データが蓄積するにつれてより現実的なモデルを構築することが可能になり、しかもその際AICのように、考え得るモデルのうちでどれが一番よいモデルであるかを判定する客観的な規準がある。

MOLPHYでは、各遺伝子で得られた結果を総合的に評価することができる。

```
% protml -mfv -u -l ND1 sequence_file topology_file > outfile
```

その場合自動的にND1.llsファイルができる

```
% totalml *.lls > total_file
```

totalml 1.2 (01/26/00) 24 data sets 8155 sites.

tree	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	total
1	5.0	7.1	5.8	8.4	9.6	1.6	3.0	2.5	1.5	8.5	6.4	1.0	5.2	3.8	6.3	3.2	5.1	4.8	4.5	5.9	1.8	13.8	11.4	11.6	96.7
2	8105.2	3.4	4282.5	1.9	2.0	1.5	2964.0	710.9	0.4	5.8	0.3	1748.0	2.4	3.4	4.5	5.4	4.6	5.0	6.3	7.9	2.0	8.1	9.6	6.9	26.5
3	3.1	1.7	1.0	1.9	2.0	1.5	1.4	1.4	0.9	6.3	1617.1	1.3	2.4	0.0	3.6	3.4	3.2	4.0	1.2	7.6	4.5	14.9	9.8	10.5	46.3
4	3.5	10467.3	1.3	7010.3	3764.6	1.5	1.1	1.4	2216.5	2889.0	0.1	1.4	7509.9	0.0	3.6	2.1	1.9	3.1	2.7	4.6	3.4	14.9	11.7	8.2	25.2
5	7.4	7.4	10.2	11.7	11.3	1.5	3.1	3.3	0.7	1.8	7.8	4.7	3.2	3.1	9.3	3.1	858.9	4.1	7.7	6.9	2.8	15.1	9.6	9.2	103.8
6	7.1	4.6	6.9	5.9	7.2	2.0	3.4	2.6	1.4	2.3	4.9	3.9	5.7	4.2	6.7	4.7	ml	5.4	5.1	7.7	3.7	7.8	10.3	6.2	26.9
7	5.3	10.1	8.2	14.2	13.9	2237.1	1.2	1.1	1.0	8.0	9.7	2.8	8.6	3.8	6.3	2.4	3.3	2.1	4.6	3.9	4.6	3.1	1821.0	1.9	78.6
8	9.2	5.9	10.2	9.2	10.7	1.5	3.1	3.3	0.7	1.8	7.8	4.7	5.3	3.8	8.8	2.5	2.8	3.7	7.7	6.9	0.4	13.9	13.8	3.6	100.0
9	5.3	12.3	8.2	14.2	13.9	0.1	1.1	1.1	1.0	8.0	9.7	2.7	6.4	3.8	4.7	4974.8	3.2	4.9	4.6	3.9	3.8	1837.5	0.2	9.0	80.8
10	3.9	6.1	6.2	6.6	7.5	3.1	2.0	2.3	2.3	5.5	5.4	3.0	6.6	3.4	5.4	ml	5.6	4.9	4.1	3.8	4.1	ml	1.2	7.7	23.1
11	8.0	12.3	10.7	14.2	15.3	0.1	3.4	3.3	1.7	7.5	9.7	4.0	5.3	3.1	8.7	2.2	0.5	4.9	7.7	9.9	3.3	5.4	8.0	10.7	118.7
12	7.0	6.1	7.0	6.6	8.2	3.1	3.3	2.6	2.1	4.7	5.4	3.8	7.0	4.2	7.0	2.5	3.9	4.9	5.1	5.9	4.5	4.3	9.3	7.4	27.3
13	10.6	9.0	10.7	11.3	14.9	0.0	3.6	3.3	1.7	8.8	9.7	4.7	8.7	3.8	9.1	3.9	5.7	0.9	6.9	12.3	0.4	11.0	10.4	1546.6	120.0
14	5.4	7.2	7.0	7.7	8.5	0.0	3.2	2.6	2.1	5.4	5.4	3.9	5.8	3.4	7.0	5.2	4.1	3.6	4.8	6.4	0.9	8.8	6.8	ml	26.5
15	9.7	10.2	10.7	11.3	14.9	1.5	3.6	3.3	1.7	8.8	9.7	2.6	8.4	3.8	7.8	2.6	5.1	3.7	5.5	8.0	1862.9	12.7	13.8	3.7	121.7
sites	781	1074	304	314	501	1119	225	30	163	257	101	86	416	243	473	365	138	372	140	146	99	331	332	145	8155

