Search Sequence Determination for Tree Search based Detection Algorithms

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***Abstract*—Tree search based detection algorithms provide a promising approach to solve the detection problems in MIMO systems. Depth-first, Breadth-first or Metric-first search strategies provide near max-log detection at reduced but still significant complexity. In this paper we show how the incurred complexity can be reduced substantially. In order to reduce the number of metric calculations to a minimum, we propose a novel relative determination of search sequences for QAM constellations, usable inexpensively independent of the underlying constellation size and search strategy and moreover also usable for soft-in soft-out detection. Based on its application to a sphere detector, we will demonstrate the impact on complexity and performance of the detection as well as on the detector structure. Building on the results, we propose refinements of the resulting detector providing a very good performance at minimized complexity, making the resulting detector particularly favorable for implementation.**

I. Introduction

Future mobile communication systems will make use of multiple-input multiple-output (MIMO) techniques in combination with high constellation orders to enhance spectral efficiency. While performant detection of the spacial multiplexed data streams is essential for good performance, its complexity is still a limiting factor. Many recent research try to solve this problem by introducing complexity reduced detection algorithms on the basis of tree search techniques. Application of depth-first, breadth-first or metric-first search strategies [1] lead to a large variety of detection algorithms like the sphere detector [2], m-algorithm [3], LISS-algorithm [4] or modifications of them [5]–[8].

By mapping the detection onto a tree search, the complexity is mainly given by the metric computation to be carried out and hence by the number of extended parent nodes and the amount of examined child nodes [9]. While techniques like sorted QR decomposition (SQRD) [10], MMSE preprocessing with bias reduction [11] or Schnorr-Euchner (SE) enumeration [12] in combination with adapted search strategies [13]–[15] suitably reduce the amount of node extensions, the overall number of examined nodes is still impracticable high. An efficient detection, with reduced quantity of extended nodes, requires a selection of the most advantageous search path(s) to be examined in the next steps by means of the Schnorr-Euchner (SE) enumeration [16]. Consequently, all search strategies need to select favorable child nodes out of a set of possible child nodes within a complex-valued configuration. Commonly, this requires evaluation of all child nodes and the selection of favorable node(s), causing several sequential and/or parallel computations.

Consequently several techniques have been developed to ease the amount of computations and sortations, like 1.) Partial sorting of calculated child nodes [17], 2.) Fixed determination of the nodes to be studied [13], [18], 3.) Multi-level mapping [19], 4.) Mapping the detection onto a real-valued system and direkt application of the SE enumeration [20], 5.) PSK-enumeration [9] or 6.) SE Row and Column enumeration [21]. While all these techniques reduce the overall complexity, all approaches incur also major drawbacks like a suboptimal node selection (1,2,3,4), leading to an overall increment of nodes to be extended and/or to performance degradations, a complexity increasing non linear with the constellation size (1,4,6), limited field of application (2,3) or multiple sequential and/or parallel operations (1,3,4,5,6). Additionally, non of them has been shown to be suitable for a detection with a priori information. The node selection and the required calculations are hence still unsolved problems.

In this paper we propose a novel relative determination of favorable nodes based on mapping the detection problem onto a geometrical approach: For a known relative position of the received symbol's representative to an initial reference point, within a given grid, an unique sequence of favorable nodes can be identified. More specifically, this enables a heuristic determination of favorable child nodes without their calculation, by only requiring a few inexpensive comparisons for a given parent node, independent of the constellation size. Based on this, we will demonstrate exemplarily for a selected sphere detector how the number of required metric calculations is reduced to a minimum of one calculation per examined node, redundantizing any sortations for the node selection. Furthermore we will illustrate the effects on performance and complexity of the resulting detector and show its suitability for soft-in soft-out detection. Upon the results, we propose a refined parallelized structure for the sphere detector as well as complexity reduction techniques like optimized leaf processing and study the effects of iterative detection↔decoding. Altogether, we will demonstrate the proposed search sequence determination to substantially reduce the amount of computations and hardware resources needed for the detection without significantly affecting the detection performance.

