

Evolution Sonata

1. AIMS:

1.1. Translation System

A relatively simple and intuitive system shall translate amino acids into musical notes, giving a one-to-one mapping from amino acids into notes.

1.2. Finding Melodies

Selected sequences of amino acids are translated into note sequences. Then the musically most suitable note sequences (i.e. motives) are selected.

1.3. Composition

The motives become the basis for a sonata for string quartet and piano.

Amino acid sequences that all the selected species have in common become "general" motives, appearing throughout the composition, sequences that change over the evolution (e.g. from bacteria to insect to vertebrate) are introduced over time, to exemplify the process of evolution.

2. HOW IT WORKS:

2.1. Translation system

This figure shows a simple translation system from amino acids into notes (mind that the figure gives note names in German terminology):

Name	Name kürzer	AA	Masse	Isoelektrischer Punkt	System 6 (3 Oktaven)	
Glycin	Gly	G	75	5,97	Hydrophob non sequatur non sequatur	a
Alanin	Ala	A	89,00	6,01	Hydrophob non sequatur non sequatur	g
Prolin	Pro	P	115,00	6,48	Hydrophob non sequatur non sequatur	f
Valin	Val	V	117,00	5,97	Hydrophob non sequatur non sequatur	e
Leucin	Leu	L	131,00	5,98	Hydrophob non sequatur non sequatur	d
Isoleucin	Ile	I	131,00	6,02	Hydrophob non sequatur non sequatur	c
Phenylalanin	Phe	F	165,00	5,48	Hydrophob non sequatur Aromatische Seitenketten	H
Tryptophan	Trp	W	204,00	5,89	Hydrophob non sequatur Aromatische Seitenketten	A
Tyrosin	Tyr	Y	181,00	5,66	Hydrophil non sequatur Aromatische Seitenketten	h
Serin	Ser	S	105,00	5,68	Hydrophil neutral Polare ungeladene	a1
Threonin	Thr	T	119,00	5,87	Hydrophil neutral Polare ungeladene	g1
Cystein	Cys	C	121,00	5,07	Hydrophil neutral Polare ungeladene	f1
Asparagin	Asn	N	132,00	5,41	Hydrophil neutral Polare ungeladene	e1
Glutamin	Gln	Q	146,00	5,65	Hydrophil neutral Polare ungeladene	d1
Methionin	Met	M	149,00	5,74	Hydrophil neutral Polare ungeladene	c1
Aspartat	Asp	D	133,00	2,77	Hydrophil sauer Negativ geladene Seitenketten	fs1
Glutamat	Glu	E	147,00	3,22	Hydrophil sauer Negativ geladene Seitenketten	cls1
Lysin	Lys	K	146,00	9,74	Hydrophil basisch Positiv geladene Seitenketten	as1
Histidin	His	H	155,00	7,59	Hydrophil basisch Positiv geladene Seitenketten	es1
Arginin	Arg	R	174,00	10,76	Hydrophil basisch Positiv geladene Seitenketten	b

Hydrophobic amino acids, being associated with terms like “oily”, “soft”, “viscous” (yellow) receive the notes of the A minor scale in the small octave below middle C (“deep”, “viscous”, “dark”). The bigger the mass, the deeper the note.

Neutral hydrophilic amino acids (cyan) are associated with terms such as “watery”, “bright”, and thus receive the notes of the C major scale (“bright”) in the one-line octave (“high”, “agile”). Here, too, bigger mass means deeper note.

Acidic hydrophilic (blue) are associated with terms like “sour”, “sharp”, and

therefore receive sharps following the circle of fifths, also sorted by mass.

Alkaline amino acids (purple) receive flats following the circle of fourths, for being “opposed” to acidic amino acids, also sorted by mass.

Due to its special position, Tyrosin (green) lies just in the middle between hydrophiles and hydrophobes.

In musical notation this looks like this:

Hydrophobic Hydrophilic neutral Hydrophilic acidic Hydrophilic alkaline

W F I L V P A G M Q N C T S E D R H K

W F I L V P A G Y

2.2. Finding Motives and Melodies

This figure shows amino acid sequences from different species. Sequences that most or all species have in common are marked in yellow and numbered:

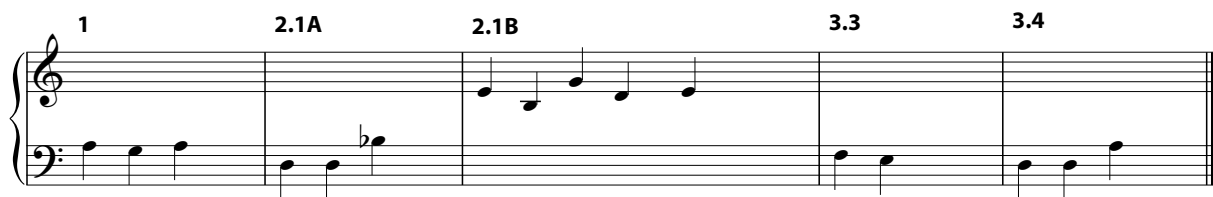
Organismus	Domäne1	Domäne2	Domäne3
Bakterium	Cryptococcus Sir2	EDRGLLRNVTQNIIDLESLAGVERVILQCHGSPKTASCLRC	KFDITTFQALDSEFDCLFKDREEDLLVIGTSLVAVPSEVLTHIPHSVQIFINLTPVYHVQPVNSILGQADS
Bakterium	PseuDomonas Sir2	AKGSYSVSIQTQNDLHERAGSVQVLIHLRGLSSTFKCFAC	RGLVWYGEDLPSDVWKSALALWKSVDLISVGTSGIIVPAADIPIRIALSYGATVIRVNTEDVSTSAQNELMLIGKATEV
Einzellier, Pilz	Hefe Sir2	QMGKLLRNVTQNIIDLESVAGIISTDKLVQCHGSPATATCVTC	KFDITTFQALDSEFDCLFKDREEDLLVIGTSLVAVPSEVLTHIPHSVQIFINLTPVYHVQPVNSILGQADS
Fadenwurm	C.elegans Sir2	ETSGKLLRNVTQNIIDLEBQVGIKRVVECHGSPKCTCTRC	KPMIVFFGEDLGRFQVTEDEKHKVDLIVIGSSLVKVPVALIPHCVDKXVPPQILINREPLHYMADIELLGCDDI
Insekt	Drosophila Sir2	TFDDVISLVKESKIIIVLTGAVSVSGCIPDFRSTNGIYA	KFDIVFFGENLPEQFRAMKYDKDEVDLLVIGSSLVKVPVALIPSSIPATVPQILINREPLHLKPFVLLGSDVI
Wirbeltier, Vogel	Ruhn Sir1a	DKEGKLLRNVTQNIIDLEQVAGIQRIIQCHGSPATASCLIC	KPDIVFFGENLPEQFRAMKYDKDEVDLLVIGSSLVKVPVALIPSSIPHEVPQILINREPLHLKPFVLLGSDVI
Wirbeltier, Nagetier	Maus Sir1a	TIEDAVKLLQECKKIIVLTGAVSVSGCIPDFRSDGIYA	KPEIVFFGENLPEQFRAMKYDKDEVDLLVIGSSLVKVPVALIPSSIPHEVPQILINREPLHLKPFVLLGSDVI
Wirbeltier, humanoID	Mensch Sir1a	TIEDAVKLLQECKKIIVLTGAVSVSGCIPDFRSDGIYA	KPEIVFFGENLPEQFRAMKYDKDEVDLLVIGSSLVKVPVALIPSSIPHEVPQILINREPLHLKPFVLLGSDVI

markiert eingeschobene Aminosäuren, die in den anderen Organismen fehlen

The sequences marked in yellow in the figure above can now be translated into notes (mind that note names are given in German terminology, again):

Domain	Sequence #	Amino Acid	German Note
1	1	G	a
1	2	A	g
1	3	G	a
2	1	L	d
2	2	L	d
2	3	R	b
2	4	N	e1
2	5	Y	h
2	6	T	g1
2	7	Q	d1
2	8	N	e1
2	9	I	c
2	10	D	cls1
3	1	F	H
3	2	F	H
3	3	G	a
3	4	L	d
3	5	K	as1
3	6	V	e
3	7	P	f
3	8	V	e
3	9	L	d
3	10	L	d
3	11	G	a
2	1	C	ff
2	2	H	es1
2	3	G	a
2	4	S	a1
2	5	F	H

In musical notation this looks like this:



These are the motives that become the harmonic and melodic basis for the "evolution sonata".

2.3. Composition

2.3.1. First Movement – “Primordial Sea”

The first movement – “Primordial Sea” – evokes the vision of the primordeal ocean, which already contains the first building blocks of life, although they have not yet formed bigger constructs. The harmonic frame results from the motives **3.4** and **2.1A**, which also form the chord progression **D minor / B-flat major** (in 2nd inversion). The polyrhythmic layering of voices indicates waves, a flowing, changing diversity of elements. After this “primitive state” is established sufficiently, the first amino acid motives begin to emerge: first the motives **1**, and **3.4**, then **3.3**. The amino acid sequences (i.e. motives) become more and more prominent, until they are finally present in every beat of every measure. The first movement ends with a rhythmic transformation of the motives **1** and **2.1A** into a melody, which will be the basic theme for the 2nd movement. For illustration, here is the end the first movement – with all musical motives (at original pitch or transposed) representing AA-sequences marked by red note heads:

The image displays a musical score for the end of the first movement, "Primordial Sea". The score is presented in two pages, 10 and 11. Page 10 contains measures 53 to 57, and page 11 contains measures 59 to 63. The score is written for piano and features a complex polyrhythmic texture with multiple staves. Red note heads are used to highlight specific musical motives throughout the piece. The dynamics are marked as mp (mezzo-piano) and f (forte).