same bootstrap likelihood occurred 1 times

tree	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	total
1	0.0101	0.0106	0.0224	0.0146	0.0137	0.0390	0.0063	0.0091	0.0129	0.0024	0.0093	0.2318	0.0166	0.0000	0.0448	0.0375	0.0030	0.0103	0.1087	0.0884	0.0422	0.0005	0.0039	0.0000	0.0000
2	0.4210	0.0141	0.5020	0.0923	0.1145	0.0123	0.3757	0.4926	0.2448	0.0711	0.0447	0.4100	0.0525	0.5010	0.6319	0.1885	0.2384	0.0239	0.4882	0.5016	0.0533	0.0173	0.1429	0.0480	0.9220
3	0.0307	0.2627	0.2277	0.1057	0.0823	0.0041	0.0553	0.1271	0.0541	0.0144	0.3420	0.0544	0.0448	0.1066	0.0386	0.0051	0.0072	0.0140	0.2625	0.0062	0.0024	0.0000	0.0133	0.0021	0.0002
4	0.0549	0.5407	0.1316	0.6894	0.7165	0.0113	0.2019	0.0332	0.3405	0.6797	0.4050	0.0558	0.5458	0.1540	0.0263	0.1017	0.1052	0.1265	0.0162	0.1379	0.0219	0.0008	0.0002	0.0340	0.0777
5	0.0130	0.0026	0.0031	0.0002	0.0067	0.0011	0.0431	0.0011	0.0290	0.1075	0.0014	0.0001	0.1900	0.0939	0.0072	0.0319	0.2839	0.0148	0.0001	0.0244	0.0919	0.0000	0.0094	0.0023	0.0000
6	0.3027	0.0367	0.0587	0.0070	0.0030	0.0001	0.0194	0.0103	0.0102	0.0029	0.1480	0.0164	0.0055	0.0001	0.0025	0.0008	0.0000	0.0147	0.0087	0.0453	0.0002	0.0000	0.0576	0.0001	0.0000
7	0.0084	0.0025	0.0322	0.0000	0.0048	0.2768	0.0757	0.1911	0.1079	0.0120	0.0000	0.0315	0.0001	0.0041	0.0049	0.0189	0.0186	0.0322	0.0408	0.0322	0.0020	0.2251	0.3164	0.2811	0.0001
8	0.0001	0.0743	0.0066	0.0676	0.0525	0.0009	0.0123	0.0007	0.1602	0.0859	0.0077	0.0000	0.0077	0.0005	0.0122	0.1026	0.0122	0.0196	0.0000	0.0135	0.0833	0.0013	0.0000	0.0778	0.0000
9	0.0191	0.0000	0.0101	0.0000	0.0008	0.1564	0.1755	0.1272	0.0136	0.0081	0.0000	0.0304	0.0140	0.0090	0.1209	0.2600	0.0192	0.0057	0.0117	0.0302	0.0153	0.5209	0.2268	0.0056	0.0000
10	0.1359	0.0003	0.0013	0.0000	0.0001	0.0099	0.0029	0.0009	0.0011	0.0052	0.0222	0.0049	0.0124	0.0134	0.0062	0.0016	0.0323	0.0250	0.0000	0.0063	0.0172	0.0000	0.1126	0.0001	0.0000
11	0.0013	0.0000	0.0000	0.0000	0.0000	0.1019	0.0101	0.0016	0.0000	0.0055	0.0000	0.0040	0.0736	0.1153	0.0149	0.0126	0.2250	0.0054	0.0002	0.0003	0.0794	0.0139	0.0546	0.0009	0.0000
12	0.0023	0.0199	0.0030	0.0000	0.0001	0.1267	0.0022	0.0035	0.0093	0.0004	0.0192	0.0039	0.0000	0.0020	0.0000	0.0000	0.0002	0.4300	0.0028	0.0033	0.0001	0.0025	0.0612	0.0120	0.0000
13	0.0000	0.0347	0.0008	0.0092	0.0011	0.0845	0.0012	0.0003	0.0091	0.0028	0.0000	0.0003	0.0000	0.0000	0.0032	0.0039	0.0002	0.2178	0.0039	0.0000	0.0982	0.0402	0.0008	0.5006	0.0000
14	0.0002	0.0000	0.0003	0.0000	0.0002	0.1665	0.0177	0.0013	0.0017	0.0002	0.0001	0.1079	0.0359	0.0000	0.0155	0.1624	0.0449	0.0005	0.0283	0.1008	0.1913	0.1640	0.0003	0.0026	0.0000
15	0.0003	0.0009	0.0002	0.0140	0.0037	0.0085	0.0007	0.0000	0.0056	0.0019	0.0004	0.0486	0.0011	0.0001	0.0709	0.0725	0.0097	0.0596	0.0279	0.0096	0.3513	0.0135	0.0000	0.0328	0.0000