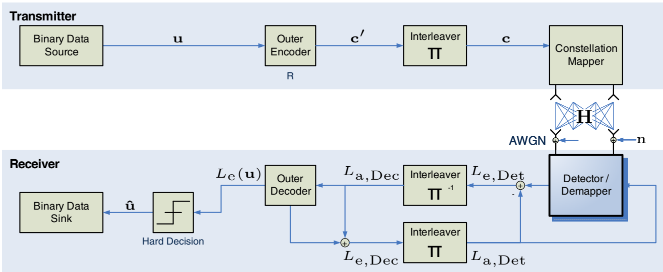


Fig. 1. System model with BICM transmitter and iterative receiver.

II. System model

Throughout this paper, we consider a $N_{\mathrm{T}} \times N_{\mathrm{R}}$ MIMO system based on a BICM transmission strategy with N_{T} transmit and N_{R} receive antennas, as depicted in Fig. 1. A vector $\mathbf{u}$ of i.i.d. information bits is encoded by the outer channel code with rate R. The resulting stream of vectors $\mathbf{c}'$ is bit-interleaved and portioned into blocks $\mathbf{c}$ of $N_{\mathrm{T}} \cdot L$ bits, where L denotes the number of bits per transmit symbol. For the transmission, the corresponding bits $\mathbf{c} \in \mathcal{C}$, covered in the set of permitted bit vectors, are mapped (e.g. gray mapping) onto complex constellation symbols $\mathbf{x}(\mathbf{c}) = [x_0, ...x_{N_{\mathrm{T}}-1}]^T = map(\mathbf{c}) \in \mathcal{X}$, the set of valid transmit symbols with cardinality $\#\mathcal{X} = \#\mathcal{C} = 2^L = Q$. We normalize the transmit energy such that $\mathcal{E}\{\mathbf{x}\mathbf{x}^{\mathrm{H}}\} = E_{\mathrm{S}}/N_{\mathrm{T}}\mathbf{I}$. On behalf of the transmission, we consider a flat fading channel and an additive noise vector $\mathbf{n} \in \mathbb{C}^{\mathbf{N}_{\mathrm{R}}\times\mathbf{1}}$ at the receiver with complex components of zero mean i.i.d. gaussian random variables of variance $N_0/2$ per real dimension ($\mathcal{E}\{\mathbf{n}\mathbf{n}^{\mathrm{H}}\} = N_0\mathbf{I}$). The considered passive channel is represented by $\mathbf{H} \in \mathbb{C}^{N_{\mathrm{T}}\times N_{\mathrm{R}}}$ with entries of a zero mean i.i.d. gaussian random process of variance 1 and is assumed to be perfectly known at the receiver. The received signal $\mathbf{y}$ is therefore given by:

$$\mathbf{y} = \mathbf{H}\mathbf{x} + \mathbf{n}$$

and the signal-to-noise-ratio ($SNR = E_s/N_0$) at the receiver applied to the energy of one information bit can be stated as: $E_{\mathrm{b}}/N_0 = E_s N_{\mathrm{R}}/N_0 N_{\mathrm{T}} L R$.
In order to ensure comparability of the results, we use for our simulations a setup equivalent to the one used in e.g. [5], [11]. The simulations are carried out for a rate $1/2$ PCCC with $(7_R, 5)$ convolutional codes, an information block size of 9216 bits (including tail bits), gray mapping, a 4×4 MIMO channel and spatial and temporal fading. The detection of the transmitted bits is carried out by complex-valued sample sphere detectors in conjunction with a BCJR based decoder with 8 internal iterations. Futhermore, a priori information is included monotonously, as described in [6].

III. Tree search based MIMO detection

A. Fundamentals

Task of the focused detector is the determination of bits c most likely sent and the calculation of reliability information for these bits. On behalf of the described system, this can be accomplished by calculating the corresponding log-likelihood ratios (L-values):

$$L\left(c_{m,l}|\mathbf{y}\right) = \ln\left(\frac{P\left(c_{m,l}=+1|\mathbf{y}\right)}{P\left(c_{m,l}=-1|\mathbf{y}\right)}\right) \approx -\frac{1}{N_0}\min_{\mathbf{c}|c_{m,l}=+1}\{\lambda_0\} + \frac{1}{N_0}\min_{\mathbf{c}|c_{m,l}=-1}\{\lambda_0\}, \quad (1)$$

where (1) results from application of the max-log approximation. $c_{m,l}$ represents the l-th bit of a symbol sent by the m-th antenna and