2.3.2. Second Movement – “Multiply!”

The melody that formed at the end of the 1st movement is used as the theme for a fugato in the beginning of the 2nd movement. After the elegant, dance-like first development the four-part fugue enters a stretto and afterwards the movement takes a faster pace into the vision of AA-sequences multiplying all the time, unstopably, almost mechanically producing the material for life.

2.3.3. Third Movement – “Life”

In the 3rd movement, evolution reaches its climax. AA-sequences following those that are present in all life but change over the course of evolution, namely the AA-sequences following sequence 1 (see below) are transcribed to music.

		1	2.1	2.2	3.1	3.2	3.3	3.4
Organismus	Domäne1		Domäne2		Domäne3			
Bakterium	Cryptococcus Sir2	SLDDAVSLLAASKKIIIVLSGAGI STSCGII DFRSSTGLYA	EDRGVLLRNYTQNIIDLESLAGVERVLIQ CHGSP KTASCLRC	KPDITFFGQALDSEFDECLFKDREEDVLLVIGTSLK VPV SEVLTHIPHSVPQIIFINLTPVYHVQPVSL EGD ADSI				
Bakterium	Pseudomonas Sir2	EFNNAKALLDAPFIVVPTGAGI SAESGII ITYGDFLTGIWA	AKSGYVSVVITQNIIDLERAGVVDVLIHL AGSL STPKCFAC	RPLVWYGEDLPSDVWWSAIALVKS CDVLI SVGTSGIVTPPADIPRIALSYGATVIHVWTEVST GAQ NELMLIGATEV				
Einzeller, Pilz	Hefe Sir2	FTIDRFIQKLTARKILVLTGAGVSV SLGI DFRSESGFYS	OMGKLLRNYTQNIIDLESVAGI STK L VQCHG SFATATCVTC	KPDITFFGQALDSEFDECLFKDREEDVLLVIGTSLK VPV SEVLTHIPHSVPQIIFINLTPVYHVQPVSL EGD ADSI				
Fadenwurm	C.elegans Sir2	SLADAVELFKTKHILVLTGAGVSV SLGI DFRSESGFYS	ETSGRLRNYTQNIIDLERAGVVDVLIHL AGSL STPKCFAC	KPDITFFGQALDSEFDECLFKDREEDVLLVIGTSLK VPV SEVLTHIPHSVPQIIFINLTPVYHVQPVSL EGD ADSI				
Insekt	Drosophila Sir2	TFDDVLSLVKESQKIIIVLTGAGVSV SLGI DFRSTNGIYA	ETGKLLRNYTQNIIDLERAGVVDVLIHL AGSL STPKCFAC	KPDITFFGQALDSEFDECLFKDREEDVLLVIGTSLK VPV SEVLTHIPHSVPQIIFINLTPVYHVQPVSL EGD ADSI				
Wirbeltier, Vogel	Huhn Sir1a	TIDDAVKLLQCKKIMVLTGAGVSV SLGI DFRSESGFYS	DKEGKLLRNYTQNIIDLEQVAGI QRI IQ CHG SFATASCLIC	KPEIVFFGENLPEQFRAMKYDKNEVDLLIVIGSSLK VPV SEVLTHIPHSVPQIIFINLTPVYHVQPVSL EGD ADSI				
Wirbeltier, Nagetier	Maus Sir1a	TIEDAVKLLQCKKIMVLTGAGVSV SLGI DFRSESGFYS	DKEGKLLRNYTQNIIDLEQVAGI QRI IQ CHG SFATASCLIC	KPEIVFFGENLPEQFRAMKYDKNEVDLLIVIGSSLK VPV SEVLTHIPHSVPQIIFINLTPVYHVQPVSL EGD ADSI				
Wirbeltier, humanoid	Mensch Sir1a	TIEDAVKLLQCKKIMVLTGAGVSV SLGI DFRSESGFYS	DKEGKLLRNYTQNIIDLEQVAGI QRI IQ CHG SFATASCLIC	KPEIVFFGENLPEQFRAMKYDKNEVDLLIVIGSSLK VPV SEVLTHIPHSVPQIIFINLTPVYHVQPVSL EGD ADSI				

markiert eingeschobene Aminosäuren, die in Den anderen Organismen fehlen

The sequence after sequence 1, marked in orange, translates into the chord progression **F major / A minor**, both in second inversion. This harmonic relation becomes the basis for the chord progression of the 3rd movement, while the melodic material is derived from the motives known from the previous movements. As evolution takes its way, tempo and complexity increase in several steps towards the final climax.