分子系統樹作成の手順:

- 3. 系統樹の構築 (MOLPHYを例に)

- c) 配列内の進化速度の不均質性への考慮

- 進化速度の不均質性を考慮するためにはガンマ分布を取り入れた解析が有力である.

- PAUP、PAML、TREE-PUZZLEなどのソフトウェアがある。

分子系統樹作成の手順:

- 1. アミノ酸配列や塩基配列などの分子データの収集
(EMBL/NCBI/DDBJなどのデータベースから)
- 2. 配列データの整列(alignment)
- 3. 最尤法による系統樹の構築
 - a) アミノ酸組成、塩基組成の変化の確認
 - b) アミノ酸置換、塩基置換モデルの選択
 - c) 配列内の進化速度の不均質性への考慮
- 4. 推定された最尤系統樹の信頼性の評価

Comparison of log-likelihood scores among the 15 possible trees among Aves(Bi), Crocodylia(Al), Testudines(Tu), Squamata(Li) for nucleotides with the HKY model and HKY + Γ model. The log-likelihood values of the highest likelihood trees are given in angle brackets, and the differences in log-likelihood of alternative trees from that of the ML tree are shown with their S.E. following \pm .

AU: Approximate unbiased, BP: RELL bootstrap probability, KH: Kishino-Hasegawa test, SH: Shimodaira-Hasegawa test.

topology	HKY model						HKY + Γ model					
	l \pm SE	AU	BP	KH	SH	l \pm SE	AU	BP	KH	SH		
01 ((Bi,(Tu,Al)),Li)	<-15531.0>	0.968	0.918	0.944	0.999	<-14984.7>	0.837	0.698	0.778	0.972		
02 (Bi,((Tu,Al),Li))	-21.8 \pm 13.8	0.081	0.046	0.056	0.377	-4.2 \pm 5.6	0.356	0.172	0.222	0.669		
03 ((Bi,Li),(Tu,Al))	-23.6 \pm 13.4	0.064	0.029	0.043	0.333	-5.0 \pm 5.3	0.248	0.108	0.169	0.630		
04 (((Bi,Al),Tu),Li)	-54.7 \pm 16.4	0.001	0.000	0.000	0.022	-23.0 \pm 9.1	0.009	0.002	0.009	0.036		
05 (Bi,((Tu,Li),Al))	-57.2 \pm 23.5	0.015	0.005	0.008	0.015	-21.2 \pm 11.4	0.036	0.012	0.032	0.051		
06 (((Bi,Tu),Al),Li)	-61.5 \pm 15.3	0.002	0.000	0.000	0.007	-24.1 \pm 8.7	0.014	0.001	0.005	0.024		
07 (((Bi,Li),Tu),Al)	-65.2 \pm 21.9	0.002	0.000	0.002	0.004	-24.5 \pm 11.4	0.021	0.005	0.018	0.028		
08 (Bi,(Tu,(Al,Li)))	-74.0 \pm 21.6	0.001	0.000	0.000	0.001	-24.7 \pm 10.5	0.005	0.000	0.010	0.017		
09 (((Bi,Li),Al),Tu)	-75.0 \pm 20.4	0.000	0.000	0.000	0.001	-27.3 \pm 10.6	0.004	0.000	0.007	0.011		
10 ((Bi,(Tu,Li)),Al)	-87.0 \pm 24.6	0.000	0.000	0.001	0.001	-30.0 \pm 12.3	0.016	0.002	0.009	0.012		
11 ((Bi,Al),(Tu,Li))	-90.3 \pm 23.8	0.000	0.000	0.000	0.000	-31.9 \pm 11.8	0.012	0.000	0.005	0.007		
12 (((Bi,Tu),Li),Al)	-106.4 \pm 22.4	0.001	0.000	0.000	0.000	-33.3 \pm 11.6	0.022	0.000	0.003	0.004		
13 (((Bi,Al),Li),Tu)	-108.1 \pm 21.6	0.000	0.000	0.000	0.000	-35.1 \pm 11.1	0.015	0.000	0.002	0.002		
14 ((Bi,Tu),(Al,Li))	-114.4 \pm 21.2	0.000	0.000	0.000	0.000	-36.6 \pm 10.8	0.000	0.000	0.001	0.001		
15 ((Bi,(Al,Li)),Tu)	-114.9 \pm 21.3	0.000	0.000	0.000	0.000	-36.6 \pm 10.8	0.000	0.000	0.001	0.001		