$$\lambda_0\left(\mathbf{y},\mathbf{c},\mathbf{L_a}\right) = \|\mathbf{y} - \mathbf{H}\hat{\mathbf{x}}(\mathbf{c})\|^2 - \frac{N_0}{2}\sum_{i=0}^{N_T-1}\sum_{j=1}^{L} c_{i,j} L_a(c_{i,j}) \quad (2)$$

represents the distance metric for a set of received symbols $\mathbf{y}$, a given $\mathbf{c}$ and the a priori knowledge $\mathbf{L_a}$. $\hat{\mathbf{x}}$ corresponds to a possible transmission symbol. As consequence, beside the most properly sent symbol $\arg\min_{\hat{\mathbf{x}}(\mathbf{c})|\mathbf{c}\in\mathcal{C}}\{\lambda_0\}$ - the detection hypothesis - and its corresponding metric $\lambda_0(\mathbf{c}^{\mathrm{ML}})$, the detector has to determine also the counter-hypotheses $\arg\min_{\hat{\mathbf{x}}(\mathbf{c})|\mathbf{c}\in\mathcal{C},c_{m,l}\neq c_{m,l}^{\mathrm{ML}}}\{\lambda_0\}$ with their metrics for each bit.

B. Tree-Search basics

Since brute force (maxlogAPP) detection of (1) is known to be of exponential growing complexity with the number of transmit antennas, several close to optimal detection strategies have been lately proposed to find relevant $\arg\min\{\lambda_0\}$. Some of the most promising are based on tree search techniques. As depicted in detail in [5], transforming the detection problem is permitted by QR-decomposition (QRD) of $\mathbf{H} = \mathbf{Q}\mathbf{R}$, where $\mathbf{Q}$ is unitary and $\mathbf{R}$ an upper triangular matrix. With the modified receive symbols $\mathbf{y}' = \mathbf{Q}^{\mathrm{H}}\mathbf{y}$ and the potential sent symbols, the euclidian distance in the detection

$$\|\mathbf{y}' - \mathbf{R}\hat{\mathbf{x}}(\mathbf{c})\|^2 \quad (3)$$

can be interpreted as tree search. The search tree and the relevant notations are drafted in Fig. 2 for a 2 QAM, $N_T = 4$ transmit antennas and the node selection of a sample sphere detection algorithm, indicated by the numeration and further depicted in [15]. The root node of the tree is defined as layer $i = N_T$. In each of the layers i, $i = (N_T - 1)...0$, 2^L possible transmission symbols $\hat{x}_i$ are existing for one parent node, represented by the nodes of the tree and connected to the parent via branches. Layer $i = (N_T) - 1$, corresponding to the lowest row of (3) and a path from $i = (N_T) - 1$ to $i = 0$ represents a complete set of sent symbols $\hat{\mathbf{x}}$, mapped

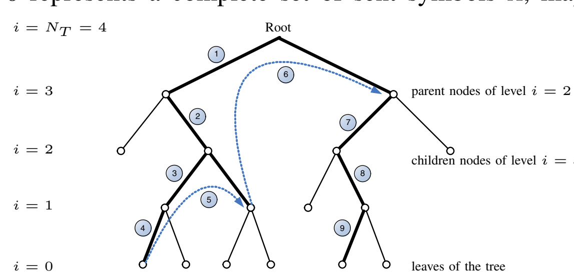


Fig. 2. Example sphere based tree search

to the leaves of the tree. Resulting from this, λ_0 (2) can be recursively calculated by the layered branch metric

$$\lambda_i = \underbrace{\lambda_{i+1}}_{\substack{\text{metric from}\\ \text{already estimated}\\ \text{symbols}}} + \Big|\underbrace{y_i''}_{\substack{\text{interference reduced}\\ \text{symbol}}} - r_{ii}\hat{x}_i\Big|^2 - \underbrace{\frac{N_0}{2}\sum_{j=1}^{L} c_{i,j} L_a(c_{i,j})}_{\text{a priori information}}, \qquad (4)$$

$$y_i'' = y_i' - \sum_{j=i+1}^{N_T-1} r_{ij}\hat{x}_j,$$

out of the squared distance between the nodes and an interference reduced symbol, a priori information and the corresponding parent node metric, whereas the root metric is defined to $\lambda_{N_\mathrm{T}} = 0$. Independent of the actual search strategy, the search is started in layer $i = N_T$ and carried out with extensions of selected nodes by analyzing at least one children node.