Comparison of log-likelihood scores among the 15 possible trees among Aves(Bi), Crocodylia(Al), Testudines(Tu), Squamata(Li) for proteins with the JTT-F model and JTT-F + Γ model. The log-likelihood values of the highest likelihood trees are given in angle brackets, and the differences in log-likelihood of alternative trees from that of the ML tree are shown with their S.E. following \pm .

AU: Approximate unbiased, BP: REll bootstrap probability, KH: Kishino-Hasegawa test, SH: Shimodaira-Hasegawa test.

topology	JTT-F model					JTT-F + Γ model				
	l \pm SE	AU	BP	KH	SH	l \pm SE	AU	BP	KH	SH
01 ((Bi,(Tu,Al)),Li)	-5.1 \pm 7.7	0.370	0.165	0.244	0.718	-3.6 \pm 4.1	0.265	0.117	0.186	0.635
02 (Bi,((Tu,Al),Li))	-5.2 \pm 7.7	0.381	0.159	0.242	0.714	-3.7 \pm 4.1	0.281	0.109	0.183	0.630
03 ((Bi,Li),(Tu,Al))	<-5890.4>	0.881	0.560	0.756	0.976	<-5789.3>	0.928	0.669	0.814	0.980
04 (((Bi,Al),Tu),Li)	-25.6 \pm 14.8	0.053	0.010	0.041	0.083	-18.5 \pm 9.3	0.038	0.004	0.025	0.037
05 (Bi,((Tu,Li),Al))	-26.1 \pm 12.7	0.003	0.000	0.026	0.060	-16.2 \pm 8.0	0.011	0.000	0.026	0.049
06 (((Bi,Tu),Al),Li)	-29.8 \pm 13.8	0.007	0.000	0.018	0.034	-19.3 \pm 9.0	0.014	0.000	0.019	0.027
07 (((Bi,Li),Tu),Al)	-15.9 \pm 10.4	0.105	0.029	0.069	0.311	-10.1 \pm 7.7	0.148	0.063	0.093	0.269
08 (Bi,(Tu,(Al,Li)))	-20.9 \pm 13.8	0.087	0.024	0.064	0.161	-15.0 \pm 8.5	0.076	0.013	0.042	0.080
09 (((Bi,Li),Al),Tu)	-14.6 \pm 10.8	0.153	0.052	0.091	0.353	-11.4 \pm 7.3	0.074	0.019	0.064	0.203
10 ((Bi,(Tu,Li)),Al)	-35.5 \pm 14.1	0.000	0.000	0.008	0.014	-18.9 \pm 9.7	0.030	0.002	0.028	0.040
11 ((Bi,Al),(Tu,Li))	-33.6 \pm 14.7	0.055	0.001	0.017	0.026	-20.4 \pm 9.5	0.004	0.000	0.018	0.027
12 (((Bi,Tu),Li),Al)	-35.0 \pm 14.3	0.001	0.000	0.010	0.016	-18.8 \pm 9.7	0.030	0.004	0.029	0.041
13 (((Bi,Al),Li),Tu)	-30.2 \pm 15.2	0.039	0.002	0.030	0.047	-19.5 \pm 9.7	0.043	0.004	0.023	0.035
14 ((Bi,Tu),(Al,Li))	-33.3 \pm 14.7	0.009	0.000	0.017	0.025	-20.0 \pm 9.6	0.016	0.000	0.022	0.032
15 ((Bi,(Al,Li)),Tu)	-30.0 \pm 15.3	0.028	0.002	0.028	0.047	-19.2 \pm 9.8	0.049	0.003	0.027	0.039

Comparison of log-likelihood scores among the 15 possible trees among Afrotheria (Elephant(Ele), Aardvark(Aar), Tenrec(Ten)) and Eulipotyphla (Shrew(Shr), Mole(Mol), Hedgehog(Hed)) for the 12 mt-proteins. The analyses are based on the Shr/Mol and Ele/Aar grouping. The log-likelihood values of the highest likelihood trees are given in angle brackets, and the differences in log-likelihood of alternative trees from that of the ML tree are shown with their S.E. following \pm .