IV. Search sequence determination

Aim of a detection algorithm is the selection and analysis of favorable nodes in order to find leaves for (1) early. Therefor a selection of child nodes by the means of the SE enumeration is essential, as described in section I. In order to avoid costly node analysis or suboptimal selection approaches, we describe in the following subsections a new view of the node selection leading to a novel technique to determine the sequence of favorable child nodes.

A. Sequence determination based on relative positions

Without a priori information the reliability of children nodes in (4) is only given by the squared euclidian distance between the interference reduced symbol y_i'' and the nodes represented by the constellation points $r_{ii}\hat{x}_i$. By normalizing[1] this relation with $\frac{1}{r_{ii}}$, the reliability is only dependant on the squared distances between a representative of the received symbol y_i''' to a fixed grid of possible sent symbols $\hat{x}_i$ with given lattice spacing a:

$$|y_i''' - \hat{x}_i|^2, \text{ with } y''' = \frac{y''}{r_{ii}},$$

as illustrated in Fig. 3 for a given y_i''' and the sequence of the tree most favorable nodes indicated by the numbering.

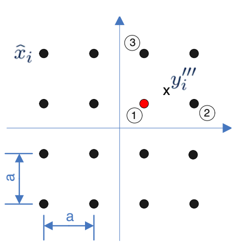
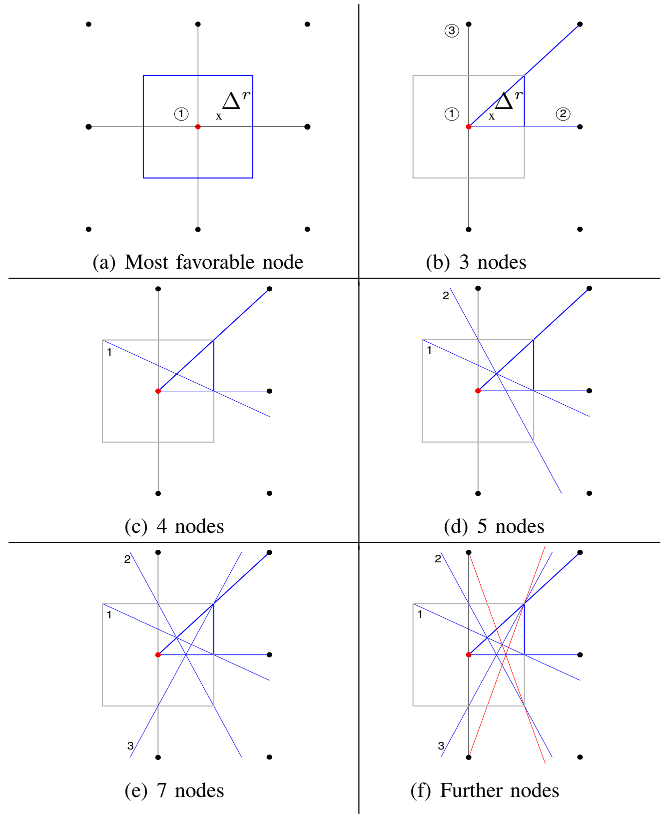


Fig. 3. Sample grid and most favorable nodes for a 16 QAM

With growing distance $|y_i''' - \hat{x}_i|$ the resulting metric $\lambda_i(\hat{x}_i)$ enhances and nodes become increasingly unfavorable. Based on this consideration the sequence of favorable nodes can be determined for a given position of y_i'''.

Since a consideration of all possible y_i'' leads to impracticable high complexity, we propose a heuristical approximation of this sequence determination. Independent of the absolute position within the grid, the most favorable node is the node closest to y_i''', easy to determine by rounding y_i''' to the grid points as displayed in Fig. 4(a) with a square bounded by blue solid lines. In order to further determine the sequence, we propose a geometrical examination relative to the closest node. For this purpose, we define a reference node x^r to: $x^r := \lfloor y_i''' \rceil_x$, with $\lfloor\cdot\rceil_x$ denoting a rounding operation to the closest valid node marked in red within the figures. On the basis of the relative position $\Delta^r = y_i''' - x^r$ it is now possible to determine a sequence of favorable nodes relative to x^r.



(a) Most favorable node (b) 3 nodes (c) 4 nodes (d) 5 nodes (e) 7 nodes (f) Further nodes

Fig. 4. Determination of the most reliable nodes for different accuracies

Presuming a Δ^r in quadrant 1 relative to x^r, the nodes marked with ② and ③ in Fig. 4(b) are potential 2nd favorable nodes. Consequently, for all Δ^r above the angle bisector of quadrant 1 – the perpendicular line spanned by these nodes – node ③ is the second favorable one and ② the 3rd favorable one. For all Δ^r lying inside the spanned triangle[2], ② is the second favorable node followed by node ③. The described determination is hence possible with a comparison of real- and imaginary-parts of Δ^r: $\mathfrak{Re}(\Delta^r) \geq \mathfrak{Im}(\Delta^r)$?. By taking advantage of the constellation's symmetry, it is possible to map all sectors of the square (Fig. 4(a)) to this triangle and the resulting sequence. This can be easily achieved by changing signs of real- and/or imaginary-part and/or swapping real- and imaginary-part of Δ^r and the resulting relative sequence.

For a possibly mapped Δ^r within the triangle, two possible subsequent 4th nodes are existing (lower left and upper right node in Fig. 4(c)). Similarly to the determination of the 2nd and 3rd node, a bisector line spanned by the nodes can be

[1] r_{ii} only contains positive real-values for a convenient chosen QRD.

[2] Spanned by the angle bisector, the real-axis and the vertical line resulting from the rounding operation.

used for the determination of the following node, indicated by line 1 in Fig. 4(c). Due to the symmetrical grid structure, this line corresponds to a comparison $\frac{a}{2} - \mathfrak{Re}(\Delta^r) \geq 2\mathfrak{Im}(\Delta^r)$?. Since the resulting areas and sequences are asymmetrical, a further merging of the involved sequences is frustrated.

While the 5th element (el.) for the upper right triangle is fixed by default, another case differentiation is needed for the lower triangle, resulting in a comparison with line 2 (Fig. 4(d)): $\frac{a}{2} - \mathfrak{Im}(\Delta^r) \geq 2\mathfrak{Re}(\Delta^r)$?.

Similarly the determination of the 6th and 7th favorable nodes can be carried out with line 3 (Fig. 4(e)): $2\mathfrak{Re}(\Delta^r) \geq \frac{a}{2} + \mathfrak{Im}(\Delta^r)$?.

All these case differentiations involve only inexpensive operations like shift-operations or additions with 1, convenient for hardware implementation.

Continuative determination of the sequences is possible by introduction of further case differentiations. Unlike the comparisons describe above, further comparisons would result in more complex operations, making their application unattractive. An example is given by the determination of the 8th node of the sequence, illustrated in Fig. 4(f). Due to a rising number of possible nodes, the number of comparisons and sequences increases as well as the complexity of operations required for case differentiations, caused by disadvantageous multiplications with 3.

Due to the described case differentiations, the sequence determination is mapped to an analysis of the relative position Δ^r, independent of the actual constellation size. Based on the examinations above, a determination of favorable nodes with diverse accuracy is possible depending on the accuracy of the position evaluation. For each defined region, used for the position evaluation, one sequence of favorable nodes can be determined, whose length corresponds to the given accuracy. Table I gives an overview of the possible precisions of the search sequence determination (SSD).

In order to further determinate the node enumeration without additional case differentiations, we propose an approximation using predefined sequences on the basis of reference points $\Delta^{r\prime}$. Under the postulation of sufficient sequence accuracy, the deviation in the distances resulting from Δ^r and $\Delta^{r\prime}$ is negligible small, resulting in an insignificant enumeration error. Throughout this paper, we use the triangle's centers as sample reference point for the proposed continuative enumeration.