AU: Approximate unbiased, BP: RELL bootstrap probability, KH: Kishino-Hasegawa test, SH: Shimodaira-Hasegawa test.

	mtREV-F model						mtREV-F + Γ model					
topology	l \pm SE	AU	BP	KH	SH		l \pm SE	AU	BP	KH	SH	
1 ((ShrMol,Hed),(EleAar,Ten))	-23.2 \pm 17.8	0.152	0.082	0.092	0.402		<-28553.9>	0.838	0.676	0.732	0.988	
2 ((ShrMol,(EleAar,Ten)),Hed)	<-29813.4>	0.903	0.734	0.819	0.995		-6.4 \pm 10.9	0.390	0.243	0.268	0.650	
3 (((ShrMol,Hed),Ten),EleAar)	-53.9 \pm 24.1	0.015	0.001	0.013	0.038		-13.4 \pm 7.4	0.069	0.021	0.039	0.355	
4 (((ShrMol,Hed),EleAar),Ten)	-46.3 \pm 23.8	0.031	0.005	0.026	0.068		-13.6 \pm 7.3	0.049	0.011	0.034	0.350	
5 (ShrMol,((EleAar,Ten),Hed))	-47.3 \pm 14.5	0.001	0.000	0.001	0.062		-18.5 \pm 8.4	0.005	0.001	0.017	0.181	
6 (((ShrMol,EleAar),Ten),Hed)	-15.7 \pm 17.3	0.254	0.165	0.181	0.572		-18.9 \pm 15.0	0.130	0.045	0.102	0.183	
7 (((ShrMol,Ten),EleAar),Hed)	-37.5 \pm 14.1	0.002	0.000	0.004	0.154		-26.0 \pm 13.7	0.002	0.000	0.029	0.049	
8 ((ShrMol,EleAar),(Ten,Hed))	-44.1 \pm 24.8	0.042	0.009	0.039	0.092		-28.6 \pm 14.0	0.014	0.002	0.020	0.038	
9 (ShrMol,(EleAar,(Ten,Hed)))	-54.6 \pm 22.4	0.013	0.002	0.009	0.029		-28.6 \pm 11.6	0.008	0.001	0.006	0.028	
10 (((ShrMol,EleAar),Hed),Ten)	-60.3 \pm 23.4	0.000	0.000	0.005	0.014		-30.1 \pm 13.9	0.009	0.000	0.014	0.027	
11 (ShrMol,((EleAar,Hed),Ten))	-82.1 \pm 19.9	0.000	0.000	0.000	0.000		-30.9 \pm 11.2	0.011	0.000	0.004	0.016	
12 ((ShrMol,(Ten,Hed)),EleAar)	-64.3 \pm 25.0	0.007	0.000	0.005	0.008		-35.1 \pm 12.2	0.004	0.000	0.002	0.007	
13 (((ShrMol,Ten),Hed),EleAar)	-86.9 \pm 22.7	0.013	0.000	0.000	0.000		-37.7 \pm 11.8	0.015	0.000	0.001	0.003	
14 ((ShrMol,(EleAar,Hed)),Ten)	-89.0 \pm 22.4	0.000	0.000	0.000	0.000		-40.0 \pm 11.8	0.013	0.000	0.001	0.001	
15 ((ShrMol,Ten),(EleAar,Hed))	-96.0 \pm 21.2	0.023	0.000	0.000	0.000		-41.1 \pm 11.8	0.025	0.000	0.001	0.001	

Comparison of log-likelihood scores among the 9 possible trees of the phylogenetic position of hedgehog among Afrotheria (Elephant(Ele), Aardvark(Aar), Tenrec(Ten)) and the phylogenetic position of tenrec among Eulipotyphla (Shrew(Shr), Mole(Mol), Hedgehog(Hed)) for the 12 mt-proteins. The log-likelihood values of the highest likelihood trees are given in angle brackets, and the differences in log-likelihood of alternative trees from that of the ML tree are shown with their S.E. following \pm .