B. Complexity reduction techniques

Since using multiple large sequences causes overhead to the detection hardware, limiting the amount and size is reasonable. Starting from the position of x^r, in each direction a maximum

TABLE I

OVERVIEW OF DIFFERENT SSD PRECISIONS

precision/length of a sequence	Nr. of sequences	cumulative case differentiations needed for the SSD, for $a = 2$
1. element	1	round Δ^r
3 elements	1	$\mathfrak{Re}(\Delta^r) \geq \mathfrak{Im}(\Delta^r)$?
4 elements	2	$1 - \mathfrak{Re}(\Delta^r) \geq 2\mathfrak{Im}(\Delta^r)$?
5 elements	3	$1 - \mathfrak{Im}(\Delta^r) \geq 2\mathfrak{Re}(\Delta^r)$?
7 elements	5	$2\mathfrak{Re}(\Delta^r) \geq 1 + \mathfrak{Im}(\Delta^r)$?
8 elements	9	$\mathfrak{Im}(\Delta^r) \geq 2 - 3\mathfrak{Re}(\Delta^r)$? $\mathfrak{Im}(\Delta^r) \geq 3\mathfrak{Re}(\Delta^r) - 2$?

of $\sqrt{Q} - 1$ grid points are existing. Hence, a sequence consists in theory out of $(2\sqrt{Q} - 1)^2$ elements. In practice, tree searches only examine nodes close to x^r, requiring few elements of the sequence. Additionally, the region in which nodes are selected is often limited by a clipping factor, as proposed e.g. in [5]. Consequently, this enables on behalf of tree searches without a priori a clear limitation of the sequence size, resulting also in an upper bounded complexity per parent node. While the actual list size depends on the underlying system, for the chosen simulation model and Q=64 a reduction below 14 elements per sequence is possible, causing not any performance degradations.

In addition to the clipping of the sequences, it is also possible to unite sections of the sequences. Within all sequences, nodes 1-3 are identically and might be merged. By noting in addition that the first seven elements of all sequences involve only permutations among the first seven symbols, it is possible to merge the lists subsequently. Consequently the determination of the search enumeration only requires one fixed sequence of intended length and a number of predefined sequences for the nodes 4-7 (CS), according to the envisages accuracy (table I).

A possibility to reduce the amount of examined nodes is provided by the introduction of adapted leaf sequences (LS). On behalf of tree searches without a priori information, only view leaf nodes are relevant for (1). Besides the leaf node represented by x^r, only nodes lying in straight real or imaginary direction of x^r have to be taken into account, as illustrated in Fig. 5. While this requires one small but additional sequence, it reduces the amount of examined leaf nodes significantly.

C. Application to a sample sphere decoding algorithm

In order to demonstrate the impact of the search sequence determination on a detector's structure and the resulting complexity and performance, we selected exemplarily a tuple search detector presented in [6], [15] as basis for our studies. To ensure an efficient detection, complexity reduction techniques like SQRD, MMSE with bias reduction, adapted candidate determination as well as SE enumeration are included. Internal clipping is not applied to ensure comparability between the implementations, but can further reduce the complexity especially on behalf of the sequential detection algorithm, carried out in the next subsection. The flowchart of the initial detector is shown in Fig. 6, illustrating its main remaining drawbacks. As already carried out in section I, the essential SE enumeration requires calculation of all Q possible child nodes

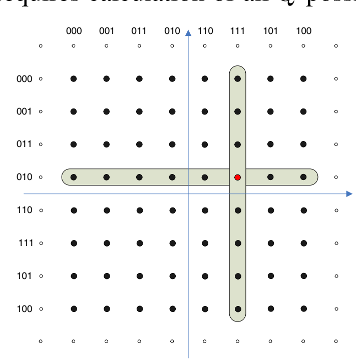


Fig. 5. Leaf nodes relevant for counter-hypothesis determination (64 QAM)

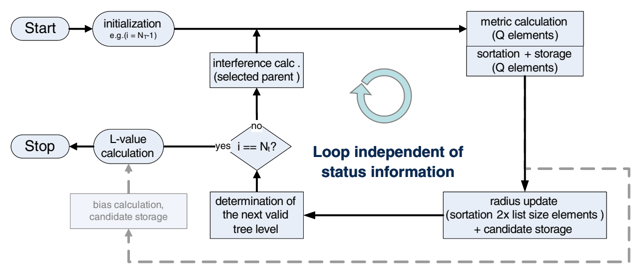


Fig. 6. Flowchart of a TS algorithm

and the selection of the most favorable one. To avoid repeated metric calculations, these nodes are sorted and stored for the selection of subsequent favorable nodes, requiring a complex sorting operation of Q nodes per parent and the storage of $N_t \times Q$ elements. Obviously, this leads to disadvantageous high hardware complexity and detection delay.

1) Sequential SSD realization: By application of the SSD, the sequence of child nodes to be examined is predefined for given parent nodes and nodes only required for the detection process have to be calculated. Consequently, only one metric calculation per loop is required. Therefrom, this dispenses the sorting, reduces complexity of subsequent radius updates and leads to significantly reduced hardware complexity. However, the proposed algorithm has to calculate also sibling nodes separately, unlike the original one. Hence, a direct selection of next extendable nodes is not always possible, requiring additional loops and limiting the level determination to the neighboring levels. The resulting sequential SSD-TS flowchart is illustrated in Fig. 7. Assuming a pipelined structure with one

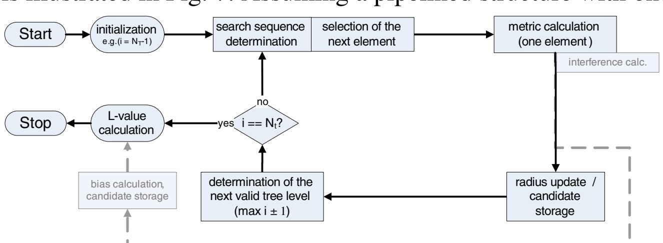
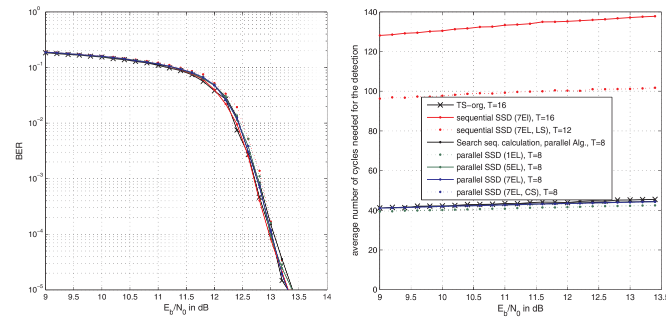


Fig. 7. Flowchart of a TS with SSD

examined node per cycle, comparable to the one proposed in [9], the throughput of a resulting implementation is mainly limited by the number of cycles needed for the detection of one symbol. Throughout this paper, hence the number of cycles is chosen as complexity measurement for the simulations. Fig. 8 shows the impact of SSD on performance and complexity of a TS. While SSD has almost independent of the SSD accuracy no effect on the performance, the overall cycle count is at first glance clearly enhanced, caused by sequential leaf and parent node processing. As displayed, easing this affect is enabled by the application of adapted leaf processing (LS), leading also to smaller radius lists. Nevertheless, the overall number of metric calculations is substantially reduced from $45cycles * 64\frac{calc.}{cycle} = 2880calc.$ required by the original detector to an average of 101 sequential calculations. $\Rightarrow$ a reduction to 3.5% of the initial required metric calculations. Under neglecting supplemental leaf processing which causes about 30% of the SSD-TS loops, a TS detection based on the PSK enumeration, preferred in implementations so far, would require more than 4.5 times the SSD-TS metric calculations

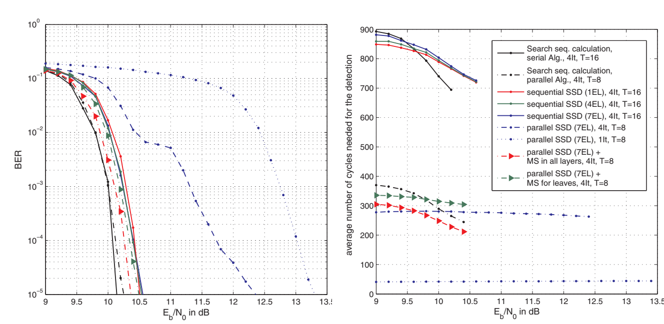


(a) Influence on the BER performance (b) Influence on complexity

Fig. 8. Comparison of the original [15] and the proposed SSD TS algorithms for 4×4 MIMO, 64QAM and without detector↔decoder iterations.