AU: Approximate unbiased, BP: RELL bootstrap probability, KH: Kishino-Hasegawa test, SH: Shimodaira-Hasegawa test.

	mtREV-F model						mtREV-F + Γ model					
topology	l \pm SE	AU	BP	KH	SH		l \pm SE	AU	BP	KH	SH	
1 (((Shr,Mol),Hed),(Ele,Aar),Ten))	<-29836.6>	0.697	0.572	0.636	0.917		<-28553.9>	0.842	0.776	0.791	0.972	
2 (((Shr,Mol),Hed),(Ele,Ten),Aar))	-4.7 \pm 14.2	0.435	0.328	0.364	0.750		-10.3 \pm 7.0	0.073	0.028	0.075	0.351	
3 (((Shr,Mol),Hed),(Ele,(Aar,Ten)))	-11.9 \pm 13.7	0.182	0.102	0.194	0.571		-6.6 \pm 8.1	0.246	0.194	0.209	0.526	
4 ((Shr,(Mol,Hed)),(Ele,Aar),Ten))	-88.6 \pm 19.3	0.001	0.000	0.000	0.000		-30.2 \pm 9.9	0.002	0.001	0.002	0.014	
5 ((Shr,(Mol,Hed)),(Ele,Ten),Aar))	-89.5 \pm 23.6	0.001	0.000	0.000	0.000		-39.9 \pm 12.0	0.001	0.000	0.001	0.001	
6 (((Shr,Hed),Mol),(Ele,Aar),Ten))	-90.3 \pm 19.0	0.000	0.000	0.000	0.000		-30.8 \pm 9.7	0.001	0.000	0.001	0.012	
7 (((Shr,Hed),Mol),(Ele,Ten),Aar))	-90.5 \pm 23.4	0.006	0.000	0.000	0.000		-40.2 \pm 11.9	0.001	0.000	0.000	0.001	
8 ((Shr,(Mol,Hed)),(Ele,(Aar,Ten)))	-97.2 \pm 23.2	0.000	0.000	0.000	0.000		-35.9 \pm 12.7	0.002	0.000	0.003	0.003	
9 (((Shr,Hed),Mol),(Ele,(Aar,Ten)))	-97.7 \pm 23.0	0.000	0.000	0.000	0.000		-36.2 \pm 12.7	0.003	0.000	0.002	0.003	