as well as additional min-searches, storage and preprocessing. The inclusion of iterative detection, as proposed in [6], leads to an additional metric increment independent to the euclidian distance due to the applied interleavers. The SSD consequently approximates the actual sequence, involving possible not optimal x^r choices or permutations in the sequence of favorable nodes. An application to breath first searches without changes is hence frustrated. By application to sequential tree searches like depth first or metric first this causes with an increased probability the selection of less favorable nodes first and hence an enhancement of the metrics limiting the search. However, since the detectors are sequential and determine multiple nodes for the soft-output calculation, this only results in a slight performance degradation and complexity enhancement. Consequently, application of the sequential SSD-TS to iterative detection is possible without any algorithmic changes. As illustrated in Fig. 9 the iterative SSD-TS only incurs a performance degradation of below 0.5 dB and an enhancement of 500 cycles. This leads to an overall complexity reduction from 14336 metric calculations to 724 calculations and hence to only 5% of the initially required metric calculations.

2) Parallel SSD realization: Main problems of sequential SSD-TS are the missing opportunity to select sibling parent notes as well as the sequential leaf processing, causing additional loops. Resolving this penalty is enabled by parallel calculation of next favorable siblings and parallel calculation of sibling leaf nodes leading to possible counter-hypotheses (see section IV-B). The adapted flowchart is given in Fig. 10. While adding 1-2 additional metric calculations per loop, these



(a) Influence on the BER performance (b) Influence on complexity

Fig. 9. Comparison of the original [15] and the proposed SSD-TS algorithms for 4×4 MIMO, 64QAM and 1 respectively 4 detector↔decoder iterations.

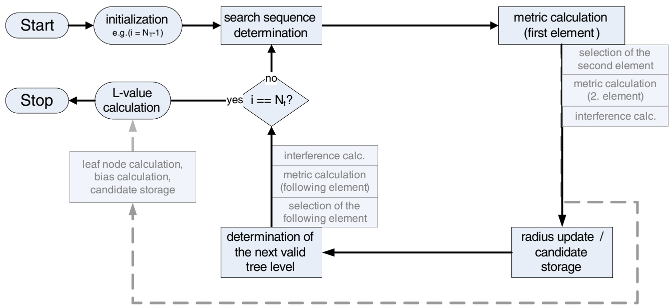


Fig. 10. Flowchart of a parallelized TS with SSD

alignments reduce the cycle count back to the original value, without any performance degradation as displayed in Fig. 8. This leads to significant reduction of the overall loop complexity, comparable to the sequential SSD-TS's complexity but moreover with reduced cycle count.

Unlike the sequential SSD, iterative detection (Fig. 9) involves an error floor, leading to an approximation of the BER curve to the non iterative BER performance. This is especially caused by the parallel leaf processing, which uses the reference point x^r as possible hypothesis and calculates only selective nodes in pure real and imaginary direction. Whenever a priori information causes non optimal x^r selection, wrong hypotheses and counter-hypotheses are calculated. Ensuring a proper chosen $x^{r\prime}$ is suitably provided by Min-Searches (MS) in real and imaginary direction of the initial x^r. The introducing of MS hence eliminates the error floor and moreover reduces the SSD-TS's performance degradation. However, the loop complexity is dramatically increased by $2 * (\sqrt{Q} - 1)$ metric calculations and 2 Min-Searches ($\sqrt{Q}$ el.), making its application unattractive. In order to avoid this drawbacks, we propose the application of MS only to the leaf processing, which also eliminates the error floor. Unlike the previous version, the added complexity is in parallel to the actual tree search and hence doesn't impact the detector significantly, enabling an efficient application of the Min-Searches.

V. Conclusion

In this publication, we presented a novel heuristic technique to determine search sequences for tree search algorithms. Based on mapping the node selection task to geometrical position analyses relative to reference nodes, it is possible to determine search sequences without continuative node analyses. The position analysis is furthermore reduced to simple case differentiation, only requiring inexpensive basic operations. This enables a sequence determination of variable accuracy, applicable independent of the actual constellation size. By utilization of the proposed sequence determination on a sample sphere decoder, we demonstrated the effects to tree searches. Without any performance loss a substantial complexity reduction is enabled, as depicted in detail in section IV-C. Moreover we have shown the proposed concepts to be suitable for soft-in soft-out detection. This enables e.g. with a TS sphere decoder, proposed in previous publications, an efficient near ML/MAP detection with minimized amount of node analyses and hardware requirements, making the proposed method particularly interesting for hardware implementations.

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