SB17F M-NFALILM-INTLLALLLMIITFWLPQLNGYMEKSTPYECGFDPMSPARVPSMKFFLVAITFLLFDLEIALLPLPWAQTNNPLMVMS-SLLIIILALSLAYEWLQKGLDWAEE----
 CHIMP M-NFVLILM-TNTLLALLLMIITFWLPQLNSYMEKSTPYECGFDPMSPARVPSMKFFLVAITFLLFDLEIALLPLPWAQTANPLMVMS-SLLITILALSLAYEWLQKGLDWAEE----
 PyGC M-NFVLILM-TNTLLALLLMIITFWLPQLNSYMEKSNPYECGFDPMSPARVPSMKFFLVAITFLLFDLEIALLPLPWAQTANPLMVMS-SLLITILALSLAYEWLQKGLDWAEE----
 GORIL M-NFALILM-TNTLLALLLMIITFWLPQLNSYMEKSTPYECGFDPMSPARVPSMKFFLVAITFLLFDLEIALLPLPWAQTNNPLMVMS-SLLIIILALSLAYEWLQKGLDWAEE----
 ORANG I-NFVLALT-INTLLALLLMIITFWLPQLNPYMEKSDPYECGFDPAYPARIPFSMKFFLVAITFLLFDLEIALLPLPWAQTNNPLMSTTS-SLMLIIILALGLTYEWSQKGLDWAEE----
 Ponpy I-NFVLALT-VNTLLALLLMIITFWLPQLNPYMEKSDPYECGFDPAYPARIPFSMKFFLVAITFLLFDLEIALLPLPWAQTNNPLMSTTS-SLMLIIILALGLTYEWSQKGLDWAEE----
 Hylla M-NLALALM-INTLLALLLMIITFWLPQLNTYMEKSTPYECGFDPSPARIPFSMKFFLVAITFLLFDLEIALLPLPWAQTNNPLSTIAS-SLTLITILILSLAYEWSQKGLDWAEE----
 Papha M-NLMLALT-VNTLLALLLMIITFWLPQLNSYAEKANPYECGFDPNPARIPFSMKFFLVAITFLLFDLEIALLPLPWAQTANPLMTIKT-SIMFITILALSLAYEWLQKGLDWAEE----
 Macsy I-NLALALM-TNTLLALLLMIITFWLPQLNSYAEKSTPYECGFDPNPARIPFSMKFFLVAITFLLFDLEIALLPLPWAQTNNPLQTMIKL-TIALIIILALSLAYEWLQKGLDWAEE----x
 Ceba1 M-NLMLTIA-TSTLLALLLMIITFWMPQLNKYTEKHNPEYECGFDPSTSAHLPFSMKFFLVAITFLLFDLEIALLPLPWAQTNNPLQTMNTM-VFTLLIILALGLAYEWLQKGLDWAEE----
 Nycco I-NTMIMLI-TNTSLASVLLVIAFWLPQLNIYTEKSPYECGFDPGTSARLPFSMKFFLVAITFLLFDLEIALLPLPWAQTNNPLNMLTM-TFLLIILALGLAYEWLQKGLDWAEE----x
 Tupbe M-NLILALV-INTSLAALLVITAFWLPQLNVYMEKSPYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAQTNNPLTMTM-ALLLISILALGLAYEWLQKGLDWAEE----
 Phovi M-NMALTLF-TNTALASLLVIAFWLPQLNTYSEKASPYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTDNLTMTM-ALLLISLLAASLAYEWTEKGLDWAEE----
 Halgr M-NMALTLF-TNTALASLLVIAFWLPQLNTYSEKASPYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTDNLTMTM-ALLLISLLAASLAYEWTEKGLDWAEE----
 Canfa M-NVMLTLM-TNVTLASLLVIAFWLPQLNIYTDKTSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTDNLTMTM-ALLLISLLAASLAYEWTEKGLDWAEE----x
 Felca M-NVMLALL-TNTLLSTLLVIAFWLPQLNIYAEKASPYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTDKLPTMTM-ALLLISLLAASLAYEWTEKGLDWAEE----x
 Equca M-NLMLTLL-TNTLLASLLVIAFWLPQLNIYAEKTSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTNNLNTMTM-ALVLSILLAISLAYEWTEKGLDWAEE----
 Equas M-NLMLTLL-TNTLLASLLVIAFWLPQLNIYAEKTSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTNNLNTMTM-ALVLSILLAISLAYEWTEKGLDWAEE----
 Cersi I-NLMLTLF-INTSLASVLLVIAFWLPQLNIYTEKASPYECGFDPMSARLPFTMKFFLVAITFLLFDLEIALLPLPWAHTNNLKTMTM-ALVLSILLAASLAYEWTEKGLDWAEE----
 Rhiun I-NLILTLL-INTLLSLLVIAFWLPQLNIYTEKSSPYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTNNLKTMTM-ALLLISLLAASLAYEWTEKGLDWAEE----
 Lampa MINLLALL-TNVTLASLLVIAFWLPQLNVYAEKTSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTNNLHTMTM-ALLLISLLAASLAYEWTEKGLDWAEE----
 Sussc M-NIMLTLT-TNVTLASLLVIAFWLPQLNAYSEKTSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTNNLKTMTM-ALFLLIILAAASLAYEWTEKGLDWAEE----
 Sussc2 M-NIMLTLT-TNVTLASLLVIAFWLPQLNAYSEKTSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTNNLKTMTM-ALFLLIILAAASLAYEWTEKGLDWAEE----
 Bosta M-NLMLALL-TNFTLATLLVIAFWLPQLNVYSEKTSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTANLNTMTM-ALFLLIILAAASLAYEWTEKGLDWAEE----x
 Oviar M-NLMLTLL-TNFTLATLLVITAFWLPQLNVYSEKTSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTANLNTMTM-ALFLLIILAAASLAYEWTEKGLDWAEE----x
 Hipam M-NLVMALL-TNTALASLLVIAFWLPQLNSYAEKTSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTNNLKTMTM-ALVLSILLAASLAYEWTEKGLDWAEE----
 Balph M-NLLLTLL-TNTTLALLLVIAFWLPQLNVYAEKTSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTSNNLNTMTM-ALFLISLLAASLAYEWTEKGLDWAEE----
 Balmu M-NLLLTLL-TNTTLALLLVIAFWLPQLNVYAEKTSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTSNNLNTMTM-ALFLISLLAASLAYEWTEKGLDWAEE----x
 Phyca M-NILLTLL-TNTTLALLLMIITAFWLPQLNAYTEKTSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTNNLKTMTM-ALFLLIILAAASLAYEWTEKGLDWAEE----
 Artja M-NMAITLL-TNTFLASLLVIAFWLPQNTNYSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTNNLQNMFLM-SLMLISLLALSLAYEWLQKGLDWAEE----*
 Pteda I-NLMVTLL-TNTLLASLLVIAFWMPQMNTYAEKSSPYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTNNLIMLTM-SLTLVLSLLAVSLAYEWFNKGLEWEE----*
 Ptesc M-NLMITLL-TNTLLASLLVIAFWMPQMNTYAEKSSPYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTNNLIMLTM-SLTLVLSLLAVSLAYEWFNKGLEWEE----*
 Chatu M-NFMLTLL-INTLLALLLVITAFWLPQNTNYSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTNNLISIMLSM-SLFLILLIILISLAYEWMQKGLDWAEE----*
 Rhipu M-NFMLTLL-TNTLLALLLVITAFWLPQNTNYSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTNNLEVMMLT-ALLLISLLAASLAYEWSQKGLDWAEE----*
 Pipab I-NFMLTLF-TNTLLALLLVITAFWLPQNTNYSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTDKLLVMLSM-SLALIMLLIISLAYEWMQKGLDWAEE----*
 Sorun I-NMLLALS-INTLLASLLVIAFWLPQLNVYAEKASPYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTQEQLNIMITM-SLALITLLAMSLAYEWTEKGLDWAEE----*
 Taleu I-NMLLTIT-VNTLLSSILVIAFWLPQLNTYSEKSSPYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTNDVKTVM-ALVLSILALSLAYEWTEKGLDWAEE----
 Dasno I-NIMITLF-INMSLASLLVIAFWLPQLNTYSEKSSPYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTQANTMTMLT-ALVLSILALGLAYEWLQKGLDWAEE----
 Orycu M-NLMLVLL-INTTISLVLVITAFWLPQLNIYSEKSSPYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTQNNLNLVLM-ALMLISILALGLAYEWLQKGLDWAEE----x
 Cavpo M-NIAISLL-TNCSLTLLLITIAFWLPQMNTYTEKTSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTSNNLMLLV-ALMLILVLSGLAYEWLQKGLDWAEE----
 Thrsu M-NMMLALS-FNYLLTLLITIAFWLPQNTNYSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTNNLPLMTMA-SLMLVFLALGLAYEWLQKGLDWAEE----*
 Gligl I-NMMLTIF-INLTLSSILITIAFWLPQLNIYTEKISPYECGFDPMSARLPFSMKFFLVAITFLLCSLEIALLPLPWAHTNNLMLMV-ALVLSILALGLAYEWLQKGLDWAEE----
 Ratno I-NLPIIT-INTLSTLILVIAFWLPQMNLYSEKANPYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTTNTTMMAT-AFLVTLVLSGLAYEWLQKGLDWAEE----*
 Musmu I-NLYTVIF-INILLSLTLVIAFWLPQMNLYSEKANPYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTIKTSTMMIM-AFLVTLVLSGLAYEWLQKGLDWAEE----*
 Musmu2 M-NLYTVIF-INILLSLTLVIAFWLPQMNLYSEKANPYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTIKTSTMMIM-AFLVTLVLSGLAYEWLQKGLDWAEE----
 Scivu M-NLLTLL-INISLILVIAFWLPQNTNYSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTNNLPLMTM-ALVLSILALGLAYEWLQKGLDWAEE----
 Loxaf MINLMITLL-TNMLTSLMVIAFWLPQNTNYSYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTQANNLSTLLM-SFLMIIILALGLAYEWLQKGLDWAEE----
 Oryaf I-NLAISLL-TNMSLASLLVIAFWLPQLNTYMEKSTPYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTNNLKLMLFM-ALLLISLLALSLAYEWMQKGLDWAEE----
 Echte I-NLMITVT-INVLLASLLVIAFWLPQLNIYAEKASPYECGFDPMSARLPFSMKFFLVAITFLLFDLEIALLPLPWAHTSNNLMLMLSM-ALFLVVLVLSGLAYEWLQKGLDWAEE